IDENTIFICATION OF ESSENTIAL GENES IN PROKARYOTES

Related Applications

This application claims priority from U.S. Provisional Patent Application Serial Number 60/191,078, filed March 21, 2000, U.S. Provisional Patent Application Serial Number 60/206,848, filed May 23, 2000, U.S. Provisional Patent Application Serial Number 60/207,727, filed May 26, 2000, U.S. Provisional Patent Application Serial Number 60/242,578, filed October 23, 2000, U.S. Provisional Patent Application Serial Number 60/253,625, filed November 27, 2000, U.S. Provisional Patent Application Serial Number 60/257,931, filed December 22, 2000, and U.S. Provisional Patent Application Serial Number 60/269,308, filed February 16, 2001 the disclosures of which are incorporated herein by reference in their entireties.

Sequence Listing

The present application is being filed along with duplicate copies of a CD-ROM marked "Copy 1" and "Copy 2" containing a Sequence Listing in electronic format. The duplicate copies of the CD-ROM each contain a file entitled SEQLIST_FINAL_9PM created on March 20, 2001 which is 37,487,912 bytes in size. The information on these duplicate CD-ROMs is incorporated herein by reference in its entirety.

Background of the Invention

Since the discovery of penicillin, the use of antibiotics to treat the ravages of bacterial infections has saved millions of lives. With the advent of these "miracle drugs," for a time it was popularly believed that humanity might, once and for all, be saved from the scourge of bacterial infections. In fact, during the 1980s and early 1990s, many large pharmaceutical companies cut back or eliminated antibiotics research and development. They believed that infectious disease caused by bacteria finally had been conquered and that markets for new drugs were limited. Unfortunately, this belief was overly optimistic.

The tide is beginning to turn in favor of the bacteria as reports of drug resistant bacteria become more frequent. The United States Centers for Disease Control announced that one of the most powerful known antibiotics, vancomycin, was unable to treat an infection of the common *Staphylococcus aureus* (staph). This organism is commonly found in our environment and is responsible for many nosocomial infections. The

import of this announcement becomes clear when one considers that vancomycin was used for years to treat infections caused by *Staphylococcus* species as well as other stubborn strains of bacteria. In short, bacteria are becoming resistant to our most powerful antibiotics. If this trend continues, it is conceivable that we will return to a time when what are presently considered minor bacterial infections are fatal diseases.

Over-prescription and improper prescription habits by some physicians have caused an indiscriminate increase in the availability of antibiotics to the public. The patients are also partly responsible, since they will often improperly use the drug, thereby generating yet another population of bacteria that is resistant, in whole or in part, to traditional antibiotics.

The bacterial pathogens that have haunted humanity remain, in spite of the development of modern scientific practices to deal with the diseases that they cause. Drug resistant bacteria are now an increasing threat to the health of humanity. A new generation of antibiotics is needed to once again deal with the pending health threat that bacteria present.

Discovery of New Antibiotics

As more and more bacterial strains become resistant to the panel of available antibiotics, new antibiotics are required to treat infections. In the past, practitioners of pharmacology would have to rely upon traditional methods of drug discovery to generate novel, safe and efficacious compounds for the treatment of disease. Traditional drug discovery methods involve blindly testing potential drug candidate-molecules, often selected at random, in the hope that one might prove to be an effective treatment for some disease. The process is painstaking and laborious, with no guarantee of success. Today, the average cost to discover and develop a new drug exceeds US $500 million, and the average time from laboratory to patient is 15 years. Improving this process, even incrementally, would represent a huge advance in the generation of novel antimicrobial agents.

Newly emerging practices in drug discovery utilize a number of biochemical techniques to provide for directed approaches to creating new drugs, rather than discovering them at random. For example, gene sequences and proteins encoded thereby that are required for the proliferation of a cell or microorganism make excellent targets since exposure of bacteria to compounds active against these targets would result

in the inactivation of the cell or microorganism. Once a target is identified, biochemical analysis of that target can be used to discover or to design molecules that interact with and alter the functions of the target. Use of physical and computational techniques to analyze structural and biochemical properties of targets in order to derive compounds that interact with such targets is called rational drug design and offers great potential. Thus, emerging drug discovery practices use molecular modeling techniques, combinatorial chemistry approaches, and other means to produce and screen and/or design large numbers of candidate compounds.

Nevertheless, while this approach to drug discovery is clearly the way of the future, problems remain. For example, the initial step of identifying molecular targets for investigation can be an extremely time consuming task. It may also be difficult to design molecules that interact with the target by using computer modeling techniques. Furthermore, in cases where the function of the target is not known or is poorly understood, it may be difficult to design assays to detect molecules that interact with and alter the functions of the target. To improve the rate of novel drug discovery and development, methods of identifying important molecular targets in pathogenic cells or microorganisms and methods for identifying molecules that interact with and alter the functions of such molecular targets are urgently required.

Staphylococcus aureus is a Gram positive microorganism which is the causative agent of many infectious diseases. Local infection by *Staphylococcus aureus* can cause abscesses on skin and cellulitis in subcutaneous tissues and can lead to toxin-related diseases such as toxic shock and scalded skin syndromes. *Staphylococcus aureus* can cause serious systemic infections such as osteomyelitis, endocarditis, pneumonia, and septicemia. *Staphylococcus aureus* is also a common cause of food poisoning, often arising from contact between prepared food and infected food industry workers. Antibiotic resistant strains of *Staphylococcus aureus* have recently been identified, including those that are now resistant to all available antibiotics, thereby severely limiting the options of care available to physicians.

Pseudomonas aeruginosa is an important Gram-negative opportunistic pathogen. It is the most common Gram-negative found in nosocomial infections. *P. aeruginosa* is responsible for 16% of nosocomial pneumonia cases, 12% of hospital-acquired urinary tract infections, 8% of surgical wound infections, and 10% of

bloodstream infections. Immunocompromised patients, such as neutropenic cancer and bone marrow transplant patients, are particular susceptible to opportunistic infections. In this group of patients, *P. aeruginosa* is responsible for pneumonia and septicemia with attributable deaths reaching 30%. *P. aeruginosa* is also one of the most common and lethal pathogens responsible for ventilator-associated pneumonia in intubated patients, with directly attributable death rates reaching 38%. Although *P. aeruginosa* outbreaks in burn patients are rare, it is associated with 60% death rates. In the AIDS population, *P. aeruginosa* is associated with 50% of deaths. Cystic fibrosis patients are characteristically susceptible to chronic infection by *P. aeruginosa*, which is responsible for high rates of illness and death. Current antibiotics work poorly for CF infections (Van Delden & Igelwski. 1998. Emerging Infectious Diseases 4:551-560; references therein).

The gram-negative enteric bacterial genus, *Salmonella*, encompasses at least 2 species. One of these, *S. enterica*, is divided into multiple subspecies and thousands of serotypes or serovars (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467). The *S. enterica* human pathogens include serovars Typhi, Paratyphi, Typhimurium, Cholerasuis, and many others deemed so closely related that they are variants of a widespread species. Worldwide, disease in humans caused by *Salmonella* is a very serious problem. In many developing countries, *S. enterica* ser. Typhi still causes often-fatal typhoid fever. This problem has been reduced or eliminated in wealthy industrial states. However, enteritis induced by Salmonella is widespread and is the second most common disease caused by contaminated food in the United States (Edwards, BH 1999 "Salmonella and Shigella species" Clin. Lab Med. 19(3):469-487). Though usually self-limiting in healthy individuals, others such as children, seniors, and those with compromising illnesses can be at much greater risk of serious illness and death.

Some *S. enterica* serovars (e.g. Typhimurium) cause a localized infection in the gastrointestinal tract. Other serovars (i.e. Typhi and Paratyphi) cause a much more serious systemic infection. In animal models, these roles can be reversed which has allowed the use of the relatively safe *S. enterica* ser. Typhimurium as a surrogate in mice for the typhoid fever agent, *S. enterica* ser. Typhi. In mice, *S. enterica* ser Typhimurium causes a systemic infection similar in outcome to typhoid fever. Years of

study of the *Salmonella* have led to the identification of many determinants of virulence in animals and humans. *Salmonella* is interesting in its ability to localize to and invade the intestinal epithelium, induce morphologic changes in target cells via injection of certain cell-remodeling proteins, and to reside intracellularly in membrane-bound vesicles (Wallis, TS and Galyov, EE 2000 "Molecular basis of *Salmonella*-induced enteritis." Molec. Microb. 36:997-1005; Falkow, S "The evolution of pathogenicity in Escherichia, Shigella, and Salmonella," Chap. 149 in Neidhardt, et al. eds pp 2723-2729; Gulig, PA "Pathogenesis of Systemic Disease," Chap. 152 in Neidhardt, et al. ppp 2774-2787). The immediate infection often results in a severe watery diarrhea but *Salmonella* also can establish and maintain a subclinical carrier state in some individuals. Spread is via food contaminated with sewage.

The gene products implicated in *Salmonella* pathogenesis include type three secretion systems (TTSS), proteins affecting cytoplasmic structure of the target cells, many proteins carrying out functions necessary for survival and proliferation of *Salmonella* in the host, as well as "traditional" factors such as endotoxin and secreted exotoxins. Additionally, there must be factors mediating species-specific illnesses. Despite this most of the genomes of *S. enterica* ser. Typhi (see http://www.sanger.ac.uk/Projects/S_typhi/ for the genome database) and *S. enterica* ser. Typhimurium (see http://genome.wustl.edu/gsc/bacterial/salmonella.shtml for the genome database) are highly conserved and are mutually useful for gene identification in multiple serovars. The Salmonella are a complex group of enteric bacteria causing disease similar to but distinct from other gram-negative enterics such as *E. coli* and have been a focus of biomedical research for the last century.

Enterococcus faecalis, a Gram-positive bacterium, is by far the most common member of the enterococci to cause infections in humans. *Enterococcus faecium* generally accounts for less than 20% of clinical isolates. Enterococci infections are mostly hospital-acquired though they are also associated with some community-acquired infections. Of nosocomial infections enterococci account for 12% of bacteremia, 15% of surgical wound infections, 14% of urinary tract infections, and 5 to15% of endocarditis cases (Huycke, M. M., D. F., Sahm and M. S. Gilmore. 1998. Emerging Infectious Diseases 4:239-249). Additionally enterococci are frequently associated with intraabdominal and pelvic infections. Enterococci infections are often

hard to treat because they are resistant to a vast array of antimicrobial drugs, including aminoglycosides, penicillin, ampicillin and vancomycin. The development of multiple-drug resistant (MDR) enterococci has made this bacteria a major concern for treating nosocomial infections.

These reasons underscore the urgency of developing new antibiotics that are effective against *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa,* and *Enterococcus faecalis*. Accordingly, there is an urgent need for more novel methods to identify and characterize bacterial genomic sequences that encode gene products involved in proliferation, and are thereby potential new targets for antibiotic development. Prior to the present invention, the discovery of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae,* and *Pseudomonas aeruginosa* and *Enterococcus faecalis* genes required for proliferation of the microorganism was a painstaking and slow process. While the detection of new cellular drug targets within a *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* cell is key for novel antibiotic development, the current methods of drug target discovery available prior to this invention have required painstaking processes requiring years of effort.

Summary of the Invention

Some aspects of the present invention are described in the numbered paragraphs below.

1. A purified or isolated nucleic acid sequence comprising a nucleotide sequence consisting essentially of one of SEQ ID NOs: 8-3795, wherein expression of said nucleic acid inhibits proliferation of a cell.

2. The nucleic acid sequence of Paragraph 1, wherein said nucleotide sequence is complementary to at least a portion of a coding sequence of a gene whose expression is required for proliferation of a cell.

3. The nucleic acid of Paragraph 1, wherein said nucleic acid sequence is complementary to at least a portion of a nucleotide sequence of an RNA required for proliferation of a cell.

4. The nucleic acid of Paragraph 3, wherein said RNA is an RNA comprising a sequence of nucleotides encoding more than one gene product.

5. A purified or isolated nucleic acid comprising a fragment of one of SEQ ID NOs.: 8-3795, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 and more than 50 consecutive nucleotides of one of SEQ ID NOs: 8-3795.

6. The fragment of Paragraph 5, wherein said fragment is included in a nucleic acid obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

7. The fragment of Paragraph 5, wherein said fragment is included in a nucleic acid obtained from an organism other than *Escherichia coli.*

8. A vector comprising a promoter operably linked to the nucleic acid of any one of Paragraphs 1-7.

9. The vector of Paragraph 8, wherein said promoter is active in a microorganism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia*

cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

10. A host cell containing the vector of Paragraph 8 or Paragraph 9.

11. A purified or isolated antisense nucleic acid comprising a nucleotide sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region within an operon comprising a proliferation-required gene whose activity or expression is inhibited by an antisense nucleic acid comprising the nucleotide sequence of one of SEQ ID NOs.: 8-3795.

12. The purified or isolated antisense nucleic acid of Paragraph 11, wherein said antisense nucleic acid is complementary to a nucleic acid from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis,*

Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

13. The purified or isolated antisense nucleic acid of Paragraph 11, wherein said nucleotide sequence is complementary to a nucleotide sequence of a nucleic acid from an organism other than *E. coli*.

14. The purified or isolated antisense nucleic acid of Paragraph 11, wherein said proliferation-required gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

15. A purified or isolated nucleic acid comprising a nucleotide sequence having at least 70% identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 8-3795, the nucleotide sequences complementary to SEQ ID NOs.: 8-3795 and the sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 8-3795 as determined using BLASTN version 2.0 with the default parameters.

16. The purified or isolated nucleic acid of Paragraph 15, wherein said nucleic acid is obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis,*

Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

17. The nucleic acid of Paragraph 15, wherein said nucleic acid is obtained from an organism other than *E. coli*.

18. A vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs.: 8-3795.

19. The vector of Paragraph 18, wherein said nucleic acid encoding said polypeptide is obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella*

pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

20. The vector of Paragraph 18, wherein said nucleotide sequence encoding said polypeptide is obtained from an organism other than *E. coli.*

21. A host cell containing the vector of Paragraph 18.

22. The vector of Paragraph 18, wherein said polypeptide comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

23. The vector of Paragraph 18, wherein said promoter is operably linked to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

24. A purified or isolated polypeptide comprising a polypeptide whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs.: 8-3795, or a fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the said polypeptides.

25. The polypeptide of Paragraph 24, wherein said polypeptide comprises an amino acid sequence of any one of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 or a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

26. The polypeptide of Paragraph 24, wherein said polypeptide is obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus*

fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

27. The polypeptide of Paragraph 24, wherein said polypeptide is obtained from an organism other than *E. coli*.

28. A purified or isolated polypeptide comprising a polypeptide having at least 25% amino acid identity to a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, or at least 25% amino acid identity to a fragment comprising at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 as determined using FASTA version 3.0t78 with the default parameters.

29. The polypeptide of Paragraph 28, wherein said polypeptide has at least 25% identity to a polypeptide comprising one of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 or at least 25% identity to a fragment comprising at least 5, at least 10, at

least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising one of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 as determined using FASTA version 3.0t78 with the default parameters.

30. The polypeptide of Paragraph 28, wherein said polypeptide is obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

31. The polypeptide of Paragraph 28, wherein said polypeptide is obtained from an organism other than *E. coli*.

32. An antibody capable of specifically binding the polypeptide of one of Paragraphs 28-31.

33. A method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid comprising a nucleotide sequence encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 8-3795 into a cell.

34. The method of Paragraph 33, further comprising the step of isolating said polypeptide.

35. The method of Paragraph 33, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

36. The method of Paragraph 33, wherein said nucleic acid encoding said polypeptide is obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

37. The method of Paragraph 33, wherein said nucleic acid encoding said polypeptide is obtained from an organism other than *E. coli*.

38. The method of Paragraph 33, wherein said promoter is operably linked to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

39. A method of inhibiting proliferation of a cell in an individual comprising inhibiting the activity or reducing the amount of a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product.

40. The method of Paragraph 39, wherein said method comprises inhibiting said activity or reducing said amount of a gene product in an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

41. The method of Paragraph 39, wherein said method comprises inhibiting said activity or reducing said amount of a gene product in an organism other than *E. coli.*

42. The method of Paragraph 39, wherein said gene product is present in an organism other than *E. coli.*

43. The method of Paragraph 39, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

44. A method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

contacting said gene product with a candidate compound; and

determining whether said compound influences the activity of said gene product.

45. The method of Paragraph 44, wherein said gene product is from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

46. The method of Paragraph 44, wherein said gene product is from an organism other than *E. coli*.

47. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is an enzymatic activity.

48. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a carbon compound catabolism activity.

49. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a biosynthetic activity.

50. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a transporter activity.

51. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a transcriptional activity.

52. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a DNA replication activity.

53. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a cell division activity.

54. The method of Paragraph 44, wherein said gene product is an RNA.

55. The method of Paragraph 44, wherein said gene product is a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

56. A compound identified using the method of Paragraph 44.

57. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

(a) contacting a target gene or RNA encoding said gene product with a candidate compound or nucleic acid; and

(b) measuring an activity of said target.

58. The method of Paragraph 57, wherein said target gene or RNA is from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida*

guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

59. The method of Paragraph 57, wherein said target gene or RNA is from an organism other than *E. coli*.

60. The method of Paragraph 57, wherein said gene product is from an organism other than *E. coli*.

61. The method of Paragraph 57, wherein said target is a messenger RNA molecule and said activity is translation of said messenger RNA.

62. The method of Paragraph 57, wherein said target is a messenger RNA molecule and said activity is transcription of a gene encoding said messenger RNA.

63. The method of Paragraph 57, wherein said target is a gene and said activity is transcription of said gene.

64. The method of Paragraph 57, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

65. The method of Paragraph 57, wherein said target is a messenger RNA molecule encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

66. The method of Paragraph 57, wherein said target comprises a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

67. A compound or nucleic acid identified using the method of Paragraph 57.

68. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a cell, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid comprising a nucleotide sequence complementary to a nucleic acid comprising a nucleotide sequence encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

69. The method of Paragraph 68, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

70. The method of Paragraph 68, wherein said cell is a Gram positive bacterium.

71. The method of Paragraph 68, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

72. The method of Paragraph 68, wherein said bacterium is *Staphylococcus aureus*.

73. The method of Paragraph 72, wherein said *Staphylococcus* species is coagulase negative.

74. The method of Paragraph 72, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

75. The method of Paragraph 68, wherein said cell is an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

76. The method of Paragraph 68, wherein said cell is not an *E. coli* cell.

77. The method of Paragraph 68, wherein said gene product is from an organism other than *E. coli*.

78. The method of Paragraph 68, wherein said antisense nucleic acid is transcribed from an inducible promoter.

79. The method of Paragraph 68, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

80. The method of Paragraph 68, wherein growth inhibition is measured by monitoring optical density of a culture growth solution.

81. The method of Paragraph 68, wherein said gene product is a polypeptide.

82. The method of Paragraph 81, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

83. The method of Paragraph 68, wherein said gene product is an RNA.

84. The method of Paragraph 68, wherein nucleic acid encoding said gene product comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

85. A compound identified using the method of Paragraph 68.

86. A method for inhibiting cellular proliferation comprising introducing an effective amount of a compound with activity against a gene whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a compound with activity against the product of said gene into a population of cells expressing said gene.

87. The method of Paragraph 86, wherein said compound is an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, or a proliferation-inhibiting portion thereof.

88. The method of Paragraph 86, wherein said proliferation inhibiting portion of one of SEQ ID NOs.: 8-3795 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

89. The method of Paragraph 86, wherein said population is a population of Gram positive bacteria.

90. The method of Paragraph 89, wherein said population of Gram positive bacteria is selected from the group consisting of a population of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

91. The method of Paragraph 86, wherein said population is a population of *Staphylococcus aureus*.

92. The method of Paragraph 91, wherein said population is a population of a bacterium selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

93. The method of Paragraph 86, wherein said population is a population of a bacterium selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

94. The method of Paragraph 86, wherein said population is a population of an organism other than *E. coli*.

95. The method of Paragraph 86, wherein said product of said gene is from an organism other than *E. coli*.

96. The method of Paragraph 86, wherein said gene encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

97. The method of Paragraph 86, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

98. A composition comprising an effective concentration of an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier.

99. The composition of Paragraph 98, wherein said proliferation-inhibiting portion of one of SEQ ID NOs.: 8-3795 comprises at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

100. A method for inhibiting the activity or expression of a gene in an operon required for proliferation wherein the activity or expression of at least one gene in said operon is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising contacting a cell in a cell population with an antisense nucleic acid complementary to at least a portion of said operon.

101. The method of Paragraph 100, wherein said antisense nucleic acid comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a proliferation-inhibiting portion thereof.

102. The method of Paragraph 100, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis,*

Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

103. The method of Paragraph 100, wherein said cell is not an *E. coli* cell.

104. The method of Paragraph 100, wherein said gene is from an organism other than *E. coli*.

105. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population.

106. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which encodes said antisense nucleic acid into said cell population.

107. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by expressing said antisense nucleic acid from the chromosome of cells in said cell population.

108. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the transcription of said antisense nucleic acid.

109. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

110. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme comprises said antisense nucleic acid.

111. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense nucleic acid into said cell.

112. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid into said cell.

113. The method of Paragraph 100, wherein said antisense nucleic acid is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

114. The method of Paragraph 100 wherein said antisense nucleic acid is a synthetic oligonucleotide.

115. The method of Paragraph 100, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

116. A method for identifying a gene which is required for proliferation of a cell comprising:

(a) contacting a cell with an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, wherein said cell is a cell other than the organism from which said nucleic acid was obtained;

(b) determining whether said nucleic acid inhibits proliferation of said cell; and

(c) identifying the gene in said cell which encodes the mRNA which is complementary to said antisense nucleic acid or a portion thereof.

117. The method of Paragraph 116, wherein said cell is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

118. The method of Paragraph 116 wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae,*

Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

119. The method of Paragraph 116, wherein said cell is not *E. coli*.

120. The method of Paragraph 116, further comprising operably linking said antisense nucleic acid to a promoter which is functional in said cell, said promoter being included in a vector, and introducing said vector into said cell.

121. A method for identifying a compound having the ability to inhibit proliferation of a cell comprising:

(a) identifying a homolog of a gene or gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 in a test cell, wherein said test cell is not the cell from which said nucleic acid was obtained;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said test cell;

(c) contacting said test cell with a sublethal level of said inhibitory nucleic acid, thus sensitizing said cell;

(d) contacting the sensitized cell of step (c) with a compound; and

(e) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said inhibitory nucleic acid.

122. The method of Paragraph 121, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

123. The method of Paragraph 121, wherein step (a) comprises identifying a nucleic acid homologous to a gene or gene product whose activity or level is inhibited

by a nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

124. The method of Paragraph 121 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid comprising a sequence of nucleotides encoding a homologous polypeptide by identifying nucleic acids which hybridize to said nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795 or the complement of said nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795.

125. The method of Paragraph 121 wherein step (a) comprises expressing a nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795 in said test cell.

126. The method of Paragraph 121, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis,*

Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

127. The method of Paragraph 121, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell other than *E. coli*.

128. The method of Paragraph 121, wherein said inhibitory nucleic acid is an antisense nucleic acid.

129. The method of Paragraph 121, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

130. The method of Paragraph 121, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

131. The method of Paragraph 121, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises directly contacting the surface of said cell with said inhibitory nucleic acid.

132. The method of Paragraph 121, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises transcribing an antisense nucleic acid complementary to at least a portion of the RNA transcribed from said homolog in said cell.

133. The method of Paragraph 121, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

134. The method of Paragraph 121, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

135. A compound identified using the method of Paragraph 121.

136. A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) contacting a test cell with a sublethal level of a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID

NOs. 8-3795 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was obtained, thus sensitizing said test cell;

(b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said nucleic acid.

137. The method of Paragraph 136, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

138. A compound identified using the method of Paragraph 136.

139. The method of Paragraph 136, wherein said test cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

140. The method of Paragraph 136, wherein the test cell is not *E. coli*.

141. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, in said cell to reduce the activity or amount of said gene product;

(b) contacting the sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

142. The method of Paragraph 141, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

143. The method of Paragraph 141, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

144. The method of Paragraph 141, wherein said cell is a Gram positive bacterium.

145. The method of Paragraph 144, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

146. The method of Paragraph 145, wherein said Gram positive bacterium is *Staphylococcus aureus*.

147. The method of Paragraph 146, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

148. The method of Paragraph 141, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida*

tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

149. The method of Paragraph 141, wherein said cell is not an *E. coli* cell.

150. The method of Paragraph 141, wherein said gene product is from an organism other than *E. coli*.

151. The method of Paragraph 141, wherein said antisense nucleic acid is transcribed from an inducible promoter.

152. The method of Paragraph 141, further comprising contacting the cell with an agent which induces transcription of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is transcribed at a sublethal level.

153. The method of Paragraph 141, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

154. The method of Paragraph 141, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

155. The method of Paragraph 141, wherein said nucleic acid encoding said gene product comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

156. A compound identified using the method of Paragraph 141.

157. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795;

(b) contacting said cell with a compound; and

(c) determining whether said compound reduces proliferation of said contacted cell by acting on said gene product.

158. The method of Paragraph 157, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

159. The method of Paragraph 157, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella*

cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

160. The method of Paragraph 157, wherein said cell is not an *E. coli* cell.

161. The method of Paragraph 157, wherein said gene product is from an organism other than *E. coli*.

162. The method of Paragraph 157, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

163. The method of Paragraph 157, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a cell.

164. The method of Paragraph 157, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

165. The method of Paragraph 157, wherein said mutation is a temperature sensitive mutation.

166. The method of Paragraph 157, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

167. A compound identified using the method of Paragraph 157.

168. A method for identifying the biological pathway in which a proliferation-required gene or its gene product lies, wherein said gene or gene product comprises a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

(a) providing a sublethal level of an antisense nucleic acid which inhibits the activity of said proliferation-required gene or gene product in a test cell;

(b) contacting said test cell with a compound known to inhibit growth or proliferation of a cell, wherein the biological pathway on which said compound acts is known; and

(c) determining the degree to which said proliferation of said test cell is inhibited relative to a cell which was not contacted with said compound.

169. The method of Paragraph 168, wherein said determining step comprises determining whether said test cell has a substantially greater sensitivity to said compound than a cell which does not express said sublethal level of said antisense nucleic acid.

170. The method of Paragraph 168, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

171. The method of Paragraph 168, wherein said test cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

172. The method of Paragraph 168, wherein said test cell is not an *E. coli* cell.

173. The method of Paragraph 168, wherein said gene product is from an organism other than *E. coli*.

174. A method for determining the biological pathway on which a test compound acts comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a first cell, wherein the activity or expression of said proliferation-required nucleic acid is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795 and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required nucleic acid lies is known,

(b) contacting said first cell with said test compound; and

(c) determining the degree to which said test compound inhibits proliferation of said first cell relative to a cell which does not contain said antisense nucleic acid.

175. The method of Paragraph 174, wherein said determining step comprises determining whether said first cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

176. The method of Paragraph 174, further comprising:

(d) providing a sublethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said first cell has a substantially greater sensitivity to said test compound than said second cell.

177. The method of Paragraph 174, wherein said first cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

178. The method of Paragraph 174, wherein said first cell is not an *E. coli* cell.

179. The method of Paragraph 174, wherein said proliferation-required nucleic acid is from an organism other than *E. coli*.

180. A purified or isolated nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795.

181. A compound which interacts with a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs.: 8-3795 to inhibit proliferation.

182. The compound of Paragraph 181, wherein said gene product is a polypeptide comprising one of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

183. The compound of Paragraph 181, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

184. A compound which interacts with a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs.: 8-3795 to inhibit proliferation.

185. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795; and

manufacturing the compound so identified.

186. The method of Paragraph 185, wherein said screening step comprises performing any one of the methods of Paragraphs 44, 68, 121, 136, 141, and 157.

187. The method of Paragraph 185, wherein said gene product is a polypeptide comprising one of SEQ ID NOs:3801-3805, 4861-5915, 10013-14110.

188. A method for inhibiting proliferation of a cell in a subject comprising administering an effective amount of a compound that reduces the activity or level of a gene product required for proliferation of said cell, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 to said subject.

189. The method of Paragraph 188 wherein said subject is selected from the group consisting of vertebrates, mammals, avians, and human beings.

190. The method of Paragraph 188, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

191. The method of Paragraph 188, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida*

tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

192. The method of Paragraph 188, wherein said cell is not *E. coli*.

193. The method of Paragraph 188, wherein said gene product is from an organism other than *E. coli*.

194. A purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012.

195. A fragment of the nucleic acid of Paragraph 8, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012.

196. A purified or isolated nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, the nucleotide sequences complementary to SEQ ID NOs.:3796-3800, 3806-4860, 5916-10012, and the nucleotide sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 as determined using BLASTN version 2.0 with the default parameters.

197. The nucleic acid of Paragraph 196, wherein said nucleic acid is from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

198. The nucleic acid of Paragraph 196, wherein said nucleic acid is from an organism other than *E. coli*.

199. A method of inhibiting proliferation of a cell comprising inhibiting the activity or reducing the amount of a gene product in said cell or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in said cell, wherein said gene product is selected from the group consisting of a gene product having having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with

the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795.

200. The method of Paragraph 199, wherein said method comprises inhibiting said activity or reducing said amount of said gene product or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis,*

Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

201. The method of Paragraph 199, wherein said method comprises inhibiting said activity or reducing said amount of said gene product or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in an organism other than *E. coli*.

202. The method of Paragraph 199, wherein said gene product is from an organism other than *E. coli*.

203. The method of Paragraph 199, wherein said gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

204. The method of Paragraph 199, wherein said gene product is encoded by a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucloetide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

205. A method for identifying a compound which influences the activity of a gene product required for proliferation comprising:

contacting a candidate compound with a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to

a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795; and

determining whether said candidate compound influences the activity of said gene product.

206. The method of Paragraph 205, wherein said gene product is from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae,*

Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

207. The method of Paragraph 205, wherein said gene product is from an organism other than *E. coli*.

208. The method of Paragraph 205, wherein said gene product is a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

209. The method of Paragraph 205, wherein said gene product is encoded by a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

210. A compound identified using the method of Paragraph 205.

211. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation comprising:

(a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid that encodes a gene product selected from the group consisting of a gene product having having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said target with a candidate compound or nucleic acid; and

(c) measuring an activity of said target.

212. The method of Paragraph 211, wherein said target gene or RNA is from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis,*

Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

213. The method of Paragraph 211, wherein said target gene or RNA is from an organism other than *E. coli*.

214. The method of Paragraph 211, wherein said gene product is from an organism other than *E. coli*.

215. The method of Paragraph 211, wherein said target is a messenger RNA molecule and said activity is translation of said messenger RNA.

216. The method of Paragraph 211, wherein said compound is a nucleic acid and said activity is translation of said gene product.

217. The method of Paragraph 211, wherein said target is a gene and said activity is transcription of said gene.

218. The method of Paragraph 211, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

219. The method of Paragraph 211, wherein said target gene is a messenger RNA molecule encoding a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and a polypeptide whose activity may be

complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

220. The method of Paragraph 11, wherein said target gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

221. A compound or nucleic acid identified using the method of Paragraph 211.

222. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a cell comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is selected from the group consisting of a gene product having having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid

comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

223. The method of Paragraph 222, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

224. The method of Paragraph 222, wherein said sensitized cell is a Gram positive bacterium.

225. The method of Paragraph 224, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

226. The method of Paragraph 225, wherein said bacterium is *Staphylococcus aureus*.

227. The method of Paragraph 224, wherein said *Staphylococcus* species is coagulase negative.

228. The method of Paragraph 226, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

229. The method of Paragraph 222, wherein said sensitized cell is an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called*

Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

230. The method of Paragraph 222, wherein said cell is an organism other than *E. coli*.

231. The method of Paragraph 222, wherein said gene product is from an organism other than *E. coli*.

232. The method of Paragraph 222, wherein said antisense nucleic acid is transcribed from an inducible promoter.

233. The method of Paragraph 222, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

234. The method of Paragraph 222, wherein growth inhibition is measured by monitoring optical density of a culture medium.

235. The method of Paragraph 222, wherein said gene product is a polypeptide.

236. The method of Paragraph 235, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 25%

amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

237. The method of Paragraph 222, wherein said gene product is an RNA.

238. The method of Paragraph 222, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

239. A compound identified using the method of Paragraph 222.

240. A method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene product or a compound with activity against a gene encoding said gene product into a population of cells expressing said gene product, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which

hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

241. The method of Paragraph 240, wherein said compound is an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, or a proliferation-inhibiting portion thereof.

242. The method of Paragraph 240, wherein said proliferation inhibiting portion of one of SEQ ID NOs.: 8-3795 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

243. The method of Paragraph 240, wherein said population is a population of Gram positive bacteria.

244. The method of Paragraph 243, wherein said population of Gram positive bacteria is selected from the group consisting of a population of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

245. The method of Paragraph 243, wherein said population is a population of *Staphylococcus aureus*.

246. The method of Paragraph 245, wherein said population is a population of a bacterium selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

247. The method of Paragraph 240, wherein said population is a population of a bacterium selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis,*

Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

248. The method of Paragraph 240, wherein said population is a population of an organism other than *E. coli*.

249. The method of Paragraph 240, wherein said product of said gene is from an organism other than *E. coli*.

250. The method of Paragraph 240, wherein said gene product is selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

251. The method of Paragraph 240, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which

hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

252. A preparation comprising an effective concentration of an antisense nucleic acid in a pharmaceutically acceptable carrier wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid comprising a sequence having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a proliferation-inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions.

253. The preparation of Paragraph 252, wherein said proliferation-inhibiting portion of one of SEQ ID NOs.: 8-3795 comprises at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

254. A method for inhibiting the activity or expression of a gene in an operon which encodes a gene product required for proliferation comprising contacting a cell in a cell population with an antisense nucleic acid comprising at least a proliferation-inhibiting portion of said operon in an antisense orientation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product

encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

255. The method of Paragraph 254, wherein said antisense nucleic acid comprises a nucleotide sequence having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide seqence selected from the group consisting of SEQ ID NOs.: 8-3795, a proliferation inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid which comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions.

256. The method of Paragraph 254, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis,*

Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

257. The method of Paragraph 254, wherein said cell is not an *E. coli* cell.

258. The method of Paragraph 254, wherein said gene is from an organism other than *E. coli*.

259. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which transcribes said antisense nucleic acid into said cell population.

260. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which transcribes said antisense nucleic acid into said cell population.

261. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by transcribing said antisense nucleic acid from the chromosome of cells in said cell population.

262. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the synthesis of said antisense nucleic acid.

263. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

264. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide.

265. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell.

266. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid into said cell.

267. The method of Paragraph 254, wherein said antisense nucleic acid has at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

268. The method of Paragraph 254 wherein said antisense nucleic acid is a synthetic oligonucleotide.

269. The method of Paragraph 254, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

270. A method for identifying a gene which is required for proliferation of a cell comprising:

(a) contacting a cell with an antisense nucleic acid selected from the group consisting of a nucleic acid at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a proliferation-inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, wherein said cell is a cell other than the organism from which said nucleic acid was obtained;

(b) determining whether said nucleic acid inhibits proliferation of said cell; and

(c) identifying the gene in said cell which encodes the mRNA which is complementary to said antisense nucleic acid or a portion thereof.

271. The method of Paragraph 270, wherein said cell is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

272. The method of Paragraph 270 wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

273. The method of Paragraph 270, wherein said cell is not *E. coli*.

274. The method of Paragraph 270, further comprising operably linking said antisense nucleic acid to a promoter which is functional in said cell, said promoter being included in a vector, and introducing said vector into said cell.

275. A method for identifying a compound having the ability to inhibit proliferation of a cell comprising:

(a) identifying a homolog of a gene or gene product whose activity or level is inhibited by an antisense nucleic acid in a test cell, wherein said test cell is not the microorgaism from which the antisense nucleic acid was obtained, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said test cell;

(c) contacting said test cell with a sublethal level of said inhibitory nucleic acid, thus sensitizing said cell;

(d) contacting the sensitized cell of step (c) with a compound; and

(e) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not express said inhibitory nucleic acid.

276. The method of Paragraph 275, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

277. The method of Paragraph 275, wherein step (a) comprises identifying a homologous nucleic acid to a gene or gene product whose activity or level is inhibited by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 by using an algorithm selected from

the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

278. The method of Paragraph 275 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids comprising nucleotide sequences which hybridize to said nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or the complement of the nucleotide sequence of said nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795.

279. The method of Paragraph 275 wherein step (a) comprises expressing a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs. 8-3795 in said test cell.

280. The method of Paragraph 275, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in an test cell selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus*

aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

281. The method of Paragraph 275, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell other than *E. coli*.

282. The method of Paragraph 275, wherein said inhibitory nucleic acid is an antisense nucleic acid.

283. The method of Paragraph 275, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

284. The method of Paragraph 275, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

285. The method of Paragraph 275, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises directly contacting said cell with said inhibitory nucleic acid.

286. The method of Paragraph 275, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises expressing an antisense nucleic acid to said homolog in said cell.

287. The method of Paragraph 275, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

288. The method of Paragraph 275, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide

sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

289. A compound identified using the method of Paragraph 275.

290. A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) sensitizing a test cell by contacting said test cell with a sublethal level of an antisense nucleic acid, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was obtained, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditionst;

(b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said antisense nucleic acid.

291. The method of Paragraph 290, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

292. A compound identified using the method of Paragraph 290.

293. The method of Paragraph 290, wherein said test cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae,*

Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

294. The method of Paragraph 290, wherein the test cell is not *E. coli*.

295. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected

from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting the sensitized cell with a compound; and

(c) determining the extent to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

296. The method of Paragraph 295, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

297. The method of Paragraph 295, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

298. The method of Paragraph 295, wherein said cell is a Gram positive bacterium.

299. The method of Paragraph 298, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

300. The method of Paragraph 299, wherein said Gram positive bacterium is *Staphylococcus aureus*.

301. The method of Paragraph 298, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

302. The method of Paragraph 295, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia*

pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

303. The method of Paragraph 295, wherein said cell is not an *E. coli* cell.

304. The method of Paragraph 295, wherein said gene product is from an organism other than *E. coli*.

305. The method of Paragraph 295, wherein said antisense nucleic acid is transcribed from an inducible promoter.

306. The method of Paragraph 305, further comprising contacting the cell with an agent which induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sublethal level.

307. The method of Paragraph 295, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

308. The method of Paragraph 295, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

309. The method of Paragraph 295, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide

sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

310. A compound identified using the method of Paragraph 295.

311. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product

whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said cell with a compound; and

(c) determining the degree to which said compound reduces proliferation of said contacted cell relative to a cell which was not contacted with said agent.

312. The method of Paragraph 311, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

313. The method of Paragraph 311, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

314. The method of Paragraph 311, wherein said cell is not an *E. coli* cell.

315. The method of Paragraph 311, wherein said gene product is from an organism other than *E. coli*.

316. The method of Paragraph 311, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

317. The method of Paragraph 311, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a cell.

318. The method of Paragraph 311, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

319. The method of Paragraph 311, wherein said mutation is a temperature sensitive mutation.

320. The method of Paragraph 311, wherein said gene product comprises a gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

321. A compound identified using the method of Paragraph 311.

322. A method for identifying the biological pathway in which a proliferation-required gene product or a gene encoding a proliferation-required gene product lies comprising:

(a) providing a sublethal level of an antisense nucleic acid which inhibits the activity or reduces the level of said gene encoding a proliferation-required gene product or said said proliferation-required gene product in a test cell, wherein said proliferation-required gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected

from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said test cell with a compound known to inhibit growth or proliferation of a cell, wherein the biological pathway on which said compound acts is known; and

(c) determining the degree to which said compound inhibits proliferation of said test cell relative to a cell which does not contain said antisense nucleic acid.

323. The method of Paragraph 322, wherein said determining step comprises determining whether said test cell has a substantially greater sensitivity to said compound than a cell which does not express said sublethal level of said antisense nucleic acid.

324. The method of Paragraph 322, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

325. The method of Paragraph 322, wherein said test cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia*

pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

326. The method of Paragraph 322, wherein said test cell is not an *E. coli* cell.

327. The method of Paragraph 322, wherein said gene product is from an organism other than *E. coli*.

328. A method for determining the biological pathway on which a test compound acts comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a cell, thereby producing a sensitized cell, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795 or a proliferation-inhibiting portion thereof,a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions and wherein the biological pathway in which said proliferation-

required nucleic acid or a protein encoded by said proliferation-required polypeptide lies is known,

(b) contacting said cell with said test compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

329. The method of Paragraph 328, wherein said determining step comprises determining whether said sensitized cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

330. The method of Paragraph 328, further comprising:

(d) providing a sublethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said sensitized cell has substantially greater sensitivity to said test compound than said second cell.

331. The method of Paragraph 328, wherein said sensitized cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae,*

Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

332. The method of Paragraph 328, wherein said sensitized cell is not an *E. coli* cell.

333. The method of Paragraph 328, wherein said proliferation-required nucleic acid is from an organism other than *E. coli.*

334. A compound which inhibits proliferation by interacting with a gene encoding a gene product required for proliferation or with a gene product required for proliferation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product

whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

335. The compound of Paragraph 334, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

336. The compound of Paragraph 334, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

337. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which

hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795 ; and

manufacturing the compound so identified.

338. The method of Paragraph 337, wherein said screening step comprises performing any one of the methods of Paragraphs 205, 211, 222, 275, 290, 295, 311.

339. The method of Paragraph 337, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

340. A method for inhibiting proliferation of a cell in a subject comprising administering an effective amount of a compound that reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.:

8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

341. The method of Paragraph 340 wherein said subject is selected from the group consisting of vertebrates, mammals, avians, and human beings.

342. The method of Paragraph 340, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

343. The method of Paragraph 340, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

344. The method of Paragraph 340, wherein said cell is not *E. coli*.

345. The method of Paragraph 340, wherein said gene product is from an organism other than *E. coli*.

Definitions

By “biological pathway” is meant any discrete cell function or process that is carried out by a gene product or a subset of gene products. Biological pathways include anabolic, catabolic, enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such as cell walls. Biological pathways that are usually required for proliferation of cells or microorganisms include, but are not limited to, cell division, DNA synthesis and replication, RNA synthesis (transcription), protein synthesis (translation), protein processing, protein transport, fatty acid biosynthesis, electron transport chains, cell wall synthesis, cell membrane production, synthesis and maintenance, and the like.

By “inhibit activity of a gene or gene product” is meant having the ability to interfere with the function of a gene or gene product in such a way as to decrease expression of the gene, in such a way as to reduce the level or activity of a product of the gene or in such a way as to inhibit the interaction of the gene or gene product with other biological molecules required for its activity. Agents which inhibit the activity of a gene include agents that inhibit transcription of the gene, agents that inhibit processing of the transcript of the gene, agents that reduce the stability of the transcript of the gene, and agents that inhibit translation of the mRNA transcribed from the gene. In microorganisms, agents which inhibit the activity of a gene can act to decrease expression of the operon in which the gene resides or alter the folding or processing of operon RNA so as to reduce the level or activity of the gene product. The gene product can be a non-translated RNA such as ribosomal RNA, a translated RNA (mRNA) or the protein product resulting from translation of the gene mRNA. Of particular utility to the present invention are antisense RNAs that have activities against the operons or genes to which they specifically hybridze.

By “activity against a gene product” is meant having the ability to inhibit the function or to reduce the level or activity of the gene product in a cell. This includes, but is not limited to, inhibiting the enzymatic activity of the gene product or the ability of the gene product to interact with other biological molecules required for its activity, including inhibiting the gene product’s assembly into a multimeric structure.

By “activity against a protein” is meant having the ability to inhibit the function or to reduce the level or activity of the protein in a cell. This includes, but is not limited

to, inhibiting the enzymatic activity of the protein or the ability of the protein to interact with other biological molecules required for its activity, including inhibiting the protein's assembly into a multimeric structure.

By "activity against a nucleic acid" is meant having the ability to inhibit the function or to reduce the level or activity of the nucleic acid in a cell. This includes, but is not limited to, inhibiting the ability of the nucleic acid interact with other biological molecules required for its activity, including inhibiting the nucleic acid's assembly into a multimeric structure.

By "activity against a gene" is meant having the ability to inhibit the function or expression of the gene in a cell. This includes, but is not limited to, inhibiting the ability of the gene to interact with other biological molecules required for its activity.

By "activity against an operon" is meant having the ability to inhibit the function or reduce the level of one or more products of the operon in a cell. This includes, but is not limited to, inhibiting the enzymatic activity of one or more products of the operon or the ability of one or more products of the operon to interact with other biological molecules required for its activity.

By "antibiotic" is meant an agent which inhibits the proliferation of a cell or microorganism.

By "*E. coli or Escherichia coli*" is meant *Escherichia coli* or any organism previously categorized as a species of *Shigella* including *Shigella boydii, Shigella flexneri, Shigella dysenteriae, Shigella sonnei, Shigella 2A.*

By "homologous coding nucleic acid" is meant a nucleic acid homologous to a nucleic acid encoding a gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 or a portion thereof. In some embodiments, the homologous coding nucleic acid may have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. In other embodiments the homologous coding nucleic acids may have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide

sequences complementary to one of SEQ ID NOs.: 8-3795 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Identity may be measured using BLASTN version 2.0 with the default parameters or tBLASTX with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety) Alternatively a "homologuous coding nucleic acid" could be identified by membership of the gene of interest to a functional orthologue cluster. All other members of that orthologue cluster would be considered homologues. Such a library of functional orthologue clusters can be found at http://www.ncbi.nlm.nih.gov/COG. A gene can be classified into a cluster of orthologous groups or COG by using the COGNITOR program available at the above web site, or by direct BLASTP comparison of the gene of interest to the members of the COGs and analysis of these results as described by Tatusov, R.L., Galperin, M.Y., Natale, D. A. and Koonin, E.V. (2000) The COG database: a tool for genome-scale analysis of protein functions and evolution. Nucleic Acids Research v. 28 n. 1, pp33-36.

The term "homologous coding nucleic acid" also includes nucleic acids comprising nucleotide sequences which encode polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% maino acid identity or similarity to a polypeptide comprising the amino acid sequence of one of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 or to a polypeptpide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs: 8-3795 or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, TBLASTN with the default parameters, or tBLASTX with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety).

The term "homologous coding nucleic acid" also includes coding nucleic acids which hybridize under stringent conditions to a nucleic acid selected from the group consisting of the nucleotide sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and coding nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 As used herein, "stringent conditions" means hybridization to filter-bound nucleic acid in 6xSSC at about 45°C followed by one or more washes in 0.1xSSC/0.2% SDS at about 68°C. Other exemplary stringent conditions may refer, *e.g.*, to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C, 48°C, 55°C, and 60°C as appropriate for the particular probe being used.

The term "homologous coding nucleic acid" also includes coding nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleotide sequence selected from the group consisting of the sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and coding nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012. As used herein, "moderate conditions" means hybridization to filter-bound DNA in 6x sodium chloride/sodium citrate (SSC) at about 45°C followed by one or more washes in 0.2xSSC/0.1% SDS at about 42-65°C.

The term "homologous coding nucleic acids" also includes nucleic acids comprising nucleotide sequences which encode a gene product whose activity may be complemented by a gene encoding a gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795. In some embodiments, the homologous coding nucleic acids may encode a gene product whose activity is complemented by the gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012. In other embodiments, the homologous coding nucleic acids may comprise a nucleotide

sequence encode a gene product whose activity is complemented by one of the polypeptides of SEQ ID NOs. 3745-4773.

The term "homologous antisense nucleic acid" includes nucleic acids comprising a nucleotide sequence having at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 8-3795 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Homologous antisense nucleic acids may also comprising nucleotide sequences which have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of the sequences complementary to one of sequences of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Nucleic acid identity may be determined as described above.

The term "homologous antisense nucleic acid" also includes antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleotide sequence complementary to one of SEQ ID NOs.: 8-3795 and antisens nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 8-3795. Homologous antisense nucleic acids also include antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

The term "homologous antisense nucleic acid" also includes antisense nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleotide sequence complementary to one of SEQ ID NOs.: 8-3795 and antisens nucleic acids comprising nucleotide seuqences which hybridize under moderate

conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 8-3795. Homologous antisense nucleic acids also include antisense nucleic acids comprising nucleotide seuqences which hybridize under moderate conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and antisense nucleic acids which comprising nucleotide sequences hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

By "homologous polypeptide" is meant a polypeptide homologous to a polypeptide whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or by a homologous antisense nucleic acid. The term "homologous polypeptide" includes polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795 or by a homologous antisense nucleic acid, or polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide to a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 or by a homologous antisense nucleic acid. Identity or similarity may be determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety).

The term homologous polypeptide also includes polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide

selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

The invention also includes polynucleotides, preferably DNA molecules, that hybridize to one of the nucleic acids of SEQ ID NOs.: 8-3795, SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 or the complements of any of the preceding nucleic acids. Such hybridization may be under stringent or moderate conditions as defined above or under other conditions which permit specific hybridization. The nucleic acid molecules of the invention that hybridize to these DNA sequences include oligodeoxynucleotides ("oligos") which hybridize to the target gene under highly stringent or stringent conditions. In general, for oligos between 14 and 70 nucleotides in length the melting temperature (Tm) is calculated using the formula:

$$Tm\ (^\circ C) = 81.5 + 16.6(\log[\text{monovalent cations (molar)}] + 0.41\ (\%\ G{+}C) - (500/N)$$

where N is the length of the probe. If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation:

$$Tm(^\circ C) = 81.5 + 16.6(\log[\text{monovalent cations (molar)}] + 0.41(\%\ G{+}C) - (0.61)(\%\ \text{formamide}) - (500/N)$$

where N is the length of the probe. In general, hybridization is carried out at about 20-25 degrees below Tm (for DNA-DNA hybrids) or about 10-15 degrees below Tm (for RNA-DNA hybrids).

Other hybridization conditions are apparent to those of skill in the art (see, for example, Ausubel, F.M. *et al.*, eds., 1989, *Current Protocols in Molecular Biology*, Vol. I, Green Publishing Associates, Inc. and John Wiley & Sons, Inc., New York, at pp.

6.3.1-6.3.6 and 2.10.3, the disclosure of which is incorporated herein by reference in its entirety).

The term, *Salmonella*, is the generic name for a large group of gram-negative enteric bacteria that are closely related to *Escherichia coli*. The diseases caused by *Salmonella* are often due to contamination of foodstuffs or the water supply and affect millions of people each year. Traditional methods of *Salmonella* taxonomy were based on assigning a separate species name to each serologically distinguishable strain (Kauffmann, F 1966 The bacteriology of the *Enterobacteriaceae*. Munksgaard, Copenhagen). Serology of *Salmonella* is based on surface antigens (O [somatic] and H [flagellar]). Over 2,400 serotypes or serovars of *Salmonella* are known (Popoff, et al. 2000 Res. Microbiol. 151:63-65). Therefore, each serotype was considered to be a separate species and often given names, accordingly (e.g. *S. paratyphi, S. typhimurium, S. typhi, S. enteriditis*, etc.).

However, by the 1970s and 1980s it was recognized that this system was not only cumbersome, but also inaccurate. Then, many *Salmonella* species were lumped into a single species (all serotypes and subgenera I, II, and IV and all serotypes of *Arizona*) with a second subspecies, *S. bongorii* also recognized (Crosa, et al., 1973, J. Bacteriol. 115:307-315). Though species designations are based on the highly variable surface antigens, the *Salmonella* are very similar otherwise with a major exception being pathogenicity determinants.

There has been some debate on the correct name for the *Salmonella* species. Currently (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467), the accepted name is *Salmonella enterica*. *S. enterica* is divided into six subspecies (I, *S. enterica* subsp. *enterica*; II, *S. enterica*, subsp. *salamae*; IIIa, *S. enterica* subsp. *arizonàe*; IIIb, *S. enterica* subsp. *diarizonae*; IV, *S. enterica* subsp. *houtenae*; and VI, *S. enterica* subsp. *indica*). Within subspecies I, serotypes are used to distinguish each of the serotypes or serovars (e.g. *S. enterica* serotype Enteriditis, *S. enterica* serotype Typhimurium, *S. enterica* serotype Typhi, and *S. enterica* serotype Choleraesuis, etc.). Current convention is to spell this out on first usage (*Salmonella enterica* ser. Typhimurium) and then use an abbreviated form (*Salmonella* Typhimurium or *S.* Typhimurium). Note, the genus and species names (*Salmonella enterica*) are italicized but not the serotype/serovar name (Typhimurium). Because the taxonomic committees have yet to

officially approve of the actual species name, this latter system is what is employed by the CDC (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467). Due to the concerns of both taxonomic priority and medical importance, some of these serotypes might ultimately receive full species designations (*S.typhi* would be the most notable).

Therefore, as used herein "*Salmonella enterica* or *S. enterica*" includes serovars Typhi, Typhimurium, Paratyphi, Choleraesuis, etc." However, appeals of the "official" name are in process and the taxonomic designations may change (*S. choleraesuis* is the species name that could replace *S. enterica* based solely on priority).

By "identifying a compound" is meant to screen one or more compounds in a collection of compounds such as a combinatorial chemical library or other library of chemical compounds or to characterize a single compound by testing the compound in a given assay and determining whether it exhibits the desired activity.

By "inducer" is meant an agent or solution which, when placed in contact with a cell or microorganism, increases transcription, or inhibitor and/or promoter clearance/fidelity, from a desired promoter.

As used herein, "nucleic acid" means DNA, RNA, or modified nucleic acids. Thus, the terminology "the nucleic acid of SEQ ID NO: X" or "the nucleic acid comprising the nucleotide sequence" includes both the DNA sequence of SEQ ID NO: X and an RNA sequence in which the thymidines in the DNA sequence have been substituted with uridines in the RNA sequence and in which the deoxyribose backbone of the DNA sequence has been substituted with a ribose backbone in the RNA sequence. Modified nucleic acids are nucleic acids having nucleotides or structures which do not occur in nature, such as nucleic acids in which the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate brides, thioester bridges, as well as many others known in the art may also be used in modified nucleic acids. Modified nucleic acids may also comprise, α-anomeric nucleotide units and modified nucleotides such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenylribofuranose, and N^4, N^4-ethano-5-methyl-cytosine are contemplated for use in the present invention. Modified nucleic acids may also be peptide nucleic acids in which the entire deoxyribose-phosphate backbone has been

exchanged with a chemically completely different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units.

As used herein, "sub-lethal" means a concentration of an agent below the concentration required to inhibit all cell growth.

Brief Description of the Drawings

Figure 1 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli* ribosomal protein *rpl*W (AS-*rplW*) which is required for protein synthesis and essential for cell proliferation, or an antisense clone to the *elaD* (AS-*elaD*) gene which is not known to be involved in protein synthesis and which is also essential for proliferation.

Figure 2A is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to *rplW* (AS-*rplW*) in the absence (0) or presence of IPTG at concentrations that result in 20% and 50% growth inhibition.

Figure 2B is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to *elaD* (AS-*elaD*)in the absence (0) or presence of IPTG at concentrations that result in 20% and 50% growth inhibition.

Figure 3 is a graph showing the fold increase in tetracycline sensitivity of *E. coli* transfected with antisense clones to essential ribosomal proteins *L23* (AS-*rplW*) and *L7/L12* and *L10* (AS-*rplLrplJ*). Antisense clones to genes known to not be directly involved in protein synthesis, *atpB/E* (AS-*atpB/E*), *visC* (AS-*visC*), *elaD* (AS-*elaD*), *yohH* (AS-*yohH*), are much less sensitive to tetracycline.

Figure 4 illustrates the results of an assay in which *Staphylococcus aureus* cells transcribing an antisense nucleic acid complementary to the *gyrB* gene encoding the β subunit of gyrase were contacted with several antibiotics whose targets were known.

Detailed Description of the Preferred Embodiments

The present invention describes a group of prokaryotic genes and gene families required for cellular proliferation. Exemplary genes and gene families from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* and *Salmonella typhi* are provided. A proliferation-

required gene or gene family is one where, in the absence or substantial reduction of a gene transcript and/or gene product, growth or viability of the cell or microorganism is reduced or eliminated. Thus, as used herein, the terminology "proliferation-required" or "required for proliferation" encompasses instances where the absence or substantial reduction of a gene transcript and/or gene product completely eliminates cell growth as well as instances where the absence of a gene transcript and/or gene product merely reduces cell growth. These proliferation-required genes can be used as potential targets for the generation of new antimicrobial agents. To achieve that goal, the present invention also encompasses assays for analyzing proliferation-required genes and for identifying compounds which interact with the gene and/or gene products of the proliferation-required genes. In addition, the present invention contemplates the expression of genes and the purification of the proteins encoded by the nucleic acid sequences identified as required proliferation genes and reported herein. The purified proteins can be used to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds.

The present invention also describes methods for identification of nucleotide sequences homologous to these genes and polypeptides described herein, including nucleic acids comprising nucleotide sequences homologous to the nucleic acids of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and polypeptides homologous to the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110. For example, these sequences may be used to identify homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides in microorganisms such as *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium*

tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments, the homologous coding nucleic acids, homologus antisense nucleic acids, or homologous polypeptides are identified in an organism other than *E. coli.*

The homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides, may then be used in each of the methods described herein, including methods to identify compounds which inhibit the proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods of inhibiting the growth of the organism containing the homologous coding nucleic acid, homologus antisense nucleic acid or homologous polypeptide, methods of identifying compounds which influence the activity or level of a gene product required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for identifying compounds or nucleic acids having the ability to reduce the level or activity of a gene product required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods of inhibiting the activity or expression of a gene in an operon required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for identifying a gene required proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for identifying the biological pathway in which a gene or gene product required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide lies, methods for identifying compounds having activity against biological pathway required for

proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for determining the biological pathway on which a test compound acts, and methods of inhibiting the proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide in a subject. In some embodiments of the present invention, the methods are performed using an organism, other than *E. coli* or a gene or gene product from an organism other than *E. coli.*

The present invention utilizes a novel method to identify proliferation-required sequences. Generally, a library of nucleic acid sequences from a given source are subcloned or otherwise inserted immediately downstream of an inducible promoter on an appropriate vector, such as a *Staphylococcus aureus/E. coli* or *Pseudomonas aeruginosa/ E. coli* shuttle vector, or a vector which will replicate in both *Salmonella typhimurium* and *Klebsiella pneumoniae,* or other vector or shuttle vector capable of functioning in the intended organism., thus forming an expression library. It is generally preferred that expression is directed by a regulatable promoter sequence such that expression level can be adjusted by addition of variable concentrations of an inducer molecule or of an inhibitor molecule to the medium. Temperature activated promoters, such as promoters regulated by temperature sensitive repressors, such as the lambda C_{I857} repressor, are also envisioned. Although the insert nucleic acids may be derived from the chromosome of the cell or microorganism into which the expression vector is to be introduced, because the insert is not in its natural chromosomal location, the insert nucleic acid is an exogenous nucleic acid for the purposes of the discussion herein. The term "expression" is defined as the production of a sense or antisense RNA molecule from a gene, gene fragment, genomic fragment, chromosome, operon or portion thereof. Expression can also be used to refer to the process of peptide or polypeptide synthesis. An expression vector is defined as a vehicle by which a ribonucleic acid (RNA) sequence is transcribed from a nucleic acid sequence carried within the expression vehicle. The expression vector can also contain features that permit translation of a protein product from the transcribed RNA message expressed from the exogenous nucleic acid sequence carried by the expression vector. Accordingly, an expression vector can produce an RNA molecule as its sole product or the

expression vector can produce a RNA molecule that is ultimately translated into a protein product.

Once generated, the expression library containing the exogenous nucleic acid sequences is introduced into a population of cells (such as the organism from which the exogenous nucleic acid sequences were obtained) to search for genes that are required for bacterial proliferation. Because the library molecules are foreign, in context, to the population of cells, the expression vectors and the nucleic acid segments contained therein are considered exogenous nucleic acid.

Expression of the exogenous nucleic acid fragments in the test population of cells containing the expression library is then activated. Activation of the expression vectors consists of subjecting the cells containing the vectors to conditions that result in the expression of the exogenous nucleic acid sequences carried by the expression library. The test population of cells is then assayed to determine the effect of expressing the exogenous nucleic acid fragments on the test population of cells. Those expression vectors that negatively impacted the growth of the cells upon induction of expression of the random sequences contained therein were identified, isolated, and purified for further study.

A variety of assays are contemplated to identify nucleic acid sequences that negatively impact growth upon expression. In one embodiment, growth in cultures expressing exogenous nucleic acid sequences and growth in cultures not expressing these sequences is compared. Growth measurements are assayed by examining the extent of growth by measuring optical densities. Alternatively, enzymatic assays can be used to measure bacterial growth rates to identify exogenous nucleic acid sequences of interest. Colony size, colony morphology, and cell morphology are additional factors used to evaluate growth of the host cells. Those cultures that fail to grow or grow at a reduced rate under expression conditions are identified as containing an expression vector encoding a nucleic acid fragment that negatively affects a proliferation-required gene.

Once exogenous nucleic acids of interest are identified, they are analyzed. The first step of the analysis is to acquire the nucleotide sequence of the nucleic acid fragment of interest. To achieve this end, the insert in those expression vectors identified as containing a nucleotide sequence of interest is sequenced, using standard techniques well known in the art. The next step of the process is to determine the source of the nucleotide

sequence. As used herein "source" means the genomic region containing the cloned fragment.

Determination of the gene(s) corresponding to the nucleotide sequence was achieved by comparing the obtained sequence data with databases containing known protein and nucleotide sequences from various microorganisms. Thus, initial gene identification was made on the basis of significant sequence similarity or identity to either characterized or predicted *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* genes or their encoded proteins and/or homologues in other species.

The number of nucleotide and protein sequences available in database systems has been growing exponentially for years. For example, the complete nucleotide sequences of *Caenorhabditis elegans* and several bacterial genomes, including *E. coli, Aeropyrum pernix, Aquifex aeolicus, Archaeoglobus fulgidus, Bacillus subtilis, Borrelia burgdorferi, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium tetani, Corynebacterium diptheria, Deinococcus radiodurans, Haemophilus influenzae, Helicobacter pylori 26695, Helicobacter pylori J99, Methanobacterium thermoautotrophicum, Methanococcus jannaschii, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Pseudomonas aeruginosa, Pyrococcus abyssi, Pyrococcus horikoshii, Rickettsia prowazekii, Synechocystis PCC6803, Thermotoga maritima, Treponema pallidum, Bordetella pertussis, Campylobacter jejuni, Clostridium acetobutylicum, Mycobacterium tuberculosis CSU#93, Neisseria gonorrhoeae, Neisseria meningitidis, Pseudomonas aeruginosa, Pyrobaculum aerophilum, Pyrococcus furiosus, Rhodobacter capsulatus, Salmonella typhimurium, Streptococcus mutans, Streptococcus pyogenes, Ureaplasma urealyticum* and *Vibrio cholera* are available. This nucleotide sequence information is stored in a number of databanks, such as GenBank, the National Center for Biotechnology Information (NCBI), the Genome Sequencing Center (http://genome.wustl.edu/gsc/salmonella.shtml), and the Sanger Centre (http://www.sanger.ac.uk/projects/S___typhi) which are publicly available for searching.

A variety of computer programs are available to assist in the analysis of the sequences stored within these databases. FASTA, (W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with FASTP and FASTA" Methods in Enzymology

183:63- 98), Sequence Retrieval System (SRS), (Etzold & Argos, SRS an indexing and retrieval tool for flat file data libraries. Comput. Appl. Biosci. 9:49-57, 1993) are two examples of computer programs that can be used to analyze sequences of interest. In one embodiment of the present invention, the BLAST family of computer programs, which includes BLASTN version 2.0 with the default parameters, or BLASTX version 2.0 with the default parameters, is used to analyze nucleotide sequences.

BLAST, an acronym for "Basic Local Alignment Search Tool," is a family of programs for database similarity searching. The BLAST family of programs includes: BLASTN, a nucleotide sequence database searching program, BLASTX, a protein database searching program where the input is a nucleic acid sequence; and BLASTP, a protein database searching program. BLAST programs embody a fast algorithm for sequence matching, rigorous statistical methods for judging the significance of matches, and various options for tailoring the program for special situations. Assistance in using the program can be obtained by e-mail at blast@ncbi.nlm.nih.gov. tBLASTX can be used to translate a nucleotide sequence in all three potential reading frames into an amino acid sequence.

Bacterial genes are often transcribed in polycistronic groups. These groups comprise operons, which are a collection of genes and intergenic sequences under common regulation. The genes of an operon are transcribed on the same mRNA and are often related functionally. Given the nature of the screening protocol, it is possible that the identified exogenous nucleic acid corresponds to a gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a nucleotide sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual nucleotide sequence that is required for bacterial proliferation. Accordingly, it is often desirable to determine which gene(s) that is encoded within the operon is individually required for proliferation.

In one embodiment of the present invention, an operon is identified and then dissected to determine which gene or genes are required for proliferation. Operons can be identified by a variety of means known to those in the art. For example, the RegulonDB DataBase described by Huerta et al. (*Nucl. Acids Res.* 26:55-59, 1998), which may also be found on the website

http://www.cifn.unam.mx/Computational_Biology/regulondb/ , the disclosures of which are incorporated herein by reference in their entireties, provides information about operons in *Escherichia coli*. The Subtilist database (http://bioweb.pasteur.fr/GenoList/SubtiList), (Moszer, I., Glaser, P. and Danchin, A. (1995) Microbiology 141: 261-268 and Moszer, I (1998) FEBS Letters 430: 28-36, the disclosures of which are incorporated herein in their entireties), may also be used to predict operons. This database lists genes from the fully sequenced, Gram-positive bacteria, *Bacillus subtilis*, together with predicted promoters and terminator sites. This information can be used in conjunction with the *Staphylococcus aureus* genomic sequence data to predict operons and thus produce a list of the genes affected by the antisense nucleic acids of the present invention. The *Pseudomonas aeruginosa* web site (http://www.pseudomonas.com) can be used to help predict operon organization in this bacterium. The databases available from the Genome Sequencing Center (http://genome.wustl.edu/gsc/salmonella.shtml), and the Sanger Centre (http://www.sanger.ac.uk/projects/S___typhi) may be used to predict operons in *Salmonella typhimurium*. The TIGR microbial database has an incomplete version of the *E. faecalis* genome http://www.tigr.org/cgi-bin/BlastSearch/blast.cgi?organism=e_faecalis. One can take a nucleotide sequence and BLAST it for homologs.

A number of techniques that are well known in the art can be used to dissect the operon. Analysis of RNA transcripts by Northern blot or primer extension techniques are commonly used to analyze operon transcripts. In one aspect of this embodiment, gene disruption by homologous recombination is used to individually inactivate the genes of an operon that is thought to contain a gene required for proliferation.

Several gene disruption techniques have been described for the replacement of a functional gene with a mutated, non-functional (null) allele. These techniques generally involve the use of homologous recombination. One technique using homologous recombination in *Staphylococcus aureus* is described in Xia et a.. 1999, Plasmid 42: 144-149, the disclosure of which is incorporated herein by reference in its entirety. This technique uses crossover PCR to create a null allele with an in-frame deletion of the coding region of a target gene. The null allele is constructed in such a way that nucleotide sequences adjacent to the wild type gene are retained. These homologous

sequences surrounding the deletion null allele provide targets for homologous recombination so that the wild type gene on the *Staphylococcus aureus* chromosome can be replaced by the constructed null allele. This method can be used with other bacteria as well, including *Salmonella* and *Klebsiella* species. Similar gene disruption methods that employ the counter selectable marker *sacB* (Schweizer, H. P., Klassen, T. and Hoang, T. (1996) Mol. Biol. of *Pseudomonas*. ASM press, 229-237, the disclosure of which is incorporated herein by reference in its entirety) are available for *Pseudomonas, Salmonella* and *Klebsiella* species. *E. faecalis* genes can be disrupted by recombining in a non-replicating plasmid that contains an internal fragment to that gene (Leboeuf, C., L. Leblanc, Y. Auffray and A. Hartke. 2000. J. Bacteriol. 182:5799-5806, the disclosure of which is incorporated herein by reference in its entirety).

The crossover PCR amplification product is subcloned into a suitable vector having a selectable marker, such as a drug resistance marker. In some embodiments the vector may have an origin of replication which is functional in *E. coli* or another organism distinct from the organism in which homologous recombination is to occur, allowing the plasmid to be grown in *E. coli* or the organism other than that in which homologous recombination is to occur, but may lack an origin of replication functional in *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* such that selection of the selectable marker requires integration of the vector into the homologous region of the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* chromosome. Usually a single crossover event is responsible for this integration event such that the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* chromosome now contains a tandem duplication of the target gene consisting of one wild type allele and one deletion

null allele separated by vector sequence. Subsequent resolution of the duplication results in both removal of the vector sequence and either restoration of the wild type gene or replacement by the in-frame deletion. The latter outcome will not occur if the gene should prove essential. A more detailed description of this method is provided in Example 5 below. It will be appreciated that this method may be practiced with any of the nucleic acids or organisms described herein.

Recombinant DNA techniques can be used to express the entire coding sequences of the gene identified as required for proliferation, or portions thereof. The over-expressed proteins can be used as reagents for further study. The identified exogenous sequences are isolated, purified, and cloned into a suitable expression vector using methods well known in the art. If desired, the nucleic acids can contain the nucleotide sequences encoding a signal peptide to facilitate secretion of the expressed protein.

Expression of fragments of the bacterial genes identified as required for proliferation is also contemplated by the present invention. The fragments of the identified genes can encode a polypeptide comprising at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 75, or more than 75 consecutive amino acids of a gene complementary to one of the identified sequences of the present invention. The nucleic acids inserted into the expression vectors can also contain endogenous sequences upstream and downstream of the coding sequence.

When expressing the encoded protien of the idnetified required for bacterial proliferation or a fragment thereof, the nucleotide sequence to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector can be any of the bacterial, insect, yeast, or mammalian expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon usage and codon bias of the sequence can be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No. 5,082,767, incorporated herein by this reference. Fusion protein expression systems are also contemplated by the present invention.

Following expression of the protein encoded by the identified exogenous nucleic acid, the protein may be purified. Protein purification techniques are well known in the art. Proteins encoded and expressed from identified exogenous nucleic acids can be partially purified using precipitation techniques, such as precipitation with polyethylene glycol. Alternatively, epitope tagging of the protein can be used to allow simple one step purification of the protein. In addition, chromatographic methods such as ion-exchange chromatography, gel filtration, use of hydroxyapaptite columns, immobilized reactive dyes, chromatofocusing, and use of high-performance liquid chromatography, may also be used to purify the protein. Electrophoretic methods such as one-dimensional gel electrophoresis, high-resolution two-dimensional polyacrylamide electrophoresis, isoelectric focusing, and others are contemplated as purification methods. Also, affinity chromatographic methods, comprising antibody columns, ligand presenting columns and other affinity chromatographic matrices are contemplated as purification methods in the present invention.

The purified proteins produced from the gene coding sequences identified as required for proliferation can be used in a variety of protocols to generate useful antimicrobial reagents. In one embodiment of the present invention, antibodies are generated against the proteins expressed from the identified exogenous nucleic acids. Both monoclonal and polyclonal antibodies can be generated against the expressed proteins. Methods for generating monoclonal and polyclonal antibodies are well known in the art. Also, antibody fragment preparations prepared from the produced antibodies discussed above are contemplated.

In addition, the purified protein, fragments thereof, or derivatives thereof may be administered to an individual in a pharmaceutically acceptable carrier to induce an immune response against the protein. Preferably, the immune response is a protective immune response which protects the individual. Methods for determining appropriate dosages of the protein and pharmaceutically acceptable carriers may be determined empiracally and are familiar to those skilled in the art.

Another application for the purified proteins of the present invention is to screen small molecule libraries for candidate compounds active against the various target proteins of the present invention. Advances in the field of combinatorial chemistry provide methods, well known in the art, to produce large numbers of candidate compounds that can

have a binding, or otherwise inhibitory effect on a target protein. Accordingly, the screening of small molecule libraries for compounds with binding affinity or inhibitory activity for a target protein produced from an identified gene is contemplated by the present invention.

The present invention further contemplates utility against a variety of other pathogenic microorganisms in addition to *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi*. For example, homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from other pathogenic microorganisms (including nucleic acids homologous to the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, nucleic acids homologous to the antisense nucleic acids of SEQ ID NOs.: 8-3795, and polypeptides homologous to the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) may be identified using methods such as those described herein. The homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides may be used to identify compounds which inhibit the proliferation of these other pathogenic microorganisms using methods such as those described herein.

For example, the proliferation-required nucleic acids, antisense nucleic acids, and polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* described herein (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, the antisense nucleic acids of SEQ ID NOs: 8-3795, and the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) may be used to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides required for proliferation in prokaryotes and eukaryotes. For example, nucleic acids or polypeptides required for the proliferation of protists, such as *Plasmodium* spp.*;* plants; animals, such as *Entamoeba* spp. *and Contracaecum* spp*;* and fungi including *Candida* spp., (e.g., *Candida albicans*), *Cryptococcus neoformans*, and

Aspergillus fumigatus may be identified. In one embodiment of the present invention, monera, specifically bacteria, including both Gram positive and Gram negative bacteria, are probed in search of novel gene sequences required for proliferation. Likewise, homologous antisense nucleic acids which may be used to inhibit growth of these organisms or to identify antibiotics may also be identified. These embodiments are particularly important given the rise of drug resistant bacteria.

The number of bacterial species that are becoming resistant to existing antibiotics is growing. A partial list of these microorganisms includes: *Escherichia* spp., such as *E. coli*, *Enterococcus* spp, such as *E. faecalis*; *Pseudomonas* spp., *such as P. aeruginosa*, *Clostridium* spp., such as *C. botulinum, Haemophilus* spp., such as *H. influenzae*, *Enterobacter* spp., such as *E. cloacae, Vibrio* spp., such as *V. cholera; Moraxala* spp., such as *M. catarrhalis*; *Streptococcus* spp., such as *S. pneumoniae, Neisseria* spp., such as *N. gonorrhoeae; Mycoplasma* spp., such as *Mycoplasma pneumoniae; Salmonella typhimurium*; *Helicobacter pylori*; *Escherichia coli;* and *Mycobacterium tuberculosis*. The genes and polypeptides identified as required for the proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, the sequences complementary to the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) can be used to identify homologous coding nucleic acids or homologous polypeptides required for proliferation from these and other organisms using methods such as nucleic acid hybridization and computer database analysis. Likewise, the antisense nucleic acids which inhibit proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* (including the antisense nucleic acids of SEQ ID NOs.: 8-3795 or the sequences complementary thereto) may also be used to identify antisense nucleic acids which

inhibit proliferation of these and other microorganisms or cells using nucleic acid hybridization or computer database analysis.

In one embodiment of the present invention, the nucleic acid sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhii* (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 and the antisense nucleic acids of SEQ ID NOs. 8-3795) are used to screen genomic libraries generated from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* and other bacterial species of interest. For example, the genomic library may be from Gram positive bacteria, Gram negative bacteria or other organisms including *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia*

enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species, including coagulase negative species of *Staphylococcus.* In some embodiments, the genomic library may be from an organism other than *E. coli*. Standard molecular biology techniques are used to generate genomic libraries from various cells or microorganisms. In one aspect, the libraries are generated and bound to nitrocellulose paper. The identified exogenous nucleic acid sequences of the present invention can then be used as probes to screen the libraries for homologous sequences.

For example, the libraries may be screened to identify homologous coding nucleic acids or homologous antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid complementary to one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and nucleic acids

comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

The libraries may also be screened to identify homologous nucleic coding nucleic acids or homologous antisense nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid complementary to one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleic acid sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

The homologous nucleic coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides identified as above can then be used as targets or tools for the identification of new, antimicrobial compounds using methods such as those described herein. In some embodiments, the homologous coding nucleic acids, homologous

antisense nucleic acids, or homologous polypeptides may be used to identify compounds with activity against more than one microorganism.

For example, the preceding methods may be used to isolate homologous coding nucleic acids or homologous antisense nucleic acids comprising a nucleotide sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 8-3795, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. The preceding methods may also be used to isolate homologous coding nucleic acids or homologous antisense nucleic acids comprising a nucleotide sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the nucleotide sequences of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. In some embodiments, the preceding methods may be used to isolate homologous coding nucleic acids or homologous antisense nucleic acids comprising a nucleotide sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleic acid sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 3796-3800, 3806-4860, 5916-10012, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. Identity may be measured using BLASTN version 2.0 with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety). For example, the homologous polynucleotides may comprise a coding sequence which is a naturally occurring allelic variant of one of the coding sequences described herein. Such allelic variants may have a substitution, deletion or addition of one or more nucleotides when compared to the nucleic acids of SEQ ID NOs: 8-3795, SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 or the nucleotide sequences complementary thereto.

Additionally, the above procedures may be used to isolate homologous coding nucleic acids which encode polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide comprising the sequence of one of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 or to a polypeptpide whose expression is inhibited by a nucleic acid of one of SEQ ID NOs: 8-3795 or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety).

Alternatively, homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides may be identified by searching a database to identify sequences having a desired level of nucleotide or amino acid sequence homology to a nucleic acid or polypeptide involved in proliferation or an antisense nucleic acid to a nucleic acid involved in microbial proliferation. A variety of such databases are available to those skilled in the art, including GenBank and GenSeq. In some embodiments, the databases are screened to identify nucleic acids with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleic acid required for proliferation, an antisense nucleic acid which inhibits proliferation, or a portion of a nucleic acid required for proliferation or a portion of an antisense nucleic acid which inhibits proliferation. For example, homologous coding sequences may be identified by using a database to identify nucleic acids homologous to one of SEQ ID Nos. 8-3795, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, nucleic acids homologous to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids homologous to one of

SEQ ID Nos. 8-3795, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof or nucleic acids homologous to the sequences complementary to any of the preceding nucleic acids. In other embodiments, the databases are screened to identify polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid sequence identity or similarity to a polypeptide involved in proliferation or a portion thereof. For example, the database may be screened to identify polypeptides homologous to a polypeptide comprising one of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110, a polypeptide whose expression is inhibited by a nucleic acid of one of SEQ ID NOs: 8-3795 or homologous to fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of any of the preceding polypeptides. In some embodiments, the database may be screened to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from cells or microorganisms other than the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* species from which they were obtained. For example the database may be screened to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from microorganisms such as *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica,*

Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species, including coagulase negative *Staphylococcus* . In some embodiments, the homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides are from an organism other than *E. coli.*

In another embodiment, gene expression arrays and microarrays can be employed. Gene expression arrays are high density arrays of DNA samples deposited at specific locations on a glass chip, nylon membrane, or the like. Such arrays can be used by researchers to quantify relative gene expression under different conditions. Gene expression arrays are used by researchers to help identify optimal drug targets, profile new compounds, and determine disease pathways. An example of this technology is found in U.S. Patent No. 5807522, which is hereby incorporated by reference.

It is possible to study the expression of all genes in the genome of a particular microbial organism using a single array. For example, the arrays may consist of 12 x 24 cm nylon filters containing PCR products corresponding to ORFs from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012) . 10 ngs of each PCR product are spotted every 1.5 mm on the filter. Single stranded labeled cDNAs are prepared for hybridization to the array (no second strand synthesis or amplification step is done) and placed in contact with the filter. Thus the labeled cDNAs are of "antisense" orientation. Quantitative analysis is done by phosphorimager.

Hybridization of cDNA made from a sample of total cell mRNA to such an array followed by detection of binding by one or more of various techniques known to those in the art results in a signal at each location on the array to which cDNA

hybridized. The intensity of the hybridization signal obtained at each location in the array thus reflects the amount of mRNA for that specific gene that was present in the sample. Comparing the results obtained for mRNA isolated from cells grown under different conditions thus allows for a comparison of the relative amount of expression of each individual gene during growth under the different conditions.

Gene expression arrays may be used to analyze the total mRNA expression pattern at various time points after induction of an antisense nucleic acid complementary to a proliferation-required gene. Analysis of the expression pattern indicated by hybridization to the array provides information on other genes whose expression is influenced by antisense expression. For example, if the antisense is complementary to a gene for ribosomal protein L7/L12 in the 50S subunit, levels of other mRNAs may be observed to increase, decrease or stay the same following expression of antisense to the L7/L12 gene. If the antisense is complementary to a different 50S subunit ribosomal protein mRNA (e.g. L25), a different mRNA expression pattern may result. Thus, the mRNA expression pattern observed following expression of an antisense nucleic acid comprising a nucleotide sequence complementary to a proliferation required gene may identify other proliferation-required nucleic acids. In addition, the mRNA expression patterns observed when the bacteria are exposed to candidate drug compounds or known antibiotics may be compared to those observed with antisense nucleic acids comprising a nucleotide sequence complementary to a proliferation-required nucleic acid. If the mRNA expression pattern observed with the candidate drug compound is similar to that observed with the antisense nucleic acid, the drug compound may be a promising therapeutic candidate. Thus, the assay would be useful in assisting in the selection of promising candidate drug compounds for use in drug development.

In cases where the source of nucleic acid deposited on the array and the source of the nucleic acid being hybridized to the array are from two different cells or microorganisms, gene expression arrays can identify homologous nucleic acids in the two cells or microorganisms.

The present invention also contemplates additional methods for screening other microorganisms for proliferation-required genes. In one aspect of this embodiment, an antisense nucleic acid comprising a nucleotide sequence complementary to the

proliferation-required sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* or a portion thereof is transcribed in an antisense orientation in such a way as to alter the level or activity of a nucleic acid required for proliferation of an autologous or heterologous cell or microorganism. For example, the antisense nucleic acid may be a homologous antisense nucleic acid such as an antisense nucleic acid homologous to the nucleotide sequence complementary to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, an antisense nucleic acid comprising a nucleotide sequence homologous to one of SEQ ID Nos.: 8-3795, or an antisense nucleic acid comprising a nucleotide sequence complementary to a portion of any of the preceding nucleic acids. The cell or microorganism transcribing the homologous antisense nucleic acid may be used in a cell-based assay, such as those described herein, to identify candidate antibiotic compounds. In another embodiment, the conserved portions of nucleotide sequences identified as proliferation-required can be used to generate degenerate primers for use in the polymerase chain reaction (PCR). The PCR technique is well known in the art. The successful production of a PCR product using degenerate probes generated from the nucleotide sequences identified herein indicates the presence of a homologous gene sequence in the species being screened. This homologous gene is then isolated, expressed, and used as a target for candidate antibiotic compounds. In another aspect of this embodiment, the homologous gene (for example a homologous coding nucleic acid)thus identified, or a portion thereof, is transcribed in an autologous cell or microorganism or in a heterologous cell or microorganism in an antisense orientation in such a way as to alter the level or activity of a homologous gene required for proliferation in the autologous or heterologous cell or microorganism. Alternatively, a homologous antisense nucleic acid may be transcribed in an autologous or heterologous cell or microorganism in such a way as to alter the level or activity of a gene product required for proliferation in the autologous or heterologous cell or microorganism.

The nucleic acids homologous to the genes required for the proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis,*

Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, or *Salmonella typhi* or the sequences complementary thereto may be used to identify homologous coding nucleic acids or homologous antisense nucleic acids from cells or microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* to inhibit the proliferation of cells or microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* by inhibiting the activity or reducing the amount of the identified homologous coding nucleic acid or homologous polypeptide in the cell or microorganism other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa Enterococcus faecalis,Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or to identify compounds which inhibit the growth of cells or microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* as described below. For example, the nucleic acids homologous to proliferation-required genes from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* or the sequences complementary thereto may be used to identify compounds which inhibit the growth of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia*

trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species. In some embodiments of the present invention, the nucleic acids homologous to proliferation-required sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* (including nucleic acids homologous to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012) or the sequences complementary thereto (including nucleic acids homologous to one of SEQ ID NOs.: 8-3795) are used to identify proliferation-required sequences in an organism other than *E. coli.*

In another embodiment of the present invention, antisense nucleic acids complementary to the sequences identified as required for proliferation or portions thereof (including antisense nucleic acids comprising a nucleotide sequence complementary to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 or portions thereof, such as the nucleic acids of SEQ ID NOs.: 8-3795) are transferred to vectors capable of function within a species other than the species from which the sequences were obtained. For example, the vector may be functional in *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis*

glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the vector may be functional in an organism other than *E. coli*. As would be appreciated by one of ordinary skill in the art, vectors may contain certain elements that are species specific. These elements can include promoter sequences, operator sequences, repressor genes, origins of replication, ribosomal binding sequences, termination sequences, and others. To use the antisense nucleic acids, one of ordinary skill in the art would know to use standard molecular biology techniques to isolate vectors containing the sequences of interest from cultured bacterial cells, isolate and purify those sequences, and subclone those sequences into a vector adapted for use in the species of bacteria to be screened.

Vectors for a variety of other species are known in the art. For example, numerous vectors which function in *E. coli* are known in the art. Also, Pla et al. have reported an expression vector that is functional in a number of relevant hosts including: *Salmonella typhimurium, Pseudomonas putida, and Pseudomonas aeruginosa*. **J. Bacteriol.** 172(8):4448-55 (1990). Brunschwig and Darzins (Gene (1992) 111:35-4, the disclosure of which is incorporated herein by reference in its entirety) described a shuttle expression vector for *Pseudomonas aeruginosa*. Similarly many examples exist of expression vectors that are freely transferable among various Gram-positive

microorganisms. Expression vectors for *Enterococcus faecalis* may be engineered by incorporating suitable promoters into a pAK80 backbone (Israelsen, H., S. M. Madsen, A. Vrang, E. B. Hansen and E. Johansen. 1995. Appl. Environ. Microbiol. 61:2540-2547, the disclosure of which is incorporated herein by reference in its entirety).

Following the subcloning of the antisense nucleic acids complementary to proliferation-required sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* or portions thereof into a vector functional in a second cell or microorganism of interest (i.e. a cell or microorganism other than the one from which the identified nucleic acids were obtained), the antisense nucleic acids are conditionally transcribed to test for bacterial growth inhibition. The nucleotide sequences of the nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* that, when transcribed, inhibit growth of the second cell or microorganism are compared to the known genomic sequence of the second cell or microorganism to identify the homologous gene from the second organism. If the homologous sequence from the second cell or microorganism is not known, it may be identified and isolated by hybridization to the proliferation-required *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalisEscherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* sequence of interest or by amplification using PCR primers based on the proliferation-required nucleotide sequence of interest as described above. In this way, sequences which may be required for the proliferation of the second cell or microorganism may be identified. For example, the second microorganism may be *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia*

trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the second microorganism is an organism other than *E. coli*.

The homologous nucleic acid sequences from the second cell or microorganism which are identified as described above may then be operably linked to a promoter, such as an inducible promoter, in an antisense orientation and introduced into the second cell or microorganism. The techniques described herein for identifying *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* genes required for proliferation may thus be employed to determine whether the identified nucleotide sequences from a second cell or microorganism inhibit the proliferation of the second cell or microorganism. For example, the second microorganism may be *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis,*

Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the second microorganism may be an organism other than *E. coli*.

Antisense nucleic acids required for the proliferation of microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or the genes corresponding thereto, may also be hybridized to a microarray containing the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis* ORFs, *Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* and *Salmonella typhi* (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012) to gauge the homology between the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* sequences and the proliferation-required nucleic acids from other cells or microorganisms. For example, the proliferation-required nucleic acid may be from *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called*

Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the proliferation-required nucleotide sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Salmonella typhi* or homologous nucleic acids are used to identify proliferation-required sequences in an organism other than *E. coli*. In some embodiments of the present invention, the proliferation-required sequences may be from an organism other than *E. coli*. The proliferation-required nucleic acids from a cell or microorganism other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* may be hybridized to the array under a variety of conditions which permit hybridization to occur when the probe has different levels of homology to the nucleotide sequence on the microarray. This would provide an indication of homology across the cells or microorganisms as well as clues to other possible essential genes in these cells or microorganisms.

In still another embodiment, the antisense nucleic acids of the present invention (including the antisense nucelic acids of SEQ ID NOs. 8-3795 or homologous antisense nucleic acids) that inhibit bacterial growth or proliferation can be used as antisense

therapeutics for killing bacteria. The antisense sequences can be complementary to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, homologous nucleic acids, or portions thereof. Alternatively, antisense therapeutics can be complementary to operons in which proliferation-required genes reside (i.e. the antisense nucleic acid may hybridize to a nucleotide sequence of any gene in the operon in which the proliferation-required genes reside). Further, antisense therapeutics can be complementary to a proliferation-required gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation or an operon containing a proliferation-required gene.

In addition to therapeutic applications, the present invention encompasses the use of nucleic acids complementary to nucleic acids required for proliferation as diagnostic tools. For example, nucleic acid probes comprising nucleotide sequences complementary to proliferation-required sequences that are specific for particular species of cells or microorganisms can be used as probes to identify particular microorganism species or cells in clinical specimens. This utility provides a rapid and dependable method by which to identify the causative agent or agents of a bacterial infection. This utility would provide clinicians the ability to accurately identify the species responsible for the infection and amdminister a compound effective against it. In an extension of this utility, antibodies generated against proteins translated from mRNA transcribed from proliferation-required sequences can also be used to screen for specific cells or microorganisms that produce such proteins in a species-specific manner.

Other embodiments of the present invention include methods of identifying compounds which inhibit the activity of gene products required for cellular proliferation using rational drug design. As discussed in more detail below, in such methods, the structure of the gene product is determined using techniques such as x-ray crystallography or computer modeling. Compounds are screened to identify those which have a structure which would allow them to interact with the gene product or a portion thereof to inhibit its activity. The compounds may be obtained using any of a variety of methods familiar to those skilled in the art, including combinatorial chemistry. In some embodiments, the compounds may be obtained from a natural product library. In some embodiments,

compounds having a structure which allows them to interact with the active site of a gene product, such as the active site of an enzyme, or with a portion of the gene product which interacts with another biomolecule to form a complex are identified. If desired, lead compounds may be identified and further optimized to provide compounds which are highly effective against the gene product.

The following examples teach the genes of the present invention and a subset of uses for the genes identified as required for proliferation. These examples are illustrative only and are not intended to limit the scope of the present invention.

EXAMPLES

The following examples are directed to the identification and exploitation of genes required for proliferation. Methods of gene identification are discussed as well as a variety of methods to utilize the identified sequences. It will be appreciated that any of the antisense nucleic acids, proliferartion-required genes or proliferation-required gene products described herein, or portions thereof, may be used in the procedures described below, including the antisense nucleic acids of SEQ ID NOs.: 8-3795, the nucleic acids of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, or the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110. Likewise, homologous coding nucleic acids or portions thereof, may be used in any of the procedures described below.

Genes Identified as Required for Proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis*

Genomic fragments were operably linked to an inducible promoter in a vector and assayed for growth inhibition activity. Example 1 describes the examination of a library of genomic fragments cloned into vectors comprising inducible promoters. Upon induction with xylose or IPTG, the vectors produced an RNA molecule corresponding to the subcloned genomic fragments. In those instances where the genomic fragments were in an antisense orientation with respect to the promoter, the transcript produced was complementary to at least a portion of an mRNA (messenger RNA) encoding a *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* gene product such that they interacted with sense mRNA produced from various *Staphylococcus aureus, Salmonella typhimurium,*

Klebsiella pneumoniae, Pseudomonas aeruginosa or *Enterococcus faecalis* genes and thereby decreased the translation efficiency or the level of the sense messenger RNA thus decreasing production of the protein encoded by these sense mRNA molecules. In cases where the sense mRNA encoded a protein required for proliferation, bacterial cells containing a vector from which transcription from the promoter had been induced failed to grow or grew at a substantially reduced rate. Additionally, in cases where the transcript produced was complementary to at least a portion of a non-translated RNA and where that non-translated RNA was required for proliferation, bacterial cells containing a vector from which transcription from the promoter had been induced also failed to grow or grew at a substantially reduced rate.

EXAMPLE 1

Inhibition of Bacterial Proliferation after Induction of Antisense Expression

Nucleic acids involved in proliferation of *Staphylococcus aureus, Salmonella typhimurium,* and *Klebsiella pneumoniae* were identified as follows. Randomly generated fragments of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* genomic DNA were transcribed from inducible promoters.

In the case of *Staphylococcus aureus,* a novel inducible promoter system, XylT5, comprising a modified T5 promoter fused to the *xylO* operater from the *xylA* promoter of *Staphylococcus aureus* was used. The promoter is described in U.S. Provisional Patent Application Serial Number 60/259,434, the disclosure of which is incorporated herein by reference in its entirety. Transcription from this hybrid promoter is inducible by xylose.

Randomly generated fragments of *Salmonella typhimurium* genomic DNA were transcribed from an IPTG inducible promoter in pLEX5BA (Krause et al., J. Mol. Biol. 274: 365 (1997) or a derivative thereof. Randomly generated fragements of *Klebsiella pneumoniae* genomic DNA were expressed from an IPTG inducible promoter in pLEX5BA-Kan. To construct pLEX5BA-kan, pLEX5BA was digested to completion with *ClaI* in order to remove the *bla* gene. Then the plasmid was treated with a partial *Not*I digestion and blunted with T4 DNA polymerase. A 3.2 kbp fragment was then gel purified and ligated to a blunted 1.3 kbp kan gene from pKanπ. Kan resistant transformants were selected on Kan plates. Orientation of the kan gene was checked by

*Sma*I digestion. A clone, which had the kan gene in the same orientation as the bla gene, was used to identify genes required for proliferation of *Klebsiella pneumoniae*.

Randomly generated fragments of *Pseudomonas aeruginosa* genomic DNA were trancribed from a two-component inducible promoter system. Integrated on the chromosome was the T7 RNA polymerase gene regulated by *lac*UV5/ *lac*O (Brunschwig, E. and Darzins, A. 1992. Gene 111:35-41, the disclosure of which is incorporated herein by reference in its entirety). On a separate plasmid, a T7 gene 10 promoter, which is transcribed by T7 RNA polymerase, was fused with a *lac*O operator followed by a multiple cloning site.

Should the genomic DNA downstream of the promoter contain, in an antisense orientation, at least a portion of an mRNA or a non-translated RNA encoding a gene product involved in proliferation, then induction of transcription from the promoter will result in detectable inhibition of proliferation.

In the case of *Staphylococcus aureus,* a shotgun library of *Staphylococcus aureus* genomic fragments was cloned into the vector pXyIT5-P15a, which harbors the XyIT5 inducible promoter. The vector was linearized at a unique *Bam*HI site immediately downstream of the XyIT5 promoter/operator. The linearized vector was treated with shrimp alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *Staphylococcus aureus* strain RN450 was fully digested with the restriction enzyme *Sau*3A , or , alternatively, partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 0.1 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain XL1-Blue MRF' (Stratagene) and plated on LB medium with supplemented with carbenicillin at 100 μg/ml. Resulting colonies numbering 5 x 10^5 or greater were scraped and combined, and were then subjected to plasmid purification.

The purified library was then transformed into electrocompetent *Staphylococcus aureus* RN4220. Resulting transformants were plated on agar containing LB + 0.2% glucose (LBG medium) + chloramphenicol at 15 μg/ml (LBG+CM15 medium) in order

to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384 well culture dishes. Each well contained 100μl of LBG + CM15 liquid medium. Inoculated 384 well dishes were incubated 16 hours at 37°C, and each well was robotically gridded onto solid LBG + CM15 medium with or without 2% xylose. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of xylose.

Arrayed colonies that were growth-sensitive on medium containing 2% xylose, yet were able to grow on similar medium lacking xylose, were subjected to further growth sensitivity analysis as follows: Colonies from the plate lacking xylose were manually picked and inoculated into individual wells of a 96 well culture dish containing LBG + CM15, and were incubated for 16 hours at 37°C. These cultures were robotically diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilutions in a 384 well array and then gridded onto media containing 2% xylose or media lacking xylose. After growth for 16 hours at 37°C, the arrays that resulted on the two media were compared to each other. Clones that grew similarly at all dilutions on both media were scored as a negative and were no longer considered. Clones that grew on xylose medium but failed to grow at the same serial dilution on the non-xylose plate were given a score based on the differential, i.e. should the clone grow at a serial dilution of 10^4 or less on the xylose plate and grow at a serial dilution of 10^8 or less on the non-xylose plate, then the corresponding clone received a score of "4" representing the log difference in growth observed.

For *Salmonella typhimurium* and *Klebsiella pneumoniae* growth curves were carried out by back diluting cultures 1:200 into fresh media containing 1 mM IPTG or media lacking IPTG and measuring the OD_{450} every 30 minutes (min). To study the effects of transcriptional induction on solid medium, 10^2, 10^3, 10^4, 10^5, 10^6, 10^7 and 10^8 fold dilutions of overnight cultures were prepared. Aliquots of from 0.5 to 3 μl of these dilutions were spotted on selective agar plates with or without 1 mM IPTG. After overnight incubation, the plates were compared to assess the sensitivity of the clones to IPTG.

Nucleic acids involved in proliferation of *Pseudomonas aeruginosa* were identified as follows. Randomly generated fragments of *Pseudomonas aeruginosa* genomic DNA were transcribed from a two-component inducible promoter system. Integrated on the chromosome was the T7 RNA polymerase gene regulated by *lac*UV5/ *lac*O (Brunschwig, E. and Darzins, A. 1992. Gene 111:35-41). On an expression plasmid there was a T7 gene 10 promoter, which is transcribed by T7 RNA polymerase, fused with a *lac*O operator followed by a multiple cloning site. Transcription from this hybrid promoter is inducible by IPTG. Should the genomic DNA downstream of the promoter contain, in an antisense orientation, at least a portion of an mRNA encoding a gene product involved in proliferation, then induction of expression from the promoter will result in detectable inhibition of proliferation.

A shotgun library of *Pseudomonas aeruginosa* genomic fragments was cloned into the vectors pEP5, pEP5S, or other similarly constructed vectors which harbor the T7*lac*O inducible promoter. The vector was linearized at a unique *Sma*I site immediately downstream of the T7*lac*O promoter/operator. The linearized vector was treated with shrimp alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *Pseudomonas aeruginosa* strain PAO1 was partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 2 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain XL1-Blue MRF' (Stratagene) and plated on LB medium with carbenicillin at 100 μg/ml or Streptomycin 100 μg/ml. Resulting colonies numbering 5 x 10^5 or greater were scraped and combined, and were then subjected to plasmid purification.

The purified library was then transformed into electrocompetent *Pseudomonas aeruginosa* strain PAO1. Resulting transformants were plated on LB agar with carbenicillin at 100 μg/ml or Streptomycin 40 μg/ml in order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384 well culture dishes. Each well contained 100 μl of LB + CB 100 or Streptomycin 40 liquid medium. Inoculated 384 well dishes were incubated 16 hours at room temperature, and each well was robotically gridded onto solid LB +

CB100 or Streptomycin 40 medium with or without 1 mM IPTG. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of IPTG.

Arrayed colonies that were growth-sensitive on medium containing 1 mM IPTG, yet were able to grow on similar medium lacking IPTG, were subjected to further growth sensitivity analysis as follows: Colonies from the plate lacking IPTG were manually picked and inoculated into individual wells of a 96 well culture dish containing LB + CB100 or Streptomycin 40, and were incubated for 16 hours at 30°C. These cultures were robotically diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilutions in a 384 well array and then gridded onto media with and without 1 mM IPTG. After growth for 16 hours at 37°C, the arrays of serially diluted spots that resulted were compared between the two media. Clones that grew similarly at all dilutions on both media were scored as a negative and were no longer considered. Clones that grew on IPTG medium but failed to grow at the same serial dilution on the non-IPTG plate were given a score based on the differential, i.e. should the clone grow at a serial dilution of 10^4 or less on the IPTG plate and grow at a serial dilution of 10^8 or less on the IPTG plate, then the corresponding clone received a score of "4" representing the log difference in growth observed.

Following the identification of those vectors that, upon induction, negatively impacted *Pseudomonas aeruginosa* growth or proliferation, the inserts or nucleic acid fragments contained in those vectors were isolated for subsequent characterization. Vectors of interest were subjected to nucleic acid sequence determination.

Nucleic acids involved in proliferation of *E. faecalis* were identified as follows. Randomly generated fragments of genomic DNA were expressed from the vectors pEPEF3 or pEPEF14, which contain the CP25 or P59 promoter, respectively, regulated by the xyl operator/repressor. Should the genomic DNA downstream of the promoter contain, in an antisense orientation, at least a portion of a mRNA encoding a gene product involved in proliferation, then induction of expression from the promoter will result in detectable inhibition of proliferation.

A shotgun library of *E. faecalis* genomic fragments was cloned into the vector pEPEF3 or pEPEF14, which harbor xylose inducible promoters. The vector was

linearized at a unique *Sma*I site immediately downstream of the promoter/operator. The linearized vector was treated with alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *E. faecalis* strain OG1RF was partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 2 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain TOP10 cells (Invitrogen) and plated on LB medium with erythromycin (Erm) at 150 µg/ml. Resulting colonies numbering 5 x 10^5 or greater were scraped and combined, and were then subjected to plasmid purification.

The purified library was then transformed into electrocompetent *E. faecalis* strain OG1RF. Resulting transformants were plated on Todd-Hewitt (TH) agar with erythromycin at 10 µg/ml in order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384 well culture dishes. Each well contained 100 µl of THB + Erm 10 µg/ml. Inoculated 384 well dishes were incubated 16 hours at room temperature, and each well was robotically gridded onto solid TH agar + Erm with or without 5% xylose. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of xylose.

Arrayed colonies that were growth-sensitive on medium containing 5% xylose, yet were able to grow on similar medium lacking xylose, were subjected to further growth sensitivity analysis. Colonies from the plate lacking xylose were manually picked and inoculated into individual wells of a 96 well culture dish containing THB + Erm 10, and were incubated for 16 hours at 30°C. These cultures were robotically diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilution on plates containing 5% xylose or plates lacking xylose. After growth for 16 hours at 37°C, the arrays of serially diluted spots that resulted were compared between the two media. Colonies that grew similarly on both media were scored as a negative and corresponding colonies were no longer considered. Colonies on xylose medium that failed to grow to the same serial dilution compared to those on the non-xylose plate were given a score based on the differential.

For example, colonies on xylose medium that only grow to a serial dilution of -4 while they were able to grow to -8 on the non-xylose plate, then the corresponding transformant colony received a score of "4" representing the log difference in growth observed.

Following the identification of those vectors that, upon induction, negatively impacted *E. faecalis* growth or proliferation, the inserts or nucleic acid fragments contained in those expression vectors were isolated for subsequent characterization. The inserts in the vectors of interest were subjected to nucleotide sequence determination.

It will be appreciated that other restriction enzymes and other endonucleases or methodologies may be used to generate random genomic fragments. In addition, random genomic fragments may be generated by mechanical shearing. Sonication and nebulization are two such techniques commonly used for mechanical shearing of DNA.

EXAMPLE 2

<u>Nucleotide Sequence Determination of Identified Clones Transribing Nucleic Acid Fragments with Detrimental Effects on *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* Proliferation</u>

Plasmids from clones that received a dilution plating score of "2" or greater were isolated to obtain the genomic DNA insert responsible for growth inhibition as follows. *Staphylococcus aureus* were grown in standard laboratory media (LB or TB with 15 ug/ml Chloramphenicol to select for the plasmid). Growth was carried out at 37°C overnight in culture tubes or 2 ml deep well microtiter plates.

Lysis of *Staphylococcus aureus* was performed as follows. Cultures (2-5 ml) were centrifuged and the cell pellets resuspended in 1.5 mg/ml solution of lysostaphin (20 µl/ml of original culture) followed by addition of 250 µl of resuspension buffer (Qiagen). Alternatively, cell pellets were resuspended directly in 250 µl of resuspension buffer (Qiagen) to which 5-20 µl of a 1 mg/ml lysostaphin solution were added.

DNA was isolated using Qiagen miniprep kits or Wizard (Qiagen) miniprep kits according to the instructions provided by the manufacturer.

The genomic DNA inserts were amplified from the purified plasmids by PCR as follows.

1 µl of Qiagen purified plasmid was put into a total reaction volume of 25 µl Qiagen Hot Start PCR mix. For *Staphylococcus aureus,* the following primers were used in the PCR reaction:

pXylT5F: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 1)

LexL TGTTTTATCAGACCGCTT (SEQ ID NO: 2)

Similar methods were conducted for *Salmonella typhimurium* and *Klebsiella pneumoniae.* For *Salmonella typhimurium* and *Klebsiella pneumoniae* the following primers were used:

5' - TGTTTTATCAGACCGCTT - 3' (SEQ ID NO: 2) and

5'-ACAATTTCACACAGCCTC-3' (SEQ ID NO: 4)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 95° C 15 min

Step 2. 94° C 45 sec

Step 3. 54° C 45 sec

Step 4. 72° C 1 minute

Step 5. Return to step 2, 29 times

Step 6. 72° C 10 minutes

Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

For *Pseudomonas aeruginosa,* plasmids from transformant colonies that received a dilution plating score of "2" or greater were isolated to obtain the genomic DNA insert responsible for growth inhibition as follows. *Pseudomonas aeruginosa* were grown in standard laboratory media (LB with carbenicillin at 100 µg/ml or Streptomycin 40 µg/ml to select for the plasmid). Growth was carried out at 30°C overnight in 100 ul culture wells in microtiter plates. To amplify insert DNA 2 ul of culture were placed into 25 ul Qiagen Hot Start PCR mix. PCR reactions were in 96 well microtiter plates. For plasmid pEP5S the following primers were used in the PCR reaction:

T7L1+: GTCGGCGATATAGGCGCCAGCAACCG (SEQ ID NO: 5)

pStrA3: ATAATCGAGCATGAGTATCATACG (SEQ ID NO: 6)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 95° C 15 min

Step 2. 94° C 45 sec

Step 3. 54° C 45 sec

Step 4. 72° C 1 minute

Step 5. Return to step 2, 29 times

Step 6. 72° C 10 minutes

Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

The purified PCR products were then directly cycle sequenced with Qiagen Hot Start PCR mix. The following primers were used in the sequencing reaction:

T7/L2: ATGCGTCCGGCGTAGAGGAT (SEQ ID NO: 7)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 94° C 15 min

Step 2. 96° C 10 sec

Step 3. 50° C 5 sec

Step 4. 60 C 4 min

Step 5. Return to step 2, 24 times

Step 6. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

For *E. faecalis*, plasmids from transformant colonies that received a dilution plating score of "2" or greater were isolated to obtain the genomic DNA insert responsible for growth inhibition as follows. *E. faecalis* were grown in THB 10 μg/ml Erm at 30°C overnight in 100 ul culture wells in microtiter plates. To amplify insert DNA 2 ul of culture were placed into 25 μl Qiagen Hot Start PCR mix. PCR reactions were in 96 well microtiter plates. The following primers were used in the PCR reaction:

pXylT5: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 1) and the pEP/pAK1 primer.

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 95° C 15 min

Step 2. 94° C 45 sec

Step 3. 54° C 45 sec

Step 4. 72° C 1 minute

Step 5. Return to step 2, 29 times

Step 6. 72° C 10 minutes

Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

The purified PCR products were then directly cycle sequenced with Qiagen Hot Start PCR mix. The following primers were used in the PCR reaction:

pXylT5: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 1)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 94° C 15 min

Step 2. 96° C 10 sec

Step 3. 50° C 5 sec

Step 4. 60° C 4 min

Step 5. Return to step 2, 24 times

Step 6. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

The amplified genomic DNA inserts from each of the above procedures were subjected to automated sequencing. Sequence identification numbers (SEQ ID NOs) and clone names for the identified inserts are listed in Table IA and discussed below.

EXAMPLE 3

Comparison Of Isolated Nucleic Acids to Known Sequences

The nucleotide sequences of the subcloned fragments from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* obtained from the expression vectors discussed above were compared to known sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* and other microorganisms as follows. First, to confirm that each clone originated from one

location on the chromosome and was not chimeric, the nucleotide sequences of the selected clones were compared against the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* genomic sequences to align the clone to the correct position on the chromosome. The NCBI BLASTN v 2.0.9 program was used for this comparison, and the incomplete *Staphylococcus aureus* genomic sequences licensed from TIGR, as well as the NCBI nonredundant GenBank database were used as the source of genomic data. *Salmonella typhimurium* sequences were compared to sequences available from the Genome Sequencing Center (http://genome.wustl.edu/gsc/salmonella.shtml), and the Sanger Centre (http://www.sanger.ac.uk/projects/S___typhi). *Pseudomonas aeruginosa* sequences were compared to a proprietary database and the NCBI GenBank database. The *E. faecalis* sequences were compared to a proprietary database.

The BLASTN analysis was performed using the default parameters except that the filtering was turned off. No further analysis was performed on inserts which resulted from the ligation of multiple fragments.

In general, antisense molecules and their complementary genes are identified as follows. First, all possible full length open reading frames (ORFs) are extracted from available genomic databases. Such databases include the GenBank nonredundant (nr) database, the unfinished genome database available from TIGR and the PathoSeq database developed by Incyte Genomics. The latter database comprises over 40 annotated bacterial genomes including complete ORF analysis. If databases are incomplete with regard to the bacterial genome of interest, it is not necessary to extract all ORFs in the genome but only to extract the ORFs within the portions of the available genomic sequences which are complementary to the clones of interest. Computer algorithms for identifying ORFs, such as GeneMark, are available and well known to those in the art. Comparison of the clone DNA to the complementary ORF(s) allows determination of whether the clone is a sense or antisense clone. Furthermore, each ORF extracted from the database can be compared to sequences in well annotated databases including the GenBank (nr) protein database, SWISSPROT and the like. A description of the gene or of a closely related gene in a closely related microorganism is often available in these databases. Similar methods are used to identify antisense clones corresponding to genes encoding non-translated RNAs.

In order to generate the gene identification data compiled in Table IB, each of the cloned nucleic acid sequences discussed above corresponding to SEQ ID NO.s 8-3795 was used to identify the corresponding *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* ORFs in the PathoSeq v.4.1 (March 2000 release) database of microbial genomic sequences. For this purpose, the NCBI BLASTN 2.0.9 computer algorithm was used. The default parameters were used except that filtering was turned off. The default parameters for the BLASTN and BLASTX analyses were:

Expectation value (e)=10
Alignment view options: pairwise
Filter query sequence (DUST with BLASTN, SEG with others)=T
Cost to open a gap (zero invokes behavior)=0
Cost to extend a gap (zero invokes behavior)=0
X dropoff value for gapped alignment (in bits) (zero invokes behavior)=0
Show GI's in deflines=F
Penalty for a nucleotide mismatch (BLASTN only)=!3
Reward for a nucleotide match (BLASTN only)=1
Number of one-line descriptions (V)=500
Number of alignments to show (B)=250
Threshold for extending hits=default
Perform gapped alignment (not available with BLASTX)=T
Query Genetic code to use=1
DB Genetic code (for TBLAST[nx] only=1
Number of processors to use=1
SeqAlign file
Believe the query defline=F
Matrix=BLOSUM62
Word Size= default
Effective length of the database (use zero for the real size)=0
Number of best hits from a region to keep=100
Length of region used to judge hits=20
Effective length of the search space (use zero for the real size)=0
Query strands to search against database (for BLAST[nx] and TBLASTX), 3 is both, 1 is top, 2 is bottom=3
Produce HTML output=F

Alternatively, ORFs were identified and refined by conducting a survey of the public and private data sources. Full-length gene protein and nucleotide sequences for these organisms were assembled from various sources. For *Pseudomonas aeruginosa*, gene sequences were adopted from the Pseudomonas genome sequencing project (downloaded from http://www.pseudomonas.com). For *Klebsiella pneumoniae, Staphylococcus aureus, Streptococcus pneumoniae* and *Salmonella typhi,* genomic

sequences from PathoSeq v 4.1 (Mar 2000 release) was reanalyzed for ORFs using the gene finding software GeneMark v 2.4a, which was purchased from GenePro Inc. 451 Bishop St., N.W., Suite B, Atlanta, GA, 30318, USA.

Antisense clones were identified as those clones for which transcription from the inducible promoter would result in the expression of an RNA antisense to a complementary ORF, intergenic or intragenic sequence. Those clones containing single inserts and that caused growth sensitivity upon induction are listed in Table IA. ORFs complementary to the antisense nucleic acids, and their encoded polypeptides, are listed in Table IB.

The gene descriptions in the PathoSeq database derive from annotations available in the public sequence databases described above. Where a clone was found to share significant sequence identity to two or more adjacent ORFs, it was listed once for each ORF and the PathoSeq information for each ORF was compiled in Table IB.

Table IA lists the SEQ ID NOs. and clone names of the inserts which inhibited proliferation and the organism in which the clone was identified. This information was used to identify the ORFs (SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012) whose gene products (SEQ ID NOs. 3801-3805, 4861-5915, 10013-14110) were inhibited by the nucleic acids comprising the nucleotide sequences of SEQ ID NOs. 8-3795. Table IB lists the clone name, the SEQ ID NO. of the antisense clone (in the column labelled Clone SEQ ID), the PathoSeq Locus containing the clone, the SEQ ID of the ORF identified in PathoSeq (in the column labelled Gene Seq ID (protein), the refined full length gene (column labelled genemarked gene), and the SEQ ID NO of the protein encoded by the refined full length gene (column labelled full length ORF protein SEQ ID).

Table IC provides a cross reference between PathoSeq Gene Locus listed in Table IB, the SEQ ID NOs. of the PathoSeq proteins and the SEQ ID NOs. of the nucleic acids which encode them.

It will be appreciated that ORFs may also be identified using databases other than PathoSeq. For example, the ORFs may be identified using the methods described in U.S. Provisional Patent Application Serial Number 60/191,078, filed March 21, 2000, the disclosure of which is incorporated herein by reference in its entirety.

EXAMPLE 4

Identification of Genes and their Corresponding Operons Affected by Antisense Inhibition

Once the genes involved in *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* proliferation are identified as described above, the operons in which these genes lie may be identified by comparison with known microbial genomes. Since bacterial genes are transcribed in a polycistronic manner, the antisense inhibition of a single gene in an operon might affect the expression of all the other genes on the operon or the genes downstream from the single gene identified. Accordingly, each of the genes contained within an operon may be analyzed for their effect on proliferation.

Operons are predicted by looking for all adjacent genes in a genomic region that lie in the same orientation with no large noncoding gaps in between. First, full-length ORFs complementary to the antisense molecules are identified as described above. Adjacent ORFs are then identified and their relative orientation determined either by directly analyzing the genomic sequences surrounding the ORFs complementary to the antisense clones or by extracting adjacent ORFs from the collection obtained through whole genome ORF analysis described above followed by ORF alignment. Operons predicted in this way may be confirmed by comparison to the arrangement of the homologous nucleic acids in the *Bacillus subtilis* complete genome sequence, as reported by the genome database compiled at Institut Pasteur Subtilist Release R15.1 (June 24, 1999) which can be found at http://bioweb.pasteur.fr/GenoList/SubtiList/. The *Bacillus subtilis* genome is the only fully sequenced and annotated genome from a Gram-positive microorganism, and appears to have a high level of similarity to *Staphylococcus aureus* both at the level of conservation of gene sequence and genomic organization including operon structure. Operons for *Salmonella typhimurium* and *Klebsiella pneumoniae* may be identified by comparison with *E. coli, Haemophilus,* or *Pseudomonas* sequences. The *Pseudomonas aeruginosa* web site (http://www.pseudomonas.com) can also be used to help predict operon organization in this bacterium.

Extensive DNA sequences of *Salmonella typhimurium* are available through the Salmonella Genome Center (Washington University, St. Louis, MO) the Sanger Centre (United Kingdom) and the PathoSeq database (Incyte). Annotation of some of the

DNA sequences in some of the aforementioned databases is lacking, but comparisons may be made to *E. coli* using tools such as BLASTX.

Public or proprietary databases may be used to analyzed *E. faecalis* sequences as well as sequences from the organisms listed above.

The results of such an analysis as applied to clone number S1M10000001A05 from *Staphylococcus aureus* are listed in Table II. Table II lists the SEQ ID NOs. of the *Staphylococcus aureus* genes involved in proliferation, the SEQ ID NOs. of the proteins encoded by these genes, and the clone name containing the nucleic acid which inhibits *Staphylococcus aureus* proliferation. In addition, Table II lists those other genes located on the operon included in the *Staphylococcus aureus* genomic sequence determined as described above. For each of the genes described in Table II, the microorganism containing the most closely related homolog, identified in one of the public databases, is also indicated in Table II.

TABLE II

DNA Seq ID	Protein Seq ID	Molecule number	Clone name	Gene	Organism used for identification of gene
3796	3801	SaXA001	S1M10000001A05	ytmI	*B. subtilis*
3797	3802			nirR	*S. carnosus*
3798	3803			nirB	*S. carnosus*
3799	3804			nirD	*S. carnosus*
3800	3805			sirB	*S. carnosus*

The preceding analyses may be conducted for each of the sequences which are listed in Table IA which inhibit proliferation and the ORFs listed in Table IB and Table IC. Once the full length ORFs and/or the operons containing them have been identified using the methods described above, they can be obtained from a genomic library by performing a PCR amplification using primers at each end of the desired sequence. Those skilled in the art will appreciate that a comparison of the ORFs to homologous sequences in other cells or microorganisms will facilitate confirmation of the start and stop codons at the ends of the ORFs.

In some embodiments, the primers may contain restriction sites which facilitate the insertion of the gene or operon into a desired vector. For example, the gene may be inserted into an expression vector and used to produce the proliferation-required protein

as described below. Other methods for obtaining the full length ORFs and/or operons are familiar to those skilled in the art. For exmaple, natural restriction sites may be employed to insert the full length ORFs and/or operons into a desired vector.

EXAMPLE 5

Identification of Individual Genes within an Operon Required for Proliferation

The following example illustrates a method for determining if a targeted gene within an operon is required for cell proliferation by replacing the targeted allele in the chromosome with an in-frame deletion of the coding region of the targeted gene.

Deletion inactivation of a chromosomal copy of a gene in *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* can be accomplished by integrative gene replacement. The principles of this method were described in Xia, M., et al. 1999 Plasmid 42:144-149 and Hamilton, C. M., et al 1989. *J. Bacteriol.* **171**: 4617-4622, the disclosures of which are incorporated herein by reference in their entireties. A similar gene disruption method is available for *Pseudomonas aeruginosa*, except the counter selectable marker is *sacB* (Schweizer, H. P., Klassen, T. and Hoang, T. (1996) Mol. Biol. of *Pseudomonas*. ASM press, 229-237, the disclosure of which is incorporated herein by reference in its entirety). In this approach, a mutant allele of the targeted gene is constructed by way of an in-frame deletion and introduced into the chromosome using a suicide vector. This results in a tandem duplication comprising a deleted (null) allele and a wild type allele of the target gene. Cells in which the vector sequences have been deleted are isolated using a counter-selection technique. Removal of the vector sequence from the chromosomal insertion results in either restoration of the wild-type target sequence or replacement of the wild type sequence with the deletion (null) allele. *E. faecalis* genes can be disrupted using a suicide vector that contains an internal fragment to a gene of interest. With the appropriate selection this plasmid will homologously recombine into the chromosome (Nallapareddy, S. R., X. Qin, G. M. Weinstock, M. Hook, B. E. Murray. 2000. Infect. Immun. 68:5218-5224, the disclosure of which is incorporated herein by reference).

The resultant population of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia*

coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, or *Salmonella typhi* colonies can then be evaluated to determine whether the target sequence is required for proliferation by PCR amplification of the affected target sequence. If the targeted gene is not required for proliferation, then PCR analysis will show that roughly equal numbers of colonies have retained either the wild-type or the mutant allele. If the targeted gene is required for proliferation, then only wild-type alleles will be recovered in the PCR analysis.

The method of cross-over PCR is used to generate the mutant allele by amplification of nucleotide sequences flanking but not including the coding region of the gene of interest, using specifically designed primers such that overlap between the resulting two PCR amplification products allows them to hybridize. Further PCR amplification of this hybridization product using primers representing the extreme 5' and 3' ends can produce an amplification product containing an in-frame deletion of the coding region but retaining substantial flanking sequences.

For *Staphylococcus aureus,* this amplification product is subcloned into the suicide vector pSA3182 (Xia, M., et al. 1999 Plasmid 42:144-149, the disclosure of which is incorporated herein by reference in its entirety) which is host-dependent for autonomous replication. This vector includes a *tetC* tetracycline-resistance marker and the origin of replication of the well-known *Staphylococcus aureus* plasmid pT181 (Mojumdar, M and Kahn, S.A., Characterisation of the Tetracycline Resistance Gene of Plasmid pT181, J. Bacteriol. 170: 5522 (1988), the disclosure of which is incorporated herein by reference in its entirety). The vector lacks the *repC* gene which is required for autonomous replication of the vector at the pT181 origin. This vector can be propagated in a *Staphylococcus aureus* host strain such as SA3528, which expresses *repC* in trans. Once the amplified truncated target gene sequence is cloned and propagated in the pSA3182 vector, it can then be introduced into a *repC* minus strain such as RN4220 (Kreiswirth, B.N. et al., The Toxic Shock Syndrome Exotoxin Structural Gene is Not Detectably Transmitted by a Prophage, Nature 305:709-712 (1983), the disclosure of which is incorporated herein by reference in its entirety) by electroporation with selection for tetracycline resistance. In this strain, the vector must integrate by homologous recombination at the targeted gene in the chromosome to impart drug resistance. This results in a inserted truncated copy of the allele, followed

by pSA3182 vector sequence, and finally an intact and functional allele of the targeted gene.

Once a tetracycline resistant *Staphylococcus aureus* strain is isolated using the above technique and shown to include truncated and wild-type alleles of the targeted gene as described above, a second plasmid, pSA7592 (Xia, M., et al. 1999 Plasmid 42:144-149, the disclosure of which is incorporated herein by reference in its entirety) is introduced into the strain by electroporation. This gene includes an erythromycin resistance gene and a *repC* gene that is expressed at high levels. Expression of *repC* in these transformants is toxic due to interference of normal chromosomal replication at the integrated pT181 origin of replication. This selects for strains that have removed the vector sequence by homologous recombination, resulting in either of two outcomes: The selected cells either possess a wild-type allele of the targeted gene or a gene in which the wild-type allele has been replaced by the engineered in-frame deletion of the truncated allele.

PCR amplification can be used to determine the genetic outcome of the above process in the resulting erythromycin resistant, tet sensitive transformant colonies. If the targeted gene is not required for cellular replication, then PCR evidence for both wild-type and mutant alleles will be found among the population of resultant transformants. However, if the targeted gene is required for cellular proliferation, then only the wild-type form of the gene will be evident among the resulting transformants.

Similarly, for *Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* the PCR products containing the mutant allele of the target sequence may be introduced into an appropriate knockout vector and cells in which the wild type target has been disrupted are selected using the appropriate methodology.

The above methods have the advantage that insertion of an in-frame deletion mutation is far less likely to cause downstream polar effects on genes in the same operon as the targeted gene. However, it will be appreciated that other methods for disrupting *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus*

faecalis, Haemophilus influenzae, Helicobacter pylori, or *Salmonella typhi* genes which are familiar to those skilled in the art may also be used.

Each gene in the operon may be disrupted using the methodology above to determine whether it is required for proliferation.

EXAMPLE 6

Expression of the Proteins Encoded by Genes Identified as Required for *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* Proliferation

The following is provided as one exemplary method to express the proliferation-required proteins idenfied as described above. The proliferation-required proteins may be expressed using any of the bacterial, insect, yeast, or mammalian expression systems known in the art. In some embodiments, the proliferation-required proteins encoded by the identified nucleotide sequences described above (including the proteins of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 encoded by the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 are expressed using expression systems designed either for *E. coli* or for *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* . First, the initiation and termination codons for the gene are identified. If desired, methods for improving translation or expression of the protein are well known in the art. For example, if the nucleic acid encoding the polypeptide to be expressed lacks a methionine codon to serve as the initiation site, a strong Shine-Delgarno sequence, or a stop codon, these nucleotide sequences can be added. Similarly, if the identified nucleic acid lacks a transcription termination signal, this nucleotide sequence can be added to the construct by, for example, splicing out such a sequence from an appropriate donor sequence. In addition, the coding sequence may be operably linked to a strong constitutive promoter or an inducible promoter if desired. The identified nucleic acid or portion thereof encoding the polypeptide to be expressed is obtained by, for example, PCR from the bacterial expression vector or genome using oligonucleotide primers complementary to the identified nucleic acid or portion thereof and containing restriction endonuclease sequences appropriate for inserting the coding sequences into the vector such that the

coding sequences can be expressed from the vector's promoter. Alternatively, other conventional cloning techniques may be used to place the coding sequence under the control of the promoter. In some embodiments, a termination signal may be located downstream of the coding sequence such that transcription of the coding sequence ends at an appropriate position.

Several expression vector systems for protein expression in *E. coli* are well known and available to those knowledgeable in the art. The coding sequence may be inserted into any of these vectors and placed under the control of the promoter. The expression vector may then be transformed into DH5α or some other *E. coli* strain suitable for the over expression of proteins.

Alternatively, an expression vector encoding a protein required for proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae,Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* may be introduced into *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa,Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* . Protocols for introducing nucleic acids into these organisms are well known in the art. For example, the protocols described in J.C.Lee "Electroporation of Staphylococci" from Methods in Molecular Biology vol 47: Electroporation Protocols for Microorganisms Edited by : J.A. Nickoloff Humana Press Inc., Totowa, NJ. pp209-216, the disclosure of which is incorporated herein by reference in its entirety, may be used to introduce nucleic acids into *Staphylococcus aureus*. Nucleic acids may also be introduced into *Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* using methods familiar to those skilled in the art. Positive transformants are selected after growing the transformed cells on plates containing an antibiotic to which the vector confers resistance. In one embodiment, *Staphylococcus aureus* is transformed with an expression vector in which the coding sequence is operably linked to the T5 promoter containing a xylose operator such that expression of the encoded protein is inducible with xylose.

In one embodiment, the protein is expressed and maintained in the cytoplasm as the native sequence. In an alternate embodiment, the expressed protein can be modified

to include a protein tag that allows for differential cellular targeting, such as to the periplasmic space of Gram-negative or Gram-positive expression hosts or to the exterior of the cell (i.e., into the culture medium). In some embodiments, the osmotic shock cell lysis method described in Chapter 16 of **Current Protocols in Molecular Biology,** Vol. 2, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997) may be used to liberate the polypeptide from the cell. In still another embodiment, such a protein tag could also facilitate purification of the protein from either fractionated cells or from the culture medium by affinity chromatography. Each of these procedures can be used to express a proliferation-required protein.

Expressed proteins, whether in the culture medium or liberated from the periplasmic space or the cytoplasm, are then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, standard chromatography, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the polypeptide may be secreted from the host cell in a sufficiently enriched or pure state in the supernatant or growth media of the host cell to permit it to be used for its intended purpose without further enrichment. The purity of the protein product obtained can be assessed using techniques such as SDS PAGE, which is a protein resolving technique well known to those skilled in the art. Coomassie, silver staining or staining with an antibody are typical methods used to visualize the protein of interest.

Antibodies capable of specifically recognizing the protein of interest can be generated using synthetic peptides using methods well known in the art. See, **Antibodies: A Laboratory Manual**, (Harlow and Lane, Eds.) Cold Spring Harbor Laboratory (1988). For example, 15-mer peptides having an amino acid sequence encoded by the appropriate identified gene sequence of interest or portion thereof can be chemically synthesized. The synthetic peptides are injected into mice to generate antibodies to the polypeptide encoded by the identified nucleic acid sequence of interest or portion thereof. Alternatively, samples of the protein expressed from the expression vectors discussed above can be purified and subjected to amino acid sequencing analysis to confirm the identity of the recombinantly expressed protein and subsequently used to raise antibodies. An Example describing in detail the generation of monoclonal and polyclonal antibodies appears in Example 7.

The protein encoded by the identified nucleic acid of interest or portion thereof can be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically-bound secreted protein is then released from the column and recovered using standard techniques. These procedures are well known in the art.

In an alternative protein purification scheme, the identified nucleic acid of interest or portion thereof can be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the coding sequence of the identified nucleic acid of interest or portion thereof is inserted in-frame with the gene encoding the other half of the chimera. The other half of the chimera can be maltose binding protein (MBP) or a nickel binding polypeptide encoding sequence. A chromatography matrix having maltose or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites can be engineered between the MBP gene or the nickel binding polypeptide and the identified expected gene of interest, or portion thereof. Thus, the two polypeptides of the chimera can be separated from one another by protease digestion.

One useful expression vector for generating maltose binding protein fusion proteins is pMAL (New England Biolabs), which encodes the *malE* gene. In the pMal protein fusion system, the cloned gene is inserted into a pMal vector downstream from the *malE* gene. This results in the expression of an MBP-fusion protein. The fusion protein is purified by affinity chromatography. These techniques as described are well known to those skilled in the art of molecular biology.

EXAMPLE 7

Production of an Antibody to an isolated *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa ,Enterococcus faecalis,Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* Protein

Substantially pure protein or polypeptide (including one of the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) is isolated from the transformed cells as described in Example 6. The concentration of protein in the final preparation is adjusted, for example, by concentration on a 10,000 molecular weight cut off AMICON filter device (Millipore, Bedford, MA), to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., **Nature 256**:495 (1975) or any of the well-known derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody-producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells are destroyed by growth of the system on selective medium comprising aminopterin (HAT medium). The successfully-fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as described by Engvall, E., "Enzyme immunoassay ELISA and EMIT," **Meth. Enzymol. 70**:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. **Basic Methods in Molecular Biology** Elsevier, New York. Section 21-2.

Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogeneous epitopes of a single protein or a peptide can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than larger molecules and can require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and

dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. **J. Clin. Endocrinol. Metab. 33**:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. et al., Chap. 19 in: **Handbook of Experimental Immunology** D. Wier (ed) Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μM). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: **Manual of Clinical Immunology**, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies can also be used in therapeutic compositions for killing bacterial cells expressing the protein.

EXAMPLE 8

Screening Chemical Libraries

A. Protein-Based Assays

Having isolated and expressed bacterial proteins shown to be required for bacterial proliferation, the present invention further contemplates the use of these expressed target proteins in assays to screen libraries of compounds for potential drug candidates. The generation of chemical libraries is well known in the art. For example, combinatorial chemistry can be used to generate a library of compounds to be screened in the assays described herein. A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building block" reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining amino acids in every possible combination to yield peptides of a given length. Millions of chemical compounds theoretically can be synthesized through such combinatorial mixings of

chemical building blocks. For example, one commentator observed that the systematic, combinatorial mixing of 100 interchangeable chemical building blocks results in the theoretical synthesis of 100 million tetrameric compounds or 10 billion pentameric compounds. (Gallop et al., "Applications of Combinatorial Technologies to Drug Discovery, Background and Peptide Combinatorial Libraries," **Journal of Medicinal Chemistry**, Vol. 37, No. 9, 1233-1250 (1994). Other chemical libraries known to those in the art may also be used, including natural product libraries.

Once generated, combinatorial libraries can be screened for compounds that possess desirable biological properties. For example, compounds which may be useful as drugs or to develop drugs would likely have the ability to bind to the target protein identified, expressed and purified as discussed above. Further, if the identified target protein is an enzyme, candidate compounds would likely interfere with the enzymatic properties of the target protein. For example, the enzymatic function of a target protein may be to serve as a protease, nuclease, phosphatase, dehydrogenase, transporter protein, transcriptional enzyme, and any other type of enzyme known or unknown. Thus, the present invention contemplates using the protein products described above to screen combinatorial chemical libraries.

In one example, the target protein is a serine protease and the substrate of the enzyme is known. The present example is directed towards the analysis of libraries of compounds to identify compounds that function as inhibitors of the target enzyme. First, a library of small molecules is generated using methods of combinatorial library formation well known in the art. U.S. Patent Nos. 5,463,564 and 5,574, 656, to Agrafiotis, et al., entitled "System and Method of Automatically Generating Chemical Compounds with Desired Properties," the disclosures of which are incorporated herein by reference in their entireties, are two such teachings. Then the library compounds are screened to identify those compounds that possess desired structural and functional properties. U.S. Patent No. 5,684,711, the disclosure of which is incorporated herein by reference in its entirety, also discusses a method for screening libraries.

To illustrate the screening process, the target polypeptide and chemical compounds of the library are combined with one another and permitted to interact with one another. A labeled substrate is added to the incubation. The label on the substrate is such that a detectable signal is emitted from the products of the substrate molecules that result from

the activity of the target polypeptide. The emission of this signal permits one to measure the effect of the combinatorial library compounds on the enzymatic activity of target enzymes by comparing it to the signal emitted in the absence of combinatorial library compounds. The characteristics of each library compound are encoded so that compounds demonstrating activity against the enzyme can be analyzed and features common to the various compounds identified can be isolated and combined into future iterations of libraries.

Once a library of compounds is screened, subsequent libraries are generated using those chemical building blocks that possess the features shown in the first round of screen to have activity against the target enzyme. Using this method, subsequent iterations of candidate compounds will possess more and more of those structural and functional features required to inhibit the function of the target enzyme, until a group of enzyme inhibitors with high specificity for the enzyme can be found. These compounds can then be further tested for their safety and efficacy as antibiotics for use in mammals.

It will be readily appreciated that this particular screening methodology is exemplary only. Other methods are well known to those skilled in the art. For example, a wide variety of screening techniques are known for a large number of naturally-occurring targets when the biochemical function of the target protein is known. For example, some techniques involve the generation and use of small peptides to probe and analyze target proteins both biochemically and genetically in order to identify and develop drug leads. Such techniques include the methods described in PCT publications No. WO9935494, WO9819162, WO9954728, the disclosures of which are incorporated herein by reference in their entireties. Other techniques utilize natural product libraries or libraries of larger molecules such as proteins.

It will be appreciated that the above protein-based assays may be performed with any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) or portions thereof. In addition, the above protein-based assays may be performed with homologous polypeptides or portions thereof.

B. <u>Cell-Based Assays</u>

Current cell-based assays used to identify or to characterize compounds for drug discovery and development frequently depend on detecting the ability of a test compound to modulate the activity of a target molecule located within a cell or located on the surface of a cell. An advantage of cell-based assays is that they allow the effect of a compound on a target molecule's activity to be detected within the physiologically relevant environment of the cell as opposed to an *in vitro* environment. Most often such target molecules are proteins such as enzymes, receptors and the like. However, target molecules may also include other molecules such as DNAs, lipids, carbohydrates and RNAs including messenger RNAs, ribosomal RNAs, tRNAs, regulatory RNAs and the like. A number of highly sensitive cell-based assay methods are available to those of skill in the art to detect binding and interaction of test compounds with specific target molecules. However, these methods are generally not highly effective when the test compound binds to or otherwise interacts with its target molecule with moderate or low affinity. In addition, the target molecule may not be readily accessible to a test compound in solution, such as when the target molecule is located inside the cell or within a cellular compartment. Thus, current cell-based assay methods are limited in that they are not effective in identifying or characterizing compounds that interact with their targets with moderate to low affinity or compounds that interact with targets that are not readily accessible.

The cell-based assay methods of the present invention have substantial advantages over current cell-based assays. These advantages derive from the use of sensitized cells in which the level or activity of at least one proliferation-required gene product (the target molecule) has been specifically reduced to the point where the presence or absence of its function becomes a rate-determining step for cellular proliferation. Bacterial, fungal, plant, or animal cells can all be used with the present method. Such sensitized cells become much more sensitive to compounds that are active against the affected target molecule. Thus, cell-based assays of the present invention are capable of detecting compounds exhibiting low or moderate potency against the target molecule of interest because such compounds are substantially more potent on sensitized cells than on non-sensitized cells. The effect may be such that a test compound may be two to several times more potent, at least 10 times more potent, at least 20 times more potent, at least 50 times more potent, at least 100 times more

potent, at least 1000 times more potent, or even more than 1000 times more potent when tested on the sensitized cells as compared to the non-sensitized cells. The proliferation-required nucleic acids or polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi,* or portions thereof, may be employed in any of the cell-based assays described herein. Similarly, homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides or portions of the homologous nucleic acids or homologous polypeptides, may be employed in any of the cell-based assays described herein.

Due in part to the increased appearance of antibiotic resistance in pathogenic microorganisms and to the significant side-effects associated with some currently used antibiotics, novel antibiotics acting at new targets are highly sought after in the art. Yet, another limitation in the current art related to cell-based assays is the problem of repeatedly identifying hits against the same kinds of target molecules in the same limited set of biological pathways. This may occur when compounds acting at such new targets are discarded, ignored or fail to be detected because compounds acting at the "old" targets are encountered more frequently and are more potent than compounds acting at the new targets. As a result, the majority of antibiotics in use currently interact with a relatively small number of target molecules within an even more limited set of biological pathways.

The use of sensitized cells of the current invention provides a solution to the above problem in two ways. First, desired compounds acting at a target of interest, whether a new target or a previously known but poorly exploited target, can now be detected above the "noise" of compounds acting at the "old" targets due to the specific and substantial increase in potency of such desired compounds when tested on the sensitized cells of the current invention. Second, the methods used to sensitize cells to compounds acting at a target of interest may also sensitize these cells to compounds acting at other target molecules within the same biological pathway. For example, expression of an antisense molecule to a gene encoding a ribosomal protein is expected to sensitize the cell to compounds acting at that ribosomal protein and may also sensitize the cells to compounds acting at any of the ribosomal components (proteins or

rRNA) or even to compounds acting at any target which is part of the protein synthesis pathway. Thus an important advantage of the present invention is the ability to reveal new targets and pathways that were previously not readily accessible to drug discovery methods.

Sensitized cells of the present invention are prepared by reducing the activity or level of a target molecule. The target molecule may be a gene product, such as an RNA or polypeptide produced from the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including a gene product produced from the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, such as the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) or from homologous nucleic acids. For example, the target molecule may be one of the polypeptides of SEQ ID NOs. 3801-3805, 4861-5915, 10013-14110 or a homologous polypeptide. Alternatively, the target may be a gene product such as an RNA or polypeptide which is produced from a sequence within the same operon as the proliferation-required nucleic acids from*Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or from homologous nucleic acids. In addition, the target may be an RNA or polypeptide in the same biological pathway as the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or from homologous nucleic acids. Such biological pathways include, but are not limited to, enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such the cell wall.

Current methods employed in the arts of medicinal and combinatorial chemistries are able to make use of structure-activity relationship information derived from testing compounds in various biological assays including direct binding assays and cell-based assays. Occasionally compounds are directly identified in such assays that are sufficiently potent to be developed as drugs. More often, initial hit compounds

exhibit moderate or low potency. Once a hit compound is identified with low or moderate potency, directed libraries of compounds are synthesized and tested in order to identify more potent leads. Generally these directed libraries are combinatorial chemical libraries consisting of compounds with structures related to the hit compound but containing systematic variations including additions, subtractions and substitutions of various structural features. When tested for activity against the target molecule, structural features are identified that either alone or in combination with other features enhance or reduce activity. This information is used to design subsequent directed libraries containing compounds with enhanced activity against the target molecule. After one or several iterations of this process, compounds with substantially increased activity against the target molecule are identified and may be further developed as drugs. This process is facilitated by use of the sensitized cells of the present invention since compounds acting at the selected targets exhibit increased potency in such cell-based assays, thus; more compounds can now be characterized providing more useful information than would be obtained otherwise.

Thus, it is now possible using cell-based assays of the present invention to identify or characterize compounds that previously would not have been readily identified or characterized including compounds that act at targets that previously were not readily exploited using cell-based assays. The process of evolving potent drug leads from initial hit compounds is also substantially improved by the cell-based assays of the present invention because, for the same number of test compounds, more structure-function relationship information is likely to be revealed.

The method of sensitizing a cell entails selecting a suitable gene or operon. A suitable gene or operon is one whose transcription and/or expression is required for the proliferation of the cell to be sensitized. The next step is to introduce into the cells to be sensitized, an antisense RNA capable of hybridizing to the suitable gene or operon or to the RNA encoded by the suitable gene or operon. Introduction of the antisense RNA can be in the form of a vector in which antisense RNA is produced under the control of an inducible promoter. The amount of antisense RNA produced is modulated by varying an inducer concentration to which the cell is exposed and thereby varying the activity of the promoter driving transcription of the antisense RNA. Thus, cells are sensitized by exposing them to an inducer concentration that results in a sub-lethal level

of antisense RNA expression. The requisite maount of inducer may be derived empiracally by one of skill in the art.

In one embodiment of the cell-based assays, antisense nucleic acids complementary to the identified *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* nucleotide sequences or portions thereof (including antisense nucleic acids comprising a nucleotide sequence complementary to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and the antisense nucleic acids of SEQ ID NOs.: 8-3795 or antisense nucleic acids comprising a nucleotide sequence complementary to portions of the foregoing nucleic acids thereof), antisense nucleic complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids are used to inhibit the production of a proliferation-required protein. Vectors producing antisense RNA complementary to identified genes required for proliferation, or portions thereof, are used to limit the concentration of a proliferation-required protein without severely inhibiting growth. The proliferation-required protein may be one of the proteins of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 or a homologous polypeptide. To achieve that goal, a growth inhibition dose curve of inducer is calculated by plotting various doses of inducer against the corresponding growth inhibition caused by the antisense expression. From this curve, the concentration of inducer needed to achieve various percentages of antisense induced growth inhibition, from 1 to 100% can be determined.

A variety of different regulatable promoters may be used to produce the antisense nucleic acid. Transcription from the regulatable promoters may be modulated by controlling the activity of a transcription factor repressor which acts at the regulatable promoter. For example, if transcription is modulated by affecting the activity of a repressor, the choice of inducer to be used depends on the repressor/operator responsible for regulating transcription of the antisense nucleic acid. If the regulatable promoter comprises a T5 promoter fused to a *xylO* (xylose operator; e.g. derived from *Staphylococcus xylosis* (Schnappinger, D. et al., FEMS Microbiol. Let. 129: 121-128 (1995), the disclosure of which is incorporated herein by reference in its entirety) then transcription of the antisense nucleic acid may be regulated by a xylose

repressor. The xylose repressor may be provided by ectoptic expression within an *S. aureus* cell of an exogenous xylose repressor gene, e.g. derived from *S. xylosis* DNA. In such cases transcription of antisense RNA from the promoter is inducible by adding xylose to the medium and the promoter is thus "xylose inducible." Similarly, IPTG inducible promoters may be used. For example, the highest concentration of the inducer that does not reduce the growth rate significantly can be estimated from the curve. Cellular proliferation can be monitored by growth medium turbidity via OD measurements. In another example, the concentration of inducer that reduces growth by 25% can be predicted from the curve. In still another example, a concentration of inducer that reduces growth by 50% can be calculated. Additional parameters such as colony forming units (cfu) can be used to measure cellular viability.

Cells to be assayed are exposed to the above-determined concentrations of inducer. The presence of the inducer at this sub-lethal concentration reduces the amount of the proliferation required gene product to a sub-optimal amount in the cell that will still support growth. Cells grown in the presence of this concentration of inducer are therefore specifically more sensitive to inhibitors of the proliferation-required protein or RNA of interest or to inhibitors of proteins or RNAs in the same biological pathway as the proliferation-required protein or RNA of interest but not to inhibitors of unrelated proteins or RNAs.

Cells pretreated with sub-inhibitory concentrations of inducer and thus containing a reduced amount of proliferation-required target gene product are then used to screen for compounds that reduce cell growth. The sub-lethal concentration of inducer may be any concentration consistent with the intended use of the assay to identify candidate compounds to which the cells are more sensitive. For example, the sub-lethal concentration of the inducer may be such that growth inhibition is at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60% at least about 75%, or more. Cells which are pre-sensitized using the preceding method are more sensitive to inhibitors of the target protein because these cells contain less target protein to inhibit than do wild-type cells.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids comprising a nucleotide sequence complementary to any of the

proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, or homologous polypeptides.

In another embodiment of the cell-based assays of the present invention, the level or activity of a proliferation required gene product is reduced using a mutation, such as a temperature sensitive mutation, in the gene encoding a gene product required for proliferation and an antisense nucleic acid comprising a nucleotide sequence complementary to the gene encoding the gene product required for proliferation or a portion thereof. Growing the cells at an intermediate temperature between the permissive and restrictive temperatures of the temperature sensitive mutant where the mutation is in a proliferation-required gene produces cells with reduced activity of the proliferation-required gene product. The antisense RNA complementary to the proliferation-required sequence further reduces the activity of the proliferation required gene product. Drugs that may not have been found using either the temperature sensitive mutation or the antisense nucleic acid alone may be identified by determining whether cells in which transcription of the antisense nucleic acid has been induced and which are grown at a temperature between the permissive temperature and the restrictive temperature are substantially more sensitive to a test compound than cells in which expression of the antisense nucleic acid has not been induced and which are grown at a permissive temperature. Also drugs found previously from either the antisense nucleic acid alone or the temperature sensitive mutation alone may have a different sensitivity profile when used in cells combining the two approaches, and that sensitivity profile may indicate a more specific action of the drug in inhibiting one or more activities of the gene product.

Temperature sensitive mutations may be located at different sites within the gene and correspond to different domains of the protein. For example, the *dnaB* gene of *Escherichia coli* encodes the replication fork DNA helicase. DnaB has several domains, including domains for oligomerization, ATP hydrolysis, DNA binding, interaction with primase, interaction with DnaC, and interaction with DnaA [(Biswas, E.E. and Biswas, S.B. 1999. Mechanism and DnaB helicase of *Escherichia coli*: structural domains involved in ATP hydrolysis, DNA binding, and oligomerization. Biochem. **38**:10919-10928; Hiasa, H. and Marians, K.J. 1999. Initiation of bidirectional replication at the chromosomal origin is directed by the interaction between helicase and primase. J. Biol. Chem. **274**:27244-27248; San Martin, C., Radermacher, M., Wolpensinger, B., Engel, A., Miles, C.S., Dixon, N.E., and Carazo, J.M. 1998. Three-dimensional reconstructions from cryoelectron microscopy images reveal an intimate complex between helicase DnaB and its loading partner DnaC. Structure **6**:501-9; Sutton, M.D., Carr, K.M., Vicente, M., and Kaguni, J.M. 1998. *Escherichia coli* DnaA protein. The N-terminal domain and loading of DnaB helicase at the *E. coli* chromosomal origin. J. Biol. Chem. **273**:34255-62.), the disclosures of which are incorporated herein by reference in their entireties]. Temperature sensitive mutations in different domains of DnaB confer different phenotypes at the restrictive temperature, which include either an abrupt stop or slow stop in DNA replication with or without DNA breakdown (Wechsler, J.A. and Gross, J.D. 1971. *Escherichia coli* mutants temperature-sensitive for DNA synthesis. Mol. Gen. Genetics **113**:273-284, the disclosure of which is incorporated herein by reference in its entirety) and termination of growth or cell death. Combining the use of temperature sensitive mutations in the *dnaB* gene that cause cell death at the restrictive temperature with an antisense to the *dnaB* gene could lead to the discovery of very specific and effective inhibitors of one or a subset of activities exhibited by DnaB.

It will be appreciated that the above method may be performed with any mutation which reduces but does not eliminate the activity or level of the gene product which is required for proliferation.

It will be appreciated that the above cell-based assays may be performed using mutations in, such as temperature sensitive mutations, and antisense nucleic acids comprising a nucleotide sequence complementary to any of the genes encoding

proliferation-required gene products from from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* , or portions thereof (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012), mutations in and antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110), or homologous polypeptides may be reduced.

When screening for antimicrobial agents against a gene product required for proliferation, growth inhibition of cells containing a limiting amount of that proliferation-required gene product can be assayed. Growth inhibition can be measured by directly comparing the amount of growth, measured by the optical density of the growth medium, between an experimental sample and a control sample. Alternative methods for assaying cell proliferation include measuring green fluorescent protein (GFP) reporter construct emissions, various enzymatic activity assays, and other methods well known in the art.

It will be appreciated that the above method may be performed in solid phase, liquid phase or a combination of the two. For example, cells grown on nutrient agar containing the inducer of the antisense construct may be exposed to compounds spotted onto the agar surface. If desired, the cells may be grown on agar containing varying concentrations of the inducer. A compound's effect may be judged from the diameter of the resulting killing zone, the area around the compound application point in which cells do not grow. Multiple compounds may be transferred to agar plates and simultaneously tested using automated and semi-automated equipment including but not restricted to multi-channel pipettes (for example the Beckman Multimek) and multi-channel spotters (for example the Genomic Solutions Flexys). In this way multiple plates and thousands to millions of compounds may be tested per day.

The compounds may also be tested entirely in liquid phase using microtiter plates as described below. Liquid phase screening may be performed in microtiter plates containing 96, 384, 1536 or more wells per microtiter plate to screen multiple plates and thousands to millions of compounds per day. Automated and semi-automated equipment may be used for addition of reagents (for example cells and compounds) and determination of cell density.

EXAMPLE 9

Cell-Based Assay Using Antisense Complementary to Genes Encoding Ribosomal Proteins

The effectiveness of the above cell-based assay was validated using constructs transribing antisense RNA to the proliferation required *E. coli* genes *rplL*, *rplJ*, and *rplW* encoding ribosomal proteins L7/L12, L10 and L23 respectively. These proteins are essential components of the protein synthesis apparatus of the cell and as such are required for proliferation. These constructs were used to test the effect of antisense transcription on cell sensitivity to antibiotics known to bind to the ribosome and thereby inhibit protein synthesis. Constructs transcribing antisense RNA to several other genes (*elaD*, *visC*, *yohH*, and *atpE/B*), the products of which are not involved in protein synthesis were used for comparison.

First, pLex5BA (Krause et al., J. Mol. Biol. 274: 365 (1997), the disclosure of which is incorporated herein by reference in its entirety) vectors containing antisense constructs to either *rplW* or to *elaD* were introduced into separate *E. coli* cell populations. Vector introduction is a technique well known to those of ordinary skill in the art. The vectors of this example contain IPTG inducible promoters that drive the transcription of the antisense RNA in the presence of the inducer. However, those skilled in the art will appreciate that other inducible promoters may also be used. Suitable vectors are also well known in the art. Antisense clones to genes encoding different ribosomal proteins or to genes encoding proteins that are not involved in protein synthesis were utilized to test the effect of antisense transcription on cell sensitivity to the antibiotics known to bind to ribosomal proteins and inhibit protein synthesis. Antisense nucleic acids comprising a nucleotide sequence complementarty to the *elaD*, *atpB&atpE*, *visC* and *yohH* genes are referred to as AS-*elaD*, AS-*atpB/E*, AS-*visC*, AS-*yohH* respectively. These genes are not known to be involved in protein

synthesis. Antisense nucleic acids to the *rplL*, *rplL&rplJ* and *rplW* genes are referred to as AS-*rplL*, AS-*rplL/J*, and AS-*rplW* respectively. These genes encode ribosomal proteins L7/L12 (*rplL*) L10 (*rplJ*) and L23 (*rplW*). Vectors containing these antisense nucleic acids were introduced into separate *E. coli* cell populations.

The cell populations containing vectors producing AS-*elaD* or AS-*rplW* were exposed to a range of IPTG concentrations in liquid medium to obtain the growth inhibitory dose curve for each clone (Fig. 1). First, seed cultures were grown to a particular turbidity measured by the optical density (OD) of the growth solution. The OD of the solution is directly related to the number of bacterial cells contained therein. Subsequently, sixteen 200 μl liquid medium cultures were grown in a 96 well microtiter plate at 37° C with a range of IPTG concentrations in duplicate two-fold serial dilutions from 1600 uM to 12.5 μM (final concentration). Additionally, control cells were grown in duplicate without IPTG. These cultures were started from an inoculum of equal amounts of cells derived from the same initial seed culture of a clone of interest. The cells were grown for up to 15 hours and the extent of growth was determined by measuring the optical density of the cultures at 600 nm. When the control culture reached mid-log phase the percent growth (relative to the control culture) for each of the IPTG containing cultures was plotted against the log concentrations of IPTG to produce a growth inhibitory dose response curve for the IPTG. The concentration of IPTG that inhibits cell growth to 50% (IC_{50}) as compared to the 0 mM IPTG control (0% growth inhibition) was then calculated from the curve. Under these conditions, an amount of antisense RNA was produced that reduced the expression levels of *rplW* or *elaD* to a degree such that growth of cells containing their respective antisense vectors was inhibited by 50%.

Alternative methods of measuring growth are also contemplated. Examples of these methods include measurements of proteins, the expression of which is engineered into the cells being tested and can readily be measured. Examples of such proteins include green fluorescent protein (GFP), luciferase, and various enzymes.

Cells were pretreated with the selected concentration of IPTG and then used to test the sensitivity of cell populations to tetracycline, erythromycin and other known protein synthesis inhibitors. Figure 1 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the

*E. coli rpl*W gene (AS-*rplW*) which encodes ribosomal protein L23 which is required for protein synthesis and essential for cell proliferation, or an antisense clone to the *elaD* (AS-*elaD*) gene which is not known to be involved in protein synthesis.

An example of a tetracycline dose response curve is shown in Figures 2A and 2B for the *rplW* and *elaD* genes, respectively. Cells were grown to log phase and then diluted into medium alone or medium containing IPTG at concentrations which give 20% and 50% growth inhibition as determined by IPTG dose response curves. After 2.5 hours, the cells were diluted to a final OD_{600} of 0.002 into 96 well plates containing (1) +/- IPTG at the same concentrations used for the 2.5 hour pre-incubation; and (2) serial two-fold dilutions of tetracycline such that the final concentrations of tetracycline range from 1 μg/ml to 15.6 ng/ml and 0 μg/ml. The 96 well plates were incubated at 37°C and the OD_{600} was read by a plate reader every 5 minutes for up to 15 hours. For each IPTG concentration and the no IPTG control, tetracycline dose response curves were determined when the control (absence of tetracycline) reached 0.1 OD_{600}.

To compare tetracycline sensitivity with and without IPTG, tetracycline IC_{50s} were determined from the dose response curves (Figs. 3A-B). Cells transcribing antisense nucleic acids AS-*rplL* or AS-*rplW* to genes encoding ribosomal proteins L7/L12 and L23 respectively showed increased sensitivity to tetracycline (Fig. 2A) as compared to cells with reduced levels of the *elaD* gene product (AS-*elaD)* (Fig. 2B). Figure 3 shows a summary bar chart in which the ratios of tetracycline IC_{50s} determined in the presence of IPTG which gives 50% growth inhibition versus tetracycline IC_{50s} determined without IPTG (fold increase in tetracycline sensitivity) were plotted. Cells with reduced levels of either L7/L12 (encoded by genes *rplL*, *rplJ*) or L23 (encoded by the *rplW* gene) showed increased sensitivity to tetracycline (Fig. 3). Cells expressing antisense to genes not known to be involved in protein synthesis (AS-*atpB/E*, AS-*visC*, AS-*elaD*, AS-*yohH*) did not show the same increased sensitivity to tetracycline, validating the specificity of this assay (Fig. 3).

In addition to the above, it has been observed in initial experiments that clones transcribing antisense RNA to genes involved in protein synthesis (including genes encoding ribosomal proteins L7/L12 & L10, L7/L12 alone, L22, and L18, as well as genes encoding rRNA and Elongation Factor G) have increased sensitivity to the macrolide, erythromycin, whereas clones transcribing antisense to the non-protein

synthesis genes *elaD, atpB/E* and *visC* do not. Furthermore, the clone transcribing antisense to *rplL* and *rplJ* (AS-*rplL/J)* does not show increased sensitivity to nalidixic acid and ofloxacin, antibiotics which do not inhibit protein synthesis.

The results with the ribosomal protein genes *rplL, rplJ*, and *rplW* as well as the initial results using various other antisense clones and antibiotics show that limiting the concentration of an antibiotic target makes cells more sensitive to the antimicrobial agents that specifically interact with that protein. The results also show that these cells are sensitized to antimicrobial agents that inhibit the overall function in which the protein target is involved but are not sensitized to antimicrobial agents that inhibit other functions. It will be appreciated that the cell-based assays described above may be implemented using the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* antisense nucleotide sequences which inhibit the activity of genes required for proliferation described herein (including the antisense nucleic acids of SEQ ID NOs.: 8-3795) or antisense nucleic acids comprising nucleotide sequences which are complementary to the sequences of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 or portions thereof.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* , or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi,* or homologous polypeptides may be reduced.

The cell-based assay described above may also be used to identify the biological pathway in which a proliferation-required nucleic acid or its gene product lies. In such

methods, cells transcribing a sub-lethal level of antisense to a target proliferation-required nucleic acid and control cells in which transcription of the antisense has not been induced are contacted with a panel of antibiotics known to act in various pathways. If the antibiotic acts in the pathway in which the target proliferation-required nucleic acid or its gene product lies, cells in which transcription of the antisense has been induced will be more sensitive to the antibiotic than cells in which expression of the antisense has not been induced.

As a control, the results of the assay may be confirmed by contacting a panel of cells transcribing antisense nucleic acids to many different proliferation-required genes including the target proliferation-required gene. If the antibiotic is acting specifically, heightened sensitivity to the antibiotic will be observed only in the cells transcribing antisense to a target proliferation-required gene (or cells expressing antisense to other proliferation-required genes in the same pathway as the target proliferation-required gene) but will not be observed generally in all cells expressing antisense to proliferation-required genes.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* ,(including antisense nucleic acids complementary to SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012, or the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids comprising nucleotide sequences complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110), or homologous polypeptides may be reduced.

Similarly, the above method may be used to determine the pathway on which a test compound, such as a test antibiotic acts. A panel of cells, each of which transcribes

an antisense to a proliferation-required nucleic acid in a known pathway, is contacted with a compound for which it is desired to determine the pathway on which it acts. The sensitivity of the panel of cells to the test compound is determined in cells in which transcription of the antisense has been induced and in control cells in which expression of the antisense has not been induced. If the test compound acts on the pathway on which an antisense nucleic acid acts, cells in which expression of the antisense has been induced will be more sensitive to the compound than cells in which expression of the antisense has not been induced. In addition, control cells in which expression of antisense to proliferation-required genes in other pathways has been induced will not exhibit heightened sensitivity to the compound. In this way, the pathway on which the test compound acts may be determined.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids comprising nucleotide sequences complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including antisense nucleic acids complementary to SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) or homologous polypeptides may be reduced.

The Example below provides one method for performing such assays.

EXAMPLE 10

Identification of the Pathway in which a Proliferation-Required Gene Lies or the Pathway on which an Antibiotic Acts

A. Preparation of Bacterial Stocks for Assay

To provide a consistent source of cells to screen, frozen stocks of host bacteria containing the desired antisense construct are prepared using standard microbiological techniques. For example, a single clone of the microorganism can be isolated by streaking out a sample of the original stock onto an agar plate containing nutrients for cell growth and an antibiotic for which the antisense construct contains a selectable marker which confers resistance. After overnight growth an isolated colony is picked from the plate with a sterile needle and transferred to an appropriate liquid growth medium containing the antibiotic required for maintenance of the plasmid. The cells are incubated at 30°C to 37°C with vigorous shaking for 4 to 6 hours to yield a culture in exponential growth. Sterile glycerol is added to 15% (volume to volume) and 100µL to 500 µL aliquots are distributed into sterile cryotubes, snap frozen in liquid nitrogen, and stored at -80°C for future assays.

B. Growth of Bacteria for Use in the Assay

A day prior to an assay, a stock vial is removed from the freezer, rapidly thawed (37°C water bath) and a loop of culture is streaked out on an agar plate containing nutrients for cell growth and an antibiotic to which the selectable marker of the antisense construct confers resistance. After overnight growth at 37°C, ten randomly chosen, isolated colonies are transferred from the plate (sterile inoculum loop) to a sterile tube containing 5 mL of LB medium containing the antibiotic to which the antisense vector confers resistance. After vigorous mixing to form a homogeneous cell suspension, the optical density of the suspension is measured at 600 nm (OD_{600}) and if necessary an aliquot of the suspension is diluted into a second tube of 5 mL, sterile, LB medium plus antibiotic to achieve an $OD_{600} \leq 0.02$ absorbance units. The culture is then incubated at 37° C for 1-2 hrs with shaking until the OD_{600} reaches OD 0.2 – 0.3. At this point the cells are ready to be used in the assay.

C. Selection of Media to be Used in Assay

Two-fold dilution series of the inducer are generated in culture media containing the appropriate antibiotic for maintenance of the antisense construct. Several media are tested side by side and three to four wells are used to evaluate the effects of the inducer at each concentration in each media. For example, LB broth, TBD broth and Muller-Hinton media may be tested with the inducer xylose at the following concentrations, 5 mM, 10 mM, 20 mM, 40 mM, 80 mM, 120 mM and 160 mM. Equal volumes of test media-inducer and cells are added to the wells of a 384 well microtiter plate and mixed. The cells are prepared as described above and diluted 1:100 in the appropriate media containing the test antibiotic immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells of each media that do not contain inducer, for example 0 mM xylose. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD_{600} of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of inducer is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in medium without inducer. The medium yielding greatest sensitivity to inducer is selected for use in the assays described below.

D. Measurement of Test Antibiotic Sensitivity in the Absence of Antisense Construct Induction

Two-fold dilution series of antibiotics of known mechanism of action are generated in the culture medium selected for further assay development that has been supplemented with the antibiotic used to maintain the construct. A panel of test antibiotics known to act on different pathways is tested side by side with three to four wells being used to evaluate the effect of a test antibiotic on cell growth at each concentration. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the medium selected for assay development supplemented with the antibiotic required to maintain the antisense construct and are diluted 1:100 in identical medium immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells that lack antibiotic, but contain the solvent used to dissolve the antibiotics. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD_{600} of the wells over an 18-hour period. The percent inhibition of

growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in medium without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC_{50} value for each antibiotic.

E. Measurement of Test Antibiotic Sensitivity in the Presence of Antisense Construct Inducer

The culture medium selected for use in the assay is supplemented with inducer at concentrations shown to inhibit cell growth by 50% and 80% as described above, as well as the antibiotic used to maintain the construct. Two-fold dilution series of the panel of test antibiotics used above are generated in each of these media. Several antibiotics are tested side by side in each medium with three to four wells being used to evaluate the effects of an antibiotic on cell growth at each concentration. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the medium selected for use in the assay supplemented with the antibiotic required to maintain the antisense construct. The cells are diluted 1:100 into two 50 mL aliquots of identical medium containing concentrations of inducer that have been shown to inhibit cell growth by 50% and 80 % respectively and incubated at 37°C with shaking for 2.5 hours. Immediately prior to addition to the microtiter plate wells, the cultures are adjusted to an appropriate OD_{600} (typically 0.002) by dilution into warm (37°C) sterile medium supplemented with identical concentrations of the inducer and antibiotic used to maintain the antisense construct. For a control, cells are also added to several wells that contain solvent used to dissolve test antibiotics but which contain no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD_{600} of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in medium without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC_{50} value for each antibiotic.

F. Determining the Specificity of the Test Antibiotics

A comparison of the IC_{50}s generated by antibiotics of known mechanism of action under antisense induced and non-induced conditions allows the pathway in which

a proliferation-required nucleic acid lies to be identified. If cells expressing an antisense nucleic acid comprising a nucleotide sequence complementary to a proliferation-required gene are selectively sensitive to an antibiotic acting via a particular pathway, then the gene against which the antisense acts is involved in the pathway on which the antibiotic acts.

G. Identification of Pathway in which a Test Antibiotic Acts

As discussed above, the cell-based assay may also be used to determine the pathway against which a test antibiotic acts. In such an analysis, the pathways against which each member of a panel of antisense nucleic acids acts are identified as described above. A panel of cells, each containing an inducible vector which transcribes an antisense nucleic acid comprising a nucleotide sequence complementary to a gene in a known proliferation-required pathway, is contacted with a test antibiotic for which it is desired to determine the pathway on which it acts under inducing and non-inducing conditions. If heightened sensitivity is observed in induced cells transcribing antisense complementary to a gene in a particular pathway but not in induced cells transcribing antisense nucleic acids comprising nucleotide sequences complementary to genes in other pathways, then the test antibiotic acts against the pathway for which heightened sensitivity was observed.

One skilled in the art will appreciate that further optimization of the assay conditions, such as the concentration of inducer used to induce antisense transcription and/or the growth conditions used for the assay (for example incubation temperature and medium components) may further increase the selectivity and/or magnitude of the antibiotic sensitization exhibited.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids comprising nucleotide sequences complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* , (including antisense nucleic acids comprising nucleotide sequences complemenatary to SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or

homologous antisense nucleic acids In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110), or homologous polypeptides may be reduced.

The following example confirms the effectiveness of the methods described above.

EXAMPLE 11

Identification of the Biological Pathway in which a Proliferation-Required Gene Lies

The effectiveness of the above assays was validated using proliferation-required genes from *E. coli* which were identified using procedures similar to those described above. Antibiotics of various chemical classes and modes of action were purchased from Sigma Chemicals (St. Louis, MO). Stock solutions were prepared by dissolving each antibiotic in an appropriate aqueous solution based on information provided by the manufacturer. The final working solution of each antibiotic contained no more than 0.2% (w/v) of any organic solvent. To determine their potency against a bacterial strain engineered for transcription of an antisense comprising a nucleotide sequence complementary to a proliferation-required 50S ribosomal protein, each antibiotic was serially diluted two- or three- fold in growth medium supplemented with the appropriate antibiotic for maintenance of the antisense construct. At least ten dilutions were prepared for each antibiotic. 25 μL aliquots of each dilution were transferred to discrete wells of a 384-well microplate (the assay plate) using a multi-channel pipette. Quadruplicate wells were used for each dilution of an antibiotic under each treatment condition (plus and minus inducer). Each assay plate contained twenty wells for cell growth controls (growth medium replacing antibiotic), ten wells for each treatment (plus and minus inducer, in this example IPTG). Assay plates were usually divided into the two treatments: half the plate containing induced cells and an appropriate concentrations of inducer (in this example IPTG) to maintain the state of induction, the other half containing non-induced cells in the absence of IPTG.

Cells for the assay were prepared as follows. Bacterial cells containing a construct, from which transcription of antisense nucleic acid comprising a nucleotide

sequence complementary to *rplL* and *rplJ (*AS-*rplL/J)*, which encode proliferation-required 50S ribosomal subunit proteins, is inducible in the presence of IPTG, were grown into exponential growth (OD_{600} 0.2 to 0.3) and then diluted 1:100 into fresh medium containing either 400 μM or 0 μM inducer (IPTG). These cultures were incubated at 37° C for 2.5 hr. After a 2.5 hr incubation, induced and non-induced cells were respectively diluted into an assay medium at a final OD_{600} value of 0.0004. The medium contained an appropriate concentration of the antibiotic for the maintenance of the antisense construct. In addition, the medium used to dilute induced cells was supplemented with 800 μM IPTG so that addition to the assay plate would result in a final IPTG concentration of 400 μM. Induced and non-induced cell suspensions were dispensed (25 μl/well) into the appropriate wells of the assay plate as discussed previously. The plate was then loaded into a plate reader, incubated at constant temperature, and cell growth was monitored in each well by the measurement of light scattering at 595 nm. Growth was monitored every 5 minutes until the cell culture attained a stationary growth phase. For each concentration of antibiotic, a percentage inhibition of growth was calculated at the time point corresponding to mid-exponential growth for the associated control wells (no antibiotic, plus or minus IPTG). For each antibiotic and condition (plus or minus IPTG), a plot of percent inhibition versus log of antibiotic concentration was generated and the IC_{50} determined. A comparison of the IC_{50} for each antibiotic in the presence and absence of IPTG revealed whether induction of the antisense construct sensitized the cell to the mechanism of action exhibited by the antibiotic. Cells which exhibited a statistically significant decrease in the IC_{50} value in the presence of inducer were considered to have an increased sensitivity to the test antibiotic.

The results are provided in the table below, which lists the classes and names of the antibiotics used in the analysis, the targets of the antibiotics, the IC_{50} in the absence of IPTG, the IC_{50} in the presence of IPTG, the concentration units for the IC_{50s}, the fold increase in IC_{50} in the presence of IPTG, and whether increased sensitivity was observed in the presence of IPTG.

TABLE III

Effect of Expression of Antisense RNA to *rplL* and *rplJ* on Antibiotic Sensitivity

ANTIBIOTIC CLASS /Names	TARGET	IC_{50} (-IPTG)	IC_{50} (+IPTG)	Conc. Unit	Fold Increase in Sensitivity	Sensitivity Increased?
PROTEIN SYNTHESIS INHIBITOR						
AMINOGLYCOSIDES						
Gentamicin	30S ribosome function	2715	19.19	ng/ml	141	Yes
Streptomycin	30S ribosome function	11280	161	ng/ml	70	Yes
Spectinomycin	30S ribosome function	18050	<156	ng/ml		Yes
Tobramycin	30S ribosome function	3594	70.58	ng/ml	51	Yes
MACROLIDES						
Erythromycin	50S ribosome function	7467	187	ng/ml	40	Yes
AROMATIC POYKETIDES						
Tetracycline	30S ribosome function	199.7	1.83	ng/ml	109	Yes
Minocycline	30S ribosome function	668.4	3.897	ng/ml	172	Yes
Doxycycline	30S ribosome function	413.1	27.81	ng/ml	15	Yes
OTHER PROTEIN SYNTHESIS INHIBITORS						
Fusidic acid	Elongation Factor G function	59990	641	ng/ml	94	Yes
Chloramphenicol	30S ribosome function	465.4	1.516	ng/ml	307	Yes
Lincomycin	50S ribosome function	47150	324.2	ng/ml	145	Yes
OTHER ANTIBIOTIC MECHANISMS						
B-LACTAMS						
Cefoxitin	Cell wall biosynthesis	2782	2484	ng/ml	1	No
Cefotaxime	Cell wall biosynthesis	24.3	24.16	ng/ml	1	No
DNA SYNTHESIS INHIBITORS						
Nalidixic acid	DNA Gyrase activity	6973	6025	ng/ml	1	No
Ofloxacin	DNA Gyrase activity	49.61	45.89	ng/ml	1	No
OTHER						
Bacitracin	Cell membrane function	4077	4677	mg/ml	1	No
Trimethoprim	Dihydrofolate Reductase activity	128.9	181.97	ng/ml	1	No
Vancomycin	Cell wall biosynthesis	145400	72550	ng/ml	2	No

The above results demonstrate that induction of an antisense RNA complementary to genes encoding 50S ribosomal subunit proteins results in a selective and highly significant sensitization of cells to antibiotics that inhibit ribosomal function and protein synthesis. The above results further demonstrate that induction of an antisense to an essential gene sensitizes a cell or microorganism to compounds that interfere with that gene product's biological role. This sensitization is restricted to compounds that interfere with pathways associated with the targeted gene and its product.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including antisense nucleic acids complementary to SEQ ID NOs. 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi i* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110), or homologous polypeptides may be reduced.

Example 11A below describes an analysis performed in *Staphylococcus aureus.*

EXAMPLE 11A

Identification of the Biological Pathway in which a Gene Required for Proliferation of *Staphylococcus aureus* Lies

Antibiotics of various chemical classes and modes of action were purchased from chemical suppliers, for example Sigma Chemicals (St. Louis, MO). Stock solutions were prepared by dissolving each antibiotic in an appropriate aqueous solution based on information provided by the manufacturer. The final working solution of each antibiotic contained no more than 0.2% (w/v) of any organic solvent.

To determine its potency against a bacterial strain containing an antisense nucleic acid comprising a nucleotide sequence complementary to the nucleotide sequence encoding the Beta subunit of DNA gyrase (which is required for proliferation) under the control of a xylose inducible promoter, each antibiotic was serially diluted two- or three- fold in growth medium supplemented with the appropriate antibiotic for maintenance of the antisense construct. At least ten dilutions were prepared for each antibiotic.

Aliquots (25 µL) of each dilution were transferred to discrete wells of a 384-well microplate (the assay plate) using a multi-channel pipette. Quadruplicate wells were used for each dilution of an antibiotic under each treatment condition (plus and minus inducer). Each assay plate contained twenty wells for cell growth controls (growth medium, no antibiotic), ten wells for each treatment (plus and minus inducer, xylose, in this example). Half the assay plate contained induced cells (in this example *Staphylococcus aureus* cells) and appropriate concentrations of inducer (xylose, in this example) to maintain the state of induction while the other half of the assay plate contained non-induced cells maintained in the absence of inducer.

Preparation of Bacterial Cells

Cells of a bacterial clone containing a construct in which transcription of antisense comprising a nucleotide sequence complementary to the sequence encoding the Beta subunit of DNA gyrase under the control of the xylose inducible promoter (S1M10000001F08) were grown into exponential growth (OD_{600} 0.2 to 0.3) and then diluted 1:100 into fresh medium containing either 12 mM or 0 mM inducer (xylose). These cultures were incubated at 37° C for 2.5 hr. The presence of inducer (xylose) in the medium initiates and maintains production of antisense RNA from the antisense construct. After a 2.5 hr incubation, induced and non-induced cells were respectively diluted into an assay medium containing an appropriate concentration of the antibiotic for the maintenance of the antisense construct. In addition, medium used to dilute induced cells was supplemented with 24 mM xylose so that addition to the assay plate would result in a final xylose concentration of 12 mM. The cells were diluted to a final OD_{600} value of 0.0004.

Induced and non-induced cell suspensions were dispensed (25 µl/well) into the appropriate wells of the assay plate as discussed previously. The plate was then loaded

into a plate reader and incubated at constant temperature while cell growth was monitored in each well by the measurement of light scattering at 595 nm. Growth was monitored every 5 minutes until the cell culture attained a stationary growth phase. For each concentration of antibiotic, a percentage inhibition of growth was calculated at the time point corresponding to mid-exponential growth for the associated control wells (no antibiotic, plus or minus xylose). For each antibiotic and condition (plus or minus xylose), plots of percent inhibition versus Log of antibiotic concentration were generated and IC_{50s} determined.

A comparison of each antibiotic's IC_{50} in the presence and absence of inducer (xylose, in this example) reveals whether induction of the antisense construct sensitized the cell to the antibiotic's mechanism of action. If the antibiotic acts against the β subunit of DNA gyrase, the IC_{50} of induced cells will be significantly lower than the IC_{50} of uninduced cells.

Figure 4 lists the antibiotics tested, their targets, and their fold increase in potency between induced cells and uninduced cells. As illustrated in Figure 4, the potency of cefotaxime, cefoxitin, fusidic acid, lincomycin, tobramycin, trimethoprim and vancomycin, each of which act on targets other than the β subunit of gyrase, was not significantly different in induced cells as compared to uninduced cells. However, the potency of novobiocin, which is known to act against the Beta subunit of DNA gyrase, was significantly different between induced cells and uninduced cells.

Thus, induction of an antisense nucleic acid comprising a nucleotide sequence complementary to the sequence encoding the β subunit of gyrase results in a selective and significant sensitization of *Staphylococcus aureus* cells to an antibiotic which inhibits the activity of this protein. Furthermore, the results demonstrate that induction of an antisense construct to an essential gene sensitizes a cell or microorganism to compounds that interfere with that gene product's biological role. This sensitization is apparently restricted to compounds that interfere with the targeted gene and its product.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including

antisense nucleic acids complementary to SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs. 8-3795), or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa,Enterococcus faecalis Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi,* or homologous polypeptides may be reduced.

Assays utilizing antisense constructs to essential genes or portions thereof can be used to identify compounds that interfere with the activity of those gene products. Such assays could be used to identify drug leads, for example antibiotics.

Panels of cells transcribing different antisense nucleic acids can be used to characterize the point of intervention of a compound affecting an essential biochemical pathway including antibiotics with no known mechanism of action.

Assays utilizing antisense constructs to essential genes can be used to identify compounds that specifically interfere with the activity of multiple targets in a pathway. Such constructs can be used to simultaneously screen a sample against multiple targets in one pathway in one reaction (Combinatorial HTS).

Furthermore, as discussed above, panels of antisense construct-containing cells may be used to characterize the point of intervention of any compound affecting an essential biological pathway including antibiotics with no known mechanism of action.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including antisense nucleic acids comprising nucleotide sequences complementary to SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs. 8-3795), or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-

required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or homologous polypeptides may be reduced.

Another embodiment of the present invention is a method for determining the pathway against which a test antibiotic compound is active, in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sub-lethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid corresponds to a proliferation-required nucleic acid identified using the methods described above, such as the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110, or homologous polypeptides. The method is similar to those described above for determining which pathway a test antibiotic acts against, except that rather than reducing the activity or level of a proliferation-required gene product using a sub-lethal level of antisense to a proliferation-required nucleic acid, the sensitized cell is generated by reducing the activity or level of the proliferation-required gene product using a sub-lethal level of a known antibiotic which acts against the proliferation required gene product. Heightened sensitivity determines the pathway on which the test compound is active.

Interactions between drugs which affect the same biological pathway have been described in the literature. For example, Mecillinam (Amdinocillin) binds to and inactivates the penicillin binding protein 2 (PBP2, product of the *mrdA* in *E. coli*). This antibiotic interacts with other antibiotics that inhibit PBP2 as well as antibiotics that inhibit other penicillin binding proteins such as PBP3 [(Gutmann, L., Vincent, S., Billot-Klein, D., Acar, J.F., Mrena, E., and Williamson, R. (1986) Involvement of penicillin-binding protein 2 with other penicillin-binding proteins in lysis of *Escherichia coli* by some beta-lactam antibiotics alone and in synergistic lytic effect of amdinocillin (mecillinam). Antimicrobial Agents & Chemotherapy, 30:906-912), the disclosure of which is incorporated herein by reference in its entirety]. Interactions between drugs could, therefore, involve two drugs that inhibit the same target protein or nucleic acid or inhibit different proteins or nucleic acids in the same pathway [(Fukuoka, T., Domon, H., Kakuta, M., Ishii, C., Hirasawa, A., Utsui, Y., Ohya, S., and

Yasuda, H. (1997) Combination effect between panipenem and vancomycin on highly methicillin-resistant *Staphylococcus aureus*. Japan. J. Antibio. 50:411-419; Smith, C.E., Foleno, B.E., Barrett, J.F., and Frosc, M.B. (1997) Assessment of the synergistic interactions of levofloxacin and ampicillin against *Enterococcus faecium* by the checkerboard agar dilution and time-kill methods. Diagnos. Microbiol. Infect. Disease 27:85-92; den Hollander, J.G., Horrevorts, A.M., van Goor, M.L., Verbrugh, H.A., and Mouton, J.W. (1997) Synergism between tobramycin and ceftazidime against a resistant *Pseudomonas aeruginosa* strain, tested in an in vitro pharmacokinetic model. Antimicrobial Agents & Chemotherapy. 41:95-110), the disclosure of all of which are incorporated herein by reference in their entireties].

Two drugs may interact even though they inhibit different targets. For example, the proton pump inhibitor, Omeprazole, and the antibiotic, Amoxycillin, two synergistic compounds acting together, can cure *Helicobacter pylori* infection [(Gabryelewicz, A., Laszewicz, W., Dzieniszewski, J., Ciok, J., Marlicz, K., Bielecki, D., Popiela, T., Legutko, J., Knapik, Z., Poniewierka, E. (1997) Multicenter evaluation of dual-therapy (omeprazol and amoxycillin) for *Helicobacter pylori*-associated duodenal and gastric ulcer (two years of the observation). J. Physiol. Pharmacol. 48 Suppl 4:93-105), the disclosure of which is incorporated herein by reference in its entirety].

The growth inhibition from the sub-lethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sub-lethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

Cells are contacted with a combination of each member of a panel of known antibiotics at a sub-lethal level and varying concentrations of the test antibiotic. As a control, the cells are contacted with varying concentrations of the test antibiotic alone. The IC_{50} of the test antibiotic in the presence and absence of the known antibiotic is determined. If the IC_{50}s in the presence and absence of the known drug are substantially similar, then the test drug and the known drug act on different pathways.

If the IC_{50}s are substantially different, then the test drug and the known drug act on the same pathway.

It will be appreciated that the above cell-based assays may be performed using a sub-lethal concentration of a known antibiotic which acts against the product of any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the products of SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012, or portions thereof, or the products of homologous coding nucleic acids or portions thereof. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110), or homologous polypeptides may be reduced.

Another embodiment of the present invention is a method for identifying a candidate compound for use as an antibiotic in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sub-lethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described previously herein for identifying candidate compounds for use as antibiotics except that rather than reducing the activity or level of a proliferation-required gene product using a sub-lethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required gene product is reduced using a sub-lethal level of a known antibiotic which acts against the proliferation required gene product.

The growth inhibition from the sub-lethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sub-lethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

In order to characterize test compounds of interest, cells are contacted with a panel of known antibiotics at a sub-lethal level and one or more concentrations of the test compound. As a control, the cells are contacted with the same concentrations of the test compound alone. The IC_{50} of the test compound in the presence and absence of the known antibiotic is determined. If the IC_{50} of the test compound is substantially different in the presence and absence of the known drug then the test compound is a good candidate for use as an antibiotic. As discussed above, once a candidate compound is identified using the above methods its structure may be optimized using standard techniques such as combinatorial chemistry.

Representative known antibiotics which may be used in each of the above methods are provided in Table IV below. However, it will be appreciated that other antibiotics may also be used.

TABLE IV
Antibiotics and Their Targets

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
Inhibitors of Transcription		
Rifamycin, Rifampicin Rifabutin Rifaximin	Inhibits initiation of transcription/ß-subunit RNA polymerase, *rpoB*	*rpoB*, *crp*, *cyaA*
Streptolydigin	Accelerates transcription chain termination/ß-subunit RNA polymerase	*rpoB*
Streptovaricin	an acyclic ansamycin, inhibits RNA polymerase	*rpoB*
Actinomycin D+EDTA	Intercalates between 2 successive G-C pairs, *rpoB*, inhibits RNA synthesis	*pldA*

Inhibitors of Nucleic Acid Metabolism

Quinolones, Nalidixic acid Oxolinic acid	α subunit gyrase and/or topoisomerase IV, *gyrA*	*gyrAorB, icd, sloB*
Fluoroquinolones Ciprofloxacin, Norfloxacin	α subunit gyrase, *gyrA* and/or topoisomerase IV (probable target in Staph)	*gyrA* *norA* (efflux in Staph) *hipQ*
Coumerins Novobiocin	Inhibits ATPase activity of ß-subunit gyrase, *gyrB*	*gyrB, cysB, cysE, nov, ompA*
Coumermycin	Inhibits ATPase activity of ß-subunit gyrase, *gyrB*	*gyrB, hisW*
Albicidin	DNA synthesis	*tsx* (nucleoside channel)
Metronidazole	Causes single-strand breaks in DNA	*nar*

Inhibitors of Metabolic Pathways

Sulfonamides, Sulfanilamide	blocks synthesis of dihydrofolate,dihydro-pteroate synthesis, *folP*	*folP, gpt, pabA, pabB, pabC*
Trimethoprim,	Inhibits dihydrofolate reductase, *folA*	*folA, thyA*
Showdomycin	Nucleoside analogue capable of alkylating sulfhydryl groups, inhibito of thymidylate synthetase	*nupC, pnp*
Thiolactomycin	type II fatty acid synthase inhibitor	*emrB* *fadB, emrB* due to gene dosage
Psicofuranine	Adenosine glycoside antibiotic, target is GMP synthetase	*guaA,B*
Triclosan	Inhibits fatty acid synthesis	*fabI (envM)*
Diazoborines Isoniazid, Ethionamide	heterocyclic, contain boron, inhibit fatty acid synthesis, enoyl-ACP reductase, *fabI*	*fabI (envM)*

Inhibitors of Translation

Phenylpropanoids Chloramphenicol,	Binds to ribosomal peptidyl transfer center preventing peptide translocation/ binds to S6, L3, L6, L14, L16, L25, L26, L27, but preferentially to L16	*rrn, cmlA, marA, ompF, ompR*
Tetracyclines, type II polyketides Minocycline Doxycycline	Binding to 30S ribosomal subunit, "A site on 30S subunit, blocks peptide elongation, strongest binding to S7	*clmA (cmr), mar, ompF*
Macrolides (type I	Binding to 50 S ribosomal subunit,	

polyketides) Erythromycin, Carbomycin, Spiramycin etc	23S rRNA, blocks peptide translocation, L15, L4, L12	*rrn, rplC, rplD, rplV , mac*
Aminoglycosides Streptomycin,	Irreversible binding to 30S ribosomal subunit, prevents translation or causes mistranslation of mRNA/16S rRNA	*rpsL, strC,M, ubiF*
Neomycin		*atpA-E, ecfB, hemAC,D,E,G, topA,*
Spectinomycin		*rpsC,D,E, rrn, spcB*
Kanamycin		*atpA-atpE, cpxA, ecfB, hemA,B,L, topA*
Kasugamycin		*ksgA,B,C,D, rplB,K, rpsI,N,M,R*
Gentamicin, Amikacin		*rplF, ubiF*
Paromycin		*cpxA*
		rpsL
Lincosamides Lincomycin, Clindamycin	Binding to 50 S ribosomal subunit, blocks peptide translocation	*linB, rplN,O, rpsG*
Streptogramins Virginiamycin, Pristinamycin Synercid: quinupristin /dalfopristin	2 components, Streptogramins A&B, bind to the 50S ribosomal subunit blocking peptide translocation and peptide bond formation	
Fusidanes Fusidic Acid	Inhibition of elongation factor G (EF-G) prevents peptide translocation	*fusA*
Kirromycin (Mocimycin)	Inhibition of elongation factor TU (EF-Tu), prevents peptide bond formation	*tufA,B*
Pulvomycin	Binds to and inhibits EF-TU	
Thiopeptin	Sulfur-containing antibiotic, inhibits protein synthesis,EF-G	*rplE*
Tiamulin	Inhibits protein synthesis	*rplC, rplD*
Negamycin	Inhibits termination process of protein synthesis	*prfB*
Oxazolidinones Linezolid	23S rRNA	
Isoniazid		*pdx*
Nitrofurantoin	Inhibits protein synthesis, nitroreductases convert nitrofurantoin to highly reactive electrophilic intermediates which attack bacterial ribosomal	*nfnA,B*

	proteins non-specifically	
Pseudomonic Acids Mupirocin (Bactroban)	Inhibition of isoleucyl tRNA synthetase-used for Staph, topical cream, nasal spray	*ileS*
Indolmycin	Inhibits tryptophanyl-tRNA synthetase	*trpS*
Viomycin		*rrmA* (23S rRNA methyltransferase; mutant has slow growth rate, slow chain elongation rate, and viomycin resistance)
Thiopeptides	Binds to L11-23S RNA complex	
Thiostrepton	Inhibits GTP hydrolysis by EF-G	
Micrococcin	Stimulates GTP hydrolysis by EF-G	

Inhibitors of Cell Walls/Membranes

ß-lactams Penicillin, Ampicillin Methicillin,	Inhibition of one or more cell wall transpeptidases, endopeptidases, and glycosidases (PBPs), of the 12 PBPs only 2 are essential: *mrdA* (PBP2) and *ftsI (pbpB,* PBP3)	*ampC, ampD, ampE, envZ, galU, hipA, hipQ, ompC, ompF, ompR, ptsI, rfa, tolD, tolE*
Cephalosporins,		
Mecillinam (amdinocillin)	Binds to and inactivates PBP2 (*mrdA*)	*tonB*
	Inactivates PBP3 (*ftsI*)	*alaS, argS, crp, cyaA, envB, mrdA,B, mreB,C,D*
Aztreonam (Furazlocillin)		
Bacilysin, Tetaine	Dipeptide, inhib glucosamine synthase	*dppA*
Glycopeptides Vancomycin,	Inhib G+ cell wall syn, binds to terminal D-ala-D-ala of pentapeptide,	
Polypeptides Bacitracin	Prevents dephosphorylation and regeneration of lipid carrier	*rfa*
Cyclic lipopeptide Daptomycin,	Disrupts multiple aspects of membrane function, including peptidoglycan synthesis, lipoteichoic acid synthesis, and the bacterial membrane potential	

Cyclic polypeptides Polymixin,	Surfactant action disrupts cell membrane lipids, binds lipid A mioety of LPS	*pmrA*
Fosfomycin,	Analogue of P-enolpyruvate, inhibits 1st step in peptidoglycan synthesis - UDP-N-acetylglucosamine enolpyruvyl transferase, *murA*. Also acts as Immunosuppressant	*murA, crp, cyaA glpT, hipA, ptsI, uhpT*
Cycloserine	Prevents formation of D-ala dimer, inhibits D-ala ligase, *ddlA,B*	*hipA, cycA*
Alafosfalin	phosphonodipeptide, cell wall synthesis inhibitor, potentiator of ß-lactams	*pepA, tpp*
Inhibitors of Protein Processing/Transport		
Globomycin	Inhibits signal peptidase II (cleaves prolipoproteins subsequent to lipid modification, *lspA*	*lpp, dnaE*

It will be appreciated that the above cell-based assays may be performed using a sub-lethal concentration of a known antibiotic which acts against the product of any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, or portions thereof, or homologous nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, or homologous polypeptides may be reduced.

EXAMPLE 12

Transfer of Exogenous Nucleic Acid Sequences to other Bacterial Species

The ability of an antisense molecule identified in a first organism to inhibit the proliferation of a second organism (thereby confirming that a gene in the second organism which is homologous to the gene from the first organism is required for proliferation of the second organism) was validated using antisense nucleic acids which

inhibit the growth of *E. coli* which were identified using methods similar to those described above. Expression vectors which inhibited growth of *E. coli* upon induction of antisense RNA expression with IPTG were transformed directly into *Enterobacter cloacae, Klebsiella pneumonia* or *Salmonella typhimurium*. The transformed cells were then assayed for growth inhibition according to the method of Example 1. After growth in liquid culture, cells were plated at various serial dilutions and a score determined by calculating the log difference in growth for INDUCED vs. UNINDUCED antisense RNA expression as determined by the maximum 10 fold dilution at which a colony was observed. The results of these experiments are listed below in Table V. If there was no effect of antisense RNA expression in a microorganism, the clone is minus in Table V. In contrast, a positive in Table V means that at least 10 fold more cells were required to observe a colony on the induced plate than on the non-induced plate under the conditions used and in that microorganism.

TABLE V

Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation in *E. coli*

Mol. No.	*S. typhimurium*	*E. cloacae*	*K. pneumoniae*
EcXA001	+	+	-
EcXA004	+	-	-
EcXA005	+	+	+
EcXA006	-	-	-
EcXA007	-	+	-
EcXA008	+	-	+
EcXA009	-	-	-
EcXA010	+	+	+
EcXA011	-	+	-
EcXA012	-	+	-
EcXA013	+	+	+
EcXA014	+	+	-
EcXA015	+	+	+
EcXA016	+	+	+
EcXA017	+	+	+
EcXA018	+	+	+
EcXA019	+	+	+
EcXA020	+	+	+
EcXA021	+	+	+
EcXA023	+	+	+
EcXA024	+	-	+
EcXA025	-	-	-

EcXA026	+	+	-
EcXA027	+	+	-
EcXA028	+	-	-
EcXA029	-	-	-
EcXA030	+	+	+
EcXA031	+	-	-
EcXA032	+	+	-
EcXA033	+	+	+
EcXA034	+	+	+
EcXA035	-	-	-
EcXA036	+	-	+
EcXA037	+	+	-
EcXA038	+	+	+
EcXA039	+	-	-
EcXA041	+	+	+
EcXA042	-	+	+
EcXA043	-	-	-
EcXA044	-	-	-
EcXA045	+	+	+
EcXA046	-	-	-
EcXA047	+	+	-
EcXA048	-	-	-
EcXA049	+	-	-
EcXA050	-	-	-
EcXA051	+	-	-
EcXA052	+	-	-
EcXA053	+	+	+
EcXA054	-	-	+
EcXA055	+	-	-
EcXA056	+	-	+
EcXA057	+	+	-
EcXA058	-	-	-
EcXA059	+	+	+
EcXA060	-	-	-
EcXA061	-	-	-
EcXA062	-	-	-
EcXA063	+	+	-
EcXA064	-	-	-
EcXA065	+	+	-
EcXA066	-	-	-
EcXA067	-	+	-
EcXA068	-	-	-
EcXA069	-	+	-
EcXA070	-	-	-
EcXA071	+	-	-
EcXA072	+	-	+
EcXA073	+	+	+

EcXA074	+	+	+
EcXA075	+	-	-
EcXA076	-	+	-
EcXA077	+	+	-
EcXA079	+	+	+
EcXA080	+	-	-
EcXA082	-	+	-
EcXA083	-	-	-
EcXA084	-	+	-
EcXA086	-	-	-
EcXA087	-	-	-
EcXA088	-	-	-
EcXA089	-	-	-
EcXA090	-	-	-
EcXA091	-	-	-
EcXA092	-	-	-
EcXA093	-	-	-
EcXA094	+	+	+
EcXA095	+	+	-
EcXA096	-	-	-
EcXA097	+	-	-
EcXA098	+	-	-
EcXA099	-	-	-
EcXA100	-	-	-
EcXA101	-	-	-
EcXA102	-	-	-
EcXA103	-	+	-
EcXA104	+	+	+
EcXA106	+	+	-
EcXA107	-	-	-
EcXA108	-	-	-
EcXA109	-	-	-
EcXA110	+	+	-
EcXA111	-	-	-
EcXA112	-	+	-
EcXA113	+	+	+
EcXA114	-	+	-
EcXA115	-	+	-
EcXA116	+	+	-
EcXA117	+	-	-
EcXA118	-	-	-
EcXA119	+	+	-
EcXA120	-	-	-
EcXA121	-	-	-
EcXA122	+	-	+
EcXA123	+	-	-
EcXA124	-	-	-

EcXA125	-	-	-
EcXA126	-	-	-
EcXA127	+	+	-
EcXA128	-	-	-
EcXA129	-	+	-
EcXA130	+	+	-
EcXA132	-	-	-
EcXA133	-	-	-
EcXA136	-	-	-
EcXA137	-	-	-
EcXA138	+	-	-
EcXA139	-	-	-
EcXA140	+	-	-
EcXA141	+	-	-
EcXA142	-	-	-
EcXA143	-	+	-
EcXA144	+	+	-
EcXA145	-	-	-
EcXA146	-	-	-
EcXA147	-	-	-
EcXA148	-	-	-
EcXA149	+	+	+
EcXA150	-	-	-
EcXA151	+	-	-
EcXA152	-	-	-
EcXA153	+	+	-
EcXA154	-	-	-
EcXA155	-	-	**ND**
EcXA156	-	+	-
EcXA157	-	-	-
EcXA158	-	-	-
EcXA159	+	-	-
EcXA160	+	-	-
EcXA162	-	-	-
EcXA163	-	-	-
EcXA164	-	-	-
EcXA165	-	-	-
EcXA166	-	-	-
EcXA167	-	-	-
EcXA168	-	-	-
EcXA169	-	+	-
EcXA171	-	-	-
EcXA172	-	-	-
EcXA173	-	-	-
EcXA174	-	-	-
EcXA175	-	-	-
EcXA176	-	-	-

EcXA178	-	-	-
EcXA179	-	-	-
EcXA180	+	-	-
EcXA181	-	-	-
EcXA182	-	-	-
EcXA183	-	-	-
EcXA184	-	-	-
EcXA185	-	-	-
EcXA186	-	-	-
EcXA187	+	+	+
EcXA189	+	-	-
EcXA190	+	+	+
EcXA191	+	+	-
EcXA192	-	+	-

Thus, the ability of an antisense nucleic acid which inhibits the proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* to inhibit the growth of other organims may be evaluated by transforming the antisense nucleic acid directly into species other than the organism from which they were obtained. In particular, the ability of the antisense nucleic acid to inhibit the growth of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella*

dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. may be evaluated. In some embodiments of the present invention, the ability of the antisense nucleic acid to inhibit the growth of an organism other than *E. coli* may be evaluated. In such embodiments, the antisense nucleic acids are inserted into expression vectors functional in the organisms in which the antisense nucleic acids are evaluated.

It will be appreciated that the above methods for evaluating the ability of an antisense nucleic acid to inhibit the proliferation of a heterologous organism may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including antisense nucleic acids complementary to SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids.

Those skilled in the art will appreciate that a negative result in a heterologous cell or microorganism does not mean that that cell or microorganism is missing that gene nor does it mean that the gene is unessential. However, a positive result means that the heterologous cell or microorganism contains a homologous gene which is required for proliferation of that cell or microorganism. The homologous gene may be obtained using the methods described herein. Those cells that are inhibited by antisense may be used in cell-based assays as described herein for the identification and characterization of compounds in order to develop antibiotics effective in these cells or microorganisms. Those skilled in the art will appreciate that an antisense molecule which works in the microorganism from which it was obtained will not always work in a heterologous cell or microorganism.

EXAMPLE 12A

<u>Transfer of Exogenous Nucleic Acid Sequences to other Bacterial Species Using the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* Expression Vectors or Expression Vectors Functional in Bacterial Species other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* .</u>

The antisense nucleic acids that inhibit the growth of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* , or portions thereof, may also be evaluated for their ability to inhibit the growth of cells or microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* . For example, the antisense nucleic acids that inhibit the growth of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* may be evaluated for their ability to inhibit the growth of other organisms. In particular, the ability of the antisense nucleic acid to inhibit the growth of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium*

tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species may be evaluated. In some embodiments of the present invention, the ability of the antisense nucleic acid to inhibit the growth of an organism other than *E. coli* may be evaluated.

In such methods, expression vectors in which the expression of an antisense nucleic acid that inhibits the growth of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* is under the control of an inducible promoter are introduced into the cells or microorganisms in which they are to be evaluated. In some embodiments, the antisense nucleic acids may be evaluated in cells or microorganisms which are closely related to *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typh* . The ability of these antisense nucleic acids to inhibit the growth of the related cells or microorganisms in the presence of the inducer is then measured.

For example, thirty-nine antisense nucleic acids which inhibited the growth of *Staphylococcus aureus* were identified using methods such as those described herein and were inserted into an expression vector such that their expression was under the control of a xylose-inducible Xyl-T5 promoter. A vector with Green Fluorescent Protein (GFP) under control of the Xyl-T5 promoter was used to show that expression from the Xyl-T5 promoter in *Staphylococcus epidermidis* was comparable to that in *Staphylococcus aureus*.

The vectors were introduced into *Staphylococcus epidermidis* by electroporation as follows: *Staphylococcus epidermidis* was grown in liquid culture to mid-log phase

and then harvested by centrifugation. The cell pellet was resuspended in 1/3 culture volume of ice-cold EP buffer (0.625 M sucrose, 1 mM $MgCl_2$, pH=4.0), and then harvested again by centrifugation. The cell pellet was then resuspended with 1/40 volume EP buffer and allowed to incubate on ice for 1 hour. The cells were then frozen for storage at -80°C. For electroporation, 50 μl of thawed electrocompetent cells were combined with 0.5 μg plasmid DNA and then subjected to an electrical pulse of 10 kV/cm, 25 uFarads, 200 ohm using a biorad gene pulser electroporation device. The cells were immediately resuspended with 200 μl outgrowth medium and incubated for 2 hours prior to plating on solid growth medium with drug selection to maintain the plasmid vector. Colonies resulting from overnight growth of these platings were selected, cultured in liquid medium with drug selection, and then subjected to dilution plating analysis as described for *Staphylococcus aureus* in Example 10 above to test growth sensitivity in the presence of the inducer xylose.

The results are shown in Table VI below. The first column indicates the Molecule Number of the *Staphylococcus aureus* antisense nucleic acid which was introduced into *Staphylococcus epidermidis.* The second column indicates whether the antisense nucleic acid inhibited the growth of *Staphylococcus epidermidis*, with a "+" indicating that growth was inhibited. Of the 39 *Staphylococcus aureus* antisense nucleic acids evaluated, 20 inhibited the growth of *Staphylococcus epidermidis.*

TABLE VI

Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation of *Staphylococcus aureus*

Mol. No.	*S. epidermidis*
SaXA005	+
SaXA007	+
SaXA008	+
SaXA009	+
SaXA010	+
SaXA011	-
SaXA012	-
SaXA013	-
SaXA015	+

SaXA017	-
SaXA022	+
SaXA023	-
SaXA024	-
SaXA025	+
SaXA026	+
SaXA027	-
SaXA027b	-
SaXA02c	-
SaXA028	-
SaXA029	+
SaXA030	+
SaXA032	+
SaXA033	+
SaXA034	-
SaXA035	+
SaXA037	+
SaXA039	-
SaXA042	-
SaXA043	-
SaXA044	-
SaXA045	+
SaXA051	+
SaXA053	-
SaXA056b	-
SaXA059a	+
SaXA060	-
SaXA061	+
SaXA062	+
SaXA063	-
SaXA065	-

Although the results shown above were obtained using a subset of the nucleic acids of the present invention, it will be appreciated that similar analyses may be performed using the other nucleic acids of the present invention to determine whether they inhibit the proliferation of cells or microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*.

Thus, it will be appreciated that the above methods for evaluating the ability of an antisense nucleic acid to inhibit the proliferation of a heterologous organism may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, (including antisense nucleic acids complementary to SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids.

EXAMPLE 12C

As a demonstration of the methodology required to find homologues to an essential gene, nine prokaryotic organisms were analyzed and compared in detail. First, the most reliable source of gene sequences for each organism was assessed by conducting a survey of the public and private data sources. The nine organisms studied are *Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, Streptococcus pneumoniae* and *Salmonella typhi.* Full-length gene protein and nucleotide sequences for these organisms were assembled from various sources. For *Escherichia coli, Haemophilus influenzae* and *Helicobacter pylori,* gene sequences were adopted from the public sequencing projects, and derived from the GenPept 115 database (available from NCBI). For *Pseudomonas aeruginosa*, gene sequences were adopted from the Pseudomonas genome sequencing project (downloaded from

http://www.pseudomonas.com). For *Klebsiella pneumoniae, Staphylococcus aureus, Streptococcus pneumoniae* and *Salmonella typhi,* genomic sequences from PathoSeq v 4.1 (Mar 2000 release) was reanalyzed for ORFs using the gene finding software GeneMark v 2.4a, which was purchased from GenePro Inc. 451 Bishop St., N.W., Suite B, Atlanta, GA, 30318, USA.

Subsequently, the essential genes found by the antisense methodology were compared to the derived proteomes of interest, in order to find all the homologous genes to a given gene. This comparison was done using the FASTA program v3.3. Genes were considered homologues if they were greater than 25% identical and the alignment between the two genes covered more than 70% of the length of one of the genes. The best homologue for each of the nine organisms, defined as the most significantly scoring match which also fulfilled the above criteria, was reported in Table VIIA. Table VIIA lists the best ORF identified as described above (column labelled LOCUSID), the SEQ ID, % identity, and the amount of the protein which aligns well with the query sequence (coverage) for the gene identified in each of the nine organisms evaluated as described above.

Table VIIB lists the PathoSeq cluster ID for genes identified as being required for proliferation in *Enterococcus faecalis, Escherichia coli, Pseudomonas aeruginosa,* and *Staphylococcus aureus* using the methods described herein. As indicated in the column labelled PathoSeq cluster ID, these sequences share homology to one another and were consequently grouped within the same PathoSeq cluster. Thus, the methods described herein identified genes required for proliferation in several species which share homology.

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA100001	SeqID	10430	10618	10998	11603	11739		12309	13524	14040
	IDENTITY	27%	100%	28%	28%	29%		52%	55%	28%
	COVERAGE	99%	100%	101%	79%	77%		98%	98%	98%
EFA100023	SeqID		10505					12860	13392	
	IDENTITY		100%					27%	39%	
	COVERAGE		100%					95%	101%	
EFA100065	SeqID	10322	10813	11177	11351		12018	12820	13186	13733
	IDENTITY	49%	100%	49%	44%		48%	59%	65%	48%
	COVERAGE	96%	100%	95%	96%		97%	97%	98%	96%
EFA100151	SeqID	10128	10516	11247	11340		11891	12529	13362	
	IDENTITY	50%	100%	37%	46%		49%	54%	51%	
	COVERAGE	99%	100%	100%	100%		100%	99%	100%	
EFA100157	SeqID		10673		11448			12352	13176	
	IDENTITY		100%		39%			64%	74%	
	COVERAGE		100%		98%			98%	99%	
EFA100165	SeqID	10031	10637	11189	11564		12009	12614	13399	14078
	IDENTITY	31%	100%	33%	28%		32%	29%	27%	29%
	COVERAGE	97%	100%	98%	100%		96%	90%	96%	97%
EFA100190	SeqID	10364	10480	11061	11408	11659	11996	12444	13232	13966
	IDENTITY	54%	100%	57%	55%	55%	54%	78%	80%	54%
	COVERAGE	100%	101%	100%	99%	90%	100%	101%	101%	101%
EFA100194	SeqID	10336	10540	11120	11426		11989	12230	13222	14096
	IDENTITY	60%	100%	62%	62%		60%	85%	86%	61%
	COVERAGE	100%	101%	100%	102%		100%	101%	92%	101%
EFA100200	SeqID	10323	10798	11193			12020	12527	13561	13731
	IDENTITY	39%	100%	38%			40%	50%	59%	39%
	COVERAGE	85%	100%	87%			85%	85%	88%	85%
EFA100210	SeqID	10352	10560	11104	11439		5171	12260	13204	13968
	IDENTITY	53%	100%	53%	53%		54%	74%	93%	53%
	COVERAGE	95%	101%	95%	94%		95%	101%	94%	95%
EFA100211	SeqID	10351	10523	11105	11438		11992	12214	13205	
	IDENTITY	46%	100%	46%	39%		43%	69%	63%	
	COVERAGE	87%	101%	87%	81%		87%	97%	81%	

TABLE VIIA (*Continued*)

LOCUSID	***Data***	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA100289	SeqID IDENTITY COVERAGE	10284 30% 85%	10810 100% 100%				11827 31% 90%		13245 25% 84%	
EFA100295	SeqID IDENTITY COVERAGE	10045 43% 92%	10517 100% 101%	11174 41% 95%	11601 41% 97%		11937 45% 97%	12390 44% 99%	13616 45% 94%	13911 43% 72%
EFA100312	SeqID IDENTITY COVERAGE		10641 100% 100%					12178 33% 88%		
EFA100329	SeqID IDENTITY COVERAGE		10782 100% 100%							
EFA100394	SeqID IDENTITY COVERAGE	10465 43% 108%	10675 100% 100%	11238 43% 109%	11563 42% 101%		11961 44% 108%	13003 66% 99%	13684 72% 100%	13853 44% 108%
EFA100397	SeqID IDENTITY COVERAGE	10027 31% 96%	10773 100% 100%	11185 29% 98%			12012 29% 93%	12396 43% 91%	13478 46% 97%	14074 31% 93%
EFA100399	SeqID IDENTITY COVERAGE	10295 63% 98%	10766 100% 100%	11196 59% 98%	11483 59% 99%		11791 58% 101%	12281 72% 99%	13413 76% 100%	13739 63% 98%
EFA100426	SeqID IDENTITY COVERAGE	10224 28% 99%	10702 100% 101%			11638 29% 99%		12139 42% 91%	13348 41% 109%	13957 28% 99%
EFA100478	SeqID IDENTITY COVERAGE		10486 100% 100%	11135 29% 72%	11338 31% 70%			12986 44% 99%	13184 43% 98%	
EFA100615	SeqID IDENTITY COVERAGE		10501 100% 100%	11139 44% 82%			12028 47% 81%	12641 61% 100%	13331 78% 100%	
EFA100617	SeqID IDENTITY COVERAGE	10314 43% 95%	10764 100% 100%	11216 43% 96%	11391 44% 78%		5198 51% 73%	12322 63% 84%	13381 69% 82%	13765 44% 93%
EFA100641	SeqID IDENTITY COVERAGE	10205 28% 79%	10793 100% 100%				11896 31% 74%	12862 50% 85%	13334 32% 82%	

TABLE VIIA (*Continued*)

LOCUSID	***Data***	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA100642	SeqID IDENTITY COVERAGE		10792 100% 100%		11520 46% 100%		12023 46% 101%	12493 73% 100%	13367 69% 100%	
EFA100668	SeqID IDENTITY COVERAGE	10026 28% 83%	10679 100% 100%	11184 28% 76%	11613 29% 78%		12013 28% 92%	12891 29% 82%	13505 50% 99%	14073 27% 95%
EFA100689	SeqID IDENTITY COVERAGE		10717 100% 100%					12523 33% 100%	13698 33% 100%	
EFA100704	SeqID IDENTITY COVERAGE	10362 78% 100%	10482 100% 100%	11059 78% 100%	11415 77% 101%		11995 75% 101%	12442 90% 100%	13171 78% 101%	13964 77% 100%
EFA100739	SeqID IDENTITY COVERAGE	10111 71% 83%	10537 100% 101%	11052 69% 83%	11429 63% 86%	11651 70% 87%	11876 71% 83%	12228 84% 87%	13220 84% 87%	14010 70% 87%
EFA100740	SeqID IDENTITY COVERAGE	10075 45% 94%	10536 100% 100%	11008 47% 94%	11348 30% 93%	11633 45% 94%	11942 48% 82%	12227 64% 94%	13219 60% 93%	13717 44% 94%
EFA100741	SeqID IDENTITY COVERAGE	10339 40% 103%	10535 100% 100%	11118 37% 102%	11430 34% 101%		11991 39% 102%	12226 48% 101%	13218 60% 100%	14098 40% 103%
EFA100742	SeqID IDENTITY COVERAGE	10340 52% 99%	10534 100% 101%	11116 52% 99%	11431 39% 92%		5160 46% 99%	12225 79% 101%	13217 88% 101%	14099 52% 99%
EFA100748	SeqID IDENTITY COVERAGE	10287 41% 99%	10483 100% 100%	11004 39% 99%	11523 29% 94%	11690 42% 98%	11944 44% 100%	12595 52% 100%		13868 41% 100%
EFA100756	SeqID IDENTITY COVERAGE	10112 49% 75%	10575 100% 102%		11396 43% 75%		11875 45% 81%	12327 64% 94%	13343 62% 94%	14009 47% 75%
EFA100757	SeqID IDENTITY COVERAGE	10155 27% 85%	10897 100% 100%							
EFA100783	SeqID IDENTITY COVERAGE	10035 32% 104%	10811 100% 100%	10986 34% 83%	11543 86% 100%		11953 37% 78%	12738 77% 100%	13261 75% 99%	13914 31% 99%

TABLE VIIA (*Continued*)

LOCUSID	***Data***	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA100795	SeqID IDENTITY COVERAGE		10863 100% 101%						13416 50% 101%	
EFA100798	SeqID IDENTITY COVERAGE	10382 62% 95%	10818 100% 100%	11153 61% 95%	11550 56% 89%		11775 63% 92%		13641 85% 96%	
EFA100811	SeqID IDENTITY COVERAGE		10546 100% 101%					12236 48% 98%	13439 58% 99%	
EFA100870	SeqID IDENTITY COVERAGE	10439 47% 114%	10627 100% 100%	11036 46% 117%	11410 52% 79%		5179 46% 116%	12446 72% 99%	13646 78% 98%	14042 46% 114%
EFA100914	SeqID IDENTITY COVERAGE	10399 40% 102%	10579 100% 100%	11018 40% 102%	11617 34% 101%	11758 40% 102%	12111 40% 102%	12368 59% 101%	13230 63% 95%	14065 40% 102%
EFA100919	SeqID IDENTITY COVERAGE	10269 44% 101%	10491 100% 100%	11127 45% 101%	11419 40% 99%		11809 46% 101%	12556 55% 101%	13594 63% 100%	13874 45% 101%
EFA100955	SeqID IDENTITY COVERAGE	10333 48% 98%	10542 100% 101%	11123 48% 98%	11582 42% 98%	11627 49% 79%	5158 43% 98%	12232 65% 99%	13224 76% 101%	14093 48% 98%
EFA100970	SeqID IDENTITY COVERAGE		10906 100% 100%							
EFA100978	SeqID IDENTITY COVERAGE	10334 46% 100%	10541 100% 100%	11122 46% 99%	11583 35% 98%		11987 45% 102%	12231 71% 101%	13223 70% 100%	14094 46% 100%
EFA100991	SeqID IDENTITY COVERAGE	10221 42% 91%	10681 100% 100%	11210 40% 93%	11607 29% 98%	11668 42% 94%	11801 39% 91%	12289 49% 93%	13191 56% 92%	14027 30% 93%
EFA101022	SeqID IDENTITY COVERAGE	10260 59% 85%	10875 100% 101%	10982 58% 85%	11401 50% 88%		11945 61% 85%	12715 76% 85%	13251 86% 89%	14086 56% 89%
EFA101060	SeqID IDENTITY COVERAGE		10722 100% 101%		11575 35% 83%	11646 37% 77%	11957 34% 97%	12504 71% 100%	13554 67% 101%	

TABLE VIIA (*Continued*)

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
EFA101086	SeqID IDENTITY COVERAGE	10315 37% 91%	10763 100% 100%	11215 37% 89%	11454 27% 98%	11716 38% 91%	12052 35% 92%	12953 57% 98%	13662 55% 95%	13764 36% 93%
EFA101120	SeqID IDENTITY COVERAGE	10017 30% 102%	10687 100% 100%	11219 31% 102%	11331 27% 74%		12057 29% 103%	12505 26% 99%	13498 64% 98%	14012 29% 103%
EFA101121	SeqID IDENTITY COVERAGE		10686 100% 100%					12606 38% 98%	13600 50% 99%	
EFA101123	SeqID IDENTITY COVERAGE	10420 43% 98%	10748 100% 100%	11131 39% 97%	11478 33% 97%	11629 43% 94%	11820 40% 96%	12674 70% 99%	13265 70% 100%	13783 42% 98%
EFA101141	SeqID IDENTITY COVERAGE	10436 35% 94%	10614 100% 101%	11071 40% 96%	11573 35% 95%		5181 40% 95%	12450 60% 98%	13246 70% 101%	14045 31% 96%
EFA101150	SeqID IDENTITY COVERAGE	10174 35% 100%	10719 100% 100%	11221 36% 100%	11556 26% 102%		11880 33% 100%	12985 45% 100%	13385 58% 100%	13943 36% 73%
EFA101159	SeqID IDENTITY COVERAGE	10359 55% 100%	10543 100% 101%	11097 52% 100%	11442 48% 81%		5176 49% 101%	12235 58% 99%	13197 89% 99%	13974 53% 100%
EFA101160	SeqID IDENTITY COVERAGE	10358 43% 92%	10549 100% 100%	11098 43% 92%	11595 33% 96%		5175 45% 92%	12240 62% 100%	13198 74% 100%	13973 43% 93%
EFA101161	SeqID IDENTITY COVERAGE	10357 39% 86%	10551 100% 101%	11099 35% 99%			11994 37% 96%	12242 69% 93%	13199 66% 103%	13972 36% 100%
EFA101162	SeqID IDENTITY COVERAGE	10356 58% 100%	10555 100% 100%	11100 58% 100%	11441 59% 100%	11679 59% 100%	11993 57% 99%	12249 78% 100%	13200 84% 100%	13971 58% 100%
EFA101163	SeqID IDENTITY COVERAGE	10355 66% 100%	10557 100% 101%	11101 68% 99%	11594 60% 97%		5174 70% 100%	12255 84% 101%	13201 90% 100%	
EFA101164	SeqID IDENTITY COVERAGE	10354 55% 91%	10558 100% 101%	11102 58% 91%	11593 47% 91%		5173 57% 85%	12258 66% 91%	13202 81% 97%	13970 55% 91%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101165	SeqID IDENTITY COVERAGE	10353 59% 95%	10559 100% 100%	11103 60% 95%	11592 52% 99%		5172 61% 95%	12259 78% 100%	13203 88% 100%	13969 59% 95%
EFA101169	SeqID IDENTITY COVERAGE	10133 27% 93%	10574 100% 100%	11091 28% 97%			12025 26% 94%	12516 41% 100%		13849 27% 93%
EFA101253	SeqID IDENTITY COVERAGE	10389 43% 97%	10852 100% 100%	11065 42% 97%	11551 31% 96%		11838 39% 99%	13072 54% 97%	13457 67% 99%	
EFA101257	SeqID IDENTITY COVERAGE	10124 40% 99%	10917 100% 100%	10976 39% 99%	11484 39% 101%		11914 37% 97%	12528 39% 97%	13357 58% 100%	14037 38% 101%
EFA101258	SeqID IDENTITY COVERAGE	10127 40% 97%	10918 100% 101%	10973 40% 96%	11513 39% 95%		11892 36% 96%	12802 41% 92%	13358 66% 95%	13871 29% 92%
EFA101322	SeqID IDENTITY COVERAGE		10620 100% 100%					12534 66% 86%	13328 65% 86%	
EFA101339	SeqID IDENTITY COVERAGE		10743 100% 100%		11448 33% 97%			12326 46% 98%	13391 60% 98%	
EFA101340	SeqID IDENTITY COVERAGE		10745 100% 102%							
EFA101354	SeqID IDENTITY COVERAGE	10047 33% 101%	10648 100% 100%	11089 33% 104%	11608 32% 101%		11935 34% 104%	12617 38% 97%	13345 36% 100%	13913 32% 101%
EFA101370	SeqID IDENTITY COVERAGE		10738 100% 101%					13126 31% 98%		
EFA101403	SeqID IDENTITY COVERAGE		10662 100% 100%					12941 34% 100%		
EFA101404	SeqID IDENTITY COVERAGE	10210 29% 99%	10663 100% 100%	11214 28% 102%	11554 39% 98%		11921 27% 100%	12135 59% 99%	13418 64% 99%	13925 30% 99%

TABLE VIIA (*Continued*)

LOCUSID	***Data***	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101409	SeqID IDENTITY COVERAGE	10350 54% 83%	10524 100% 101%	11106 58% 80%	11437 44% 86%		5170 53% 91%	12215 81% 91%	13207 87% 91%	
EFA101410	SeqID IDENTITY COVERAGE	10349 62% 101%	10525 100% 101%	11107 64% 101%	11436 63% 100%		5169 66% 100%	12216 90% 101%	13208 90% 101%	14108 62% 102%
EFA101411	SeqID IDENTITY COVERAGE	10348 50% 97%	10526 100% 101%	11108 43% 97%			5168 49% 93%	12217 66% 96%	13209 71% 99%	14107 46% 97%
EFA101412	SeqID IDENTITY COVERAGE	10347 60% 100%	10527 100% 101%	11109 59% 100%	11589 52% 98%	11654 61% 101%	5167 58% 99%	12218 85% 92%	13210 83% 100%	14106 60% 101%
EFA101414	SeqID IDENTITY COVERAGE	10345 49% 99%	10528 100% 101%	11111 47% 99%	11435 42% 99%		5165 46% 100%	12219 79% 101%	13212 81% 101%	14104 49% 101%
EFA101415	SeqID IDENTITY COVERAGE	10344 47% 98%	10529 100% 101%	11112 50% 98%	11434 39% 100%		5164 49% 98%	12220 63% 101%	13213 74% 101%	14103 47% 98%
EFA101416	SeqID IDENTITY COVERAGE	10343 50% 97%	10530 100% 101%	11113 48% 97%	11433 42% 91%		5163 52% 94%	12221 68% 99%	13214 82% 101%	14102 51% 98%
EFA101417	SeqID IDENTITY COVERAGE	10342 55% 100%	10531 100% 101%	11114 56% 95%	11432 61% 84%		5162 52% 92%	12222 72% 95%	13215 85% 94%	14101 55% 100%
EFA101424	SeqID IDENTITY COVERAGE	10220 44% 99%	10784 100% 101%	11276 38% 97%		11765 34% 73%	11950 36% 78%	12350 65% 101%	13280 79% 99%	13934 41% 99%
EFA101425	SeqID IDENTITY COVERAGE	10240 49% 99%	10785 100% 100%	11275 50% 99%			11925 39% 99%	12351 63% 100%	13281 78% 100%	13863 47% 84%
EFA101477	SeqID IDENTITY COVERAGE	10263 52% 91%	10861 100% 100%	10965 50% 95%	11562 41% 91%		11948 49% 95%	13066 59% 94%	13525 72% 91%	14089 50% 91%
EFA101536	SeqID IDENTITY COVERAGE	10281 30% 86%	10823 100% 100%							

TABLE VIIA (*Continued)*

LOCUSID	***Data***	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101540	SeqID IDENTITY COVERAGE	10041 51% 92%	10487 100% 100%	11149 50% 90%	11456 50% 86%		11941 49% 92%	12314 73% 92%	13438 76% 99%	13907 51% 92%
EFA101541	SeqID IDENTITY COVERAGE	10042 41% 100%	10488 100% 100%	11150 45% 98%	11620 35% 121%		11940 44% 101%	12742 63% 100%	13437 44% 116%	13908 41% 100%
EFA101583	SeqID IDENTITY COVERAGE		10593 100% 100%							
EFA101670	SeqID IDENTITY COVERAGE		10511 100% 100%							
EFA101682	SeqID IDENTITY COVERAGE	10238 45% 97%	10789 100% 100%	11178 45% 98%	11517 40% 95%		11829 44% 91%	12811 57% 96%	13673 57% 95%	13864 45% 97%
EFA101685	SeqID IDENTITY COVERAGE		10791 100% 100%		11369 47% 92%		12022 51% 98%	12492 62% 97%	13368 69% 99%	
EFA101686	SeqID IDENTITY COVERAGE	10237 39% 99%	10940 100% 100%	10999 37% 99%	11325 37% 99%		11901 36% 99%	12456 64% 99%	13455 63% 99%	13956 38% 99%
EFA101695	SeqID IDENTITY COVERAGE	10204 34% 104%	10629 100% 100%	11017 32% 106%	11479 34% 76%	11715 31% 93%	12106 35% 101%	12560 51% 100%	13284 75% 99%	13928 34% 105%
EFA101736	SeqID IDENTITY COVERAGE	10219 33% 100%	10775 100% 100%	11024 29% 100%			11924 27% 99%	12300 35% 98%	13340 32% 99%	13976 28% 100%
EFA101737	SeqID IDENTITY COVERAGE	10218 39% 98%	10778 100% 100%	11023 37% 98%			11923 42% 98%	12301 43% 100%	13341 43% 103%	13774 58% 96%
EFA101753	SeqID IDENTITY COVERAGE	10134 36% 91%	10552 100% 100%	11211 37% 89%			11895 36% 90%	12151 50% 94%	13693 50% 99%	13826 37% 91%
EFA101765	SeqID IDENTITY COVERAGE		10587 100% 100%					13010 28% 98%	13353 35% 97%	

TABLE VIIA (*Continued*)

LOCUSID	***Data***	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101790	SeqID	10414	10803	11085			11915	12306		13747
	IDENTITY	42%	100%	41%			39%	46%		41%
	COVERAGE	101%	100%	101%			101%	101%		101%
EFA101791	SeqID		10804					12359		
	IDENTITY		100%					37%		
	COVERAGE		101%					77%		
EFA101792	SeqID	10030	10805	11188	11458		5187	12360	13333	14077
	IDENTITY	31%	100%	32%	27%		33%	34%	47%	31%
	COVERAGE	98%	100%	96%	98%		99%	101%	100%	98%
EFA101795	SeqID	10329	10922	11159	11322		12062	12581	13363	13886
	IDENTITY	34%	100%	36%	36%		37%	36%	47%	32%
	COVERAGE	98%	101%	98%	99%		98%	98%	99%	97%
EFA101797	SeqID	10330	10924	11160	11321		12063	13127	13364	13885
	IDENTITY	53%	100%	52%	49%		55%	59%	74%	53%
	COVERAGE	98%	100%	98%	98%		98%	98%	99%	98%
EFA101799	SeqID	10048	10926	11014	11339		11934	12908	13366	13897
	IDENTITY	53%	100%	55%	49%		55%	54%	66%	54%
	COVERAGE	97%	100%	97%	94%		97%	97%	97%	97%
EFA101833	SeqID	10429	10720		11335		12039	12340	13451	14072
	IDENTITY	31%	100%		36%		35%	51%	59%	31%
	COVERAGE	79%	100%		92%		89%	92%	91%	79%
EFA101868	SeqID		10829							
	IDENTITY		100%							
	COVERAGE		100%							
EFA101872	SeqID	10305	10815	11044	11343	11639	11797	12568	13288	13779
	IDENTITY	62%	100%	62%	38%	61%	60%	93%	92%	62%
	COVERAGE	86%	102%	86%	86%	79%	95%	97%	102%	86%
EFA101873	SeqID		10816				11796			
	IDENTITY		100%				36%			
	COVERAGE		101%				94%			
EFA101892	SeqID	10454	10506	11048	11281		12005	12142	13190	14021
	IDENTITY	47%	100%	47%	41%		53%	49%	46%	47%
	COVERAGE	100%	101%	100%	97%		100%	101%	100%	100%
EFA101924	SeqID		10891		11532			12331	13463	
	IDENTITY		100%		36%			65%	65%	
	COVERAGE		100%		101%			100%	94%	

TABLE VIIA (*Continued*)

LOCUSID	***Data***	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101925	SeqID IDENTITY COVERAGE		10893 100% 100%					12332 59% 99%		
EFA101963	SeqID IDENTITY COVERAGE	10034 48% 105%	10848 100% 100%	11148 47% 105%	11536 49% 99%		12006 47% 108%	12552 57% 101%	13648 69% 100%	13901 48% 105%
EFA102006	SeqID IDENTITY COVERAGE		10580 100% 100%				11830 33% 84%	12804 42% 99%	13315 43% 95%	
EFA102022	SeqID IDENTITY COVERAGE	10313 53% 88%	10881 100% 101%	11224 53% 88%	11502 51% 87%	11754 54% 89%	12051 55% 88%	12324 78% 89%	13485 78% 89%	13767 52% 89%
EFA102023	SeqID IDENTITY COVERAGE	10312 51% 98%	10882 100% 100%	10989 50% 99%	11576 38% 99%	11755 50% 84%	12050 50% 97%	12325 63% 99%	13699 70% 99%	13768 50% 97%
EFA102091	SeqID IDENTITY COVERAGE	10363 60% 101%	10481 100% 100%	11060 61% 101%	11568 63% 100%		11858 62% 101%	12443 75% 100%	13233 86% 100%	13965 59% 101%
EFA102110	SeqID IDENTITY COVERAGE	10193 32% 103%	10841 100% 100%	11255 34% 94%			12082 34% 100%		13430 62% 100%	13752 32% 99%
EFA102183	SeqID IDENTITY COVERAGE	10393 55% 84%	10952 100% 100%	11057 54% 86%	11330 50% 85%		11774 54% 86%	12695 67% 98%	13420 78% 100%	13920 55% 84%
EFA102185	SeqID IDENTITY COVERAGE	10458 27% 93%	10950 100% 101%	11051 29% 90%	11421 29% 94%	11632 28% 93%	12075 29% 91%	12413 63% 91%	13501 73% 96%	13858 27% 93%
EFA102186	SeqID IDENTITY COVERAGE	10448 29% 92%	10949 100% 101%	10995 29% 90%	11579 27% 94%			12412 53% 101%	13543 60% 92%	13817 30% 90%
EFA102205	SeqID IDENTITY COVERAGE	10108 46% 71%	10769 100% 102%	10985 38% 82%	11375 56% 73%				13375 55% 96%	13997 37% 104%
EFA102253	SeqID IDENTITY COVERAGE	10275 53% 100%	10727 100% 100%	11175 55% 101%	11320 48% 101%		11933 53% 101%	12372 67% 100%	13376 80% 99%	13865 54% 96%

TABLE VIIA (*Continued*)

LOCUSID	***Data***	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA102282	SeqID IDENTITY COVERAGE		10729 100% 101%					12607 40% 81%	13424 46% 76%	
EFA102338	SeqID IDENTITY COVERAGE	10250 39% 95%	10651 100% 100%	11012 38% 92%	11488 35% 86%		11954 39% 98%	12940 42% 99%	13272 50% 99%	13705 38% 99%
EFA102350	SeqID IDENTITY COVERAGE		10632 100% 101%							
EFA102351	SeqID IDENTITY COVERAGE		10634 100% 100%					12795 33% 97%	13406 38% 101%	
EFA102352	SeqID IDENTITY COVERAGE	10028 40% 101%	10635 100% 100%	11186 39% 101%	11328 35% 101%	11691 40% 101%	12011 39% 101%	12347 51% 99%	13409 55% 100%	14075 40% 101%
EFA102353	SeqID IDENTITY COVERAGE	10029 32% 99%	10636 100% 100%	11187 34% 99%	11329 28% 83%		12010 32% 98%	12348 50% 98%	13398 61% 99%	14076 31% 99%
EFA102389	SeqID IDENTITY COVERAGE	10378 41% 97%	10904 100% 100%	11094 42% 83%			11781 40% 98%	12126 54% 82%	13263 52% 100%	
EFA102453	SeqID IDENTITY COVERAGE		10931 100% 101%	10995 29% 101%	11579 33% 88%	11762 33% 105%		12412 54% 101%	13502 54% 101%	13819 29% 96%
EFA102501	SeqID IDENTITY COVERAGE	10438 45% 112%	10626 100% 100%	11037 44% 111%	11410 40% 114%		11997 44% 113%	12447 75% 93%	13187 76% 96%	14043 45% 112%
EFA102502	SeqID IDENTITY COVERAGE	10439 47% 114%	10627 100% 100%	11036 46% 117%	11410 52% 79%		5179 46% 116%	12446 72% 99%	13646 78% 98%	14042 46% 114%
EFA102503	SeqID IDENTITY COVERAGE	10016 45% 99%	10643 100% 100%		11446 37% 101%		12027 43% 101%	12995 61% 98%	13481 65% 100%	13947 41% 85%
EFA102518	SeqID IDENTITY COVERAGE	10288 33% 105%	10647 100% 100%			11681 50% 71%		12248 34% 102%	13229 54% 100%	13881 32% 105%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA102541	SeqID	10327	10602	11241	11471		5188	12237	13356	13729
	IDENTITY	59%	100%	59%	49%		59%	69%	82%	56%
	COVERAGE	77%	101%	77%	73%		77%	77%	81%	77%
EFA102542	SeqID	10326	10603	11240	11288		12016	12238	13361	13732
	IDENTITY	75%	100%	70%	67%		75%	77%	100%	76%
	COVERAGE	95%	105%	95%	100%		95%	105%	100%	100%
EFA102549	SeqID	10338	10538	11117	11428		5159			
	IDENTITY	63%	100%	63%	71%		68%			
	COVERAGE	100%	103%	100%	100%		100%			
EFA102551	SeqID	10337	10539	11119	11427	11688	11990	12229	13221	14097
	IDENTITY	59%	100%	61%	58%	30%	62%	75%	81%	58%
	COVERAGE	96%	101%	91%	99%	74%	96%	101%	101%	96%
EFA102554	SeqID	10341	10532	11115			5161	12223	13216	
	IDENTITY	45%	100%	40%			42%	62%	63%	
	COVERAGE	93%	102%	93%			97%	102%	100%	
EFA102655	SeqID	10049	10733	11086	11305		11813	12952	13228	13898
	IDENTITY	47%	100%	47%	42%		48%	57%	60%	47%
	COVERAGE	97%	100%	99%	99%		99%	98%	108%	97%
EFA102656	SeqID		10734					12321	13668	
	IDENTITY		100%					55%	55%	
	COVERAGE		100%					100%	100%	
EFA102698	SeqID	10082	10909	10956			11807			14011
	IDENTITY	56%	100%	60%			31%			55%
	COVERAGE	96%	100%	96%			96%			96%
EFA102728	SeqID	10459	10948	11050	11420		12074	12411	13503	13859
	IDENTITY	51%	100%	53%	52%		54%	76%	81%	52%
	COVERAGE	89%	101%	89%	73%		82%	96%	100%	90%
EFA102736	SeqID	10285	10556	11205	11300		11943		13401	
	IDENTITY	53%	100%	52%	44%		51%		71%	
	COVERAGE	98%	100%	100%	98%		100%		99%	
EFA102764	SeqID	10201	10478	11054				12590	13425	13822
	IDENTITY	72%	100%	56%				68%	80%	71%
	COVERAGE	99%	100%	99%				99%	100%	99%
EFA102774	SeqID	10142	10896	11261	11362		12040	12150	13235	13978
	IDENTITY	50%	100%	52%	52%		51%	68%	74%	50%
	COVERAGE	96%	100%	96%	94%		95%	98%	97%	96%

TABLE VIIA (*Continued*)

LOCUSID	***Data***	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA102780	SeqID	10395	10908	11167	11616		11772	12701	13552	
	IDENTITY	49%	100%	46%	37%		51%	51%	46%	
	COVERAGE	77%	100%	76%	77%		75%	101%	98%	
EFA102788	SeqID	10176	10661	11223	11297		11882	12630	13303	13941
	IDENTITY	59%	100%	61%	54%		63%	70%	81%	59%
	COVERAGE	94%	101%	93%	97%		94%	93%	96%	94%
EFA102802	SeqID	10274	10854	11154	11298		11932	13128	13313	13866
	IDENTITY	66%	100%	64%	58%		64%	74%	83%	65%
	COVERAGE	99%	100%	100%	96%		100%	100%	100%	99%
EFA102813	SeqID	10191	10878	11005	11347		11815	12816	13492	13754
	IDENTITY	54%	100%	53%	51%		52%	64%	65%	53%
	COVERAGE	100%	100%	100%	99%		99%	99%	99%	100%
EFA102915	SeqID	10297	10640	10964	11323		11783	13090	13664	13737
	IDENTITY	27%	100%	32%	30%		31%	50%	52%	28%
	COVERAGE	100%	100%	100%	90%		100%	98%	99%	100%
EFA103021	SeqID	10434	10612	11039	11413		11999	12451	13517	
	IDENTITY	65%	100%	66%	60%		62%	86%	86%	
	COVERAGE	101%	101%	101%	99%		101%	101%	99%	
EFA103033	SeqID	10221	10681	11210	11607	11668	11801	12289	13191	14027
	IDENTITY	42%	100%	40%	29%	42%	39%	49%	56%	30%
	COVERAGE	91%	100%	93%	98%	94%	91%	93%	92%	93%
EFA103038	SeqID	10435	10613	11038	11412		11998	12784	13397	14046
	IDENTITY	54%	100%	52%	56%		51%	73%	73%	53%
	COVERAGE	99%	100%	100%	99%		100%	100%	100%	99%
EFA103039	SeqID	10293	10850	11041	11482	11728	11793	12541	13377	13741
	IDENTITY	45%	100%	46%	44%	40%	46%	73%	69%	45%
	COVERAGE	99%	100%	101%	98%	99%	99%	102%	101%	99%
EFA103062	SeqID	10437	10615	11072	11572		5180	12449	13247	14044
	IDENTITY	59%	100%	64%	54%		65%	64%	68%	59%
	COVERAGE	101%	101%	102%	102%		101%	99%	101%	102%
EFA103081	SeqID	10262	10862	10984	11403		11947		13415	14090
	IDENTITY	41%	100%	41%	40%		41%		74%	40%
	COVERAGE	85%	101%	83%	82%		80%		95%	85%
EFA103174	SeqID	10251	10689	10969	11370		11955	12600	13518	13703
	IDENTITY	32%	100%	32%	37%		33%	63%	77%	33%
	COVERAGE	93%	100%	94%	95%		96%	100%	100%	92%

TABLE VIIA (*Continued*)

LOCUSID	***Data***	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA103210	SeqID IDENTITY COVERAGE	10071 56% 97%	10688 100% 101%	11019 63% 98%	11371 39% 99%		11850 57% 97%	12601 79% 99%	13319 76% 101%	13945 57% 99%
EFA103268	SeqID IDENTITY COVERAGE	10365 69% 100%	10479 100% 101%	11062 70% 100%	11409 68% 100%		5178 70% 99%	12445 83% 101%	13231 93% 101%	13967 70% 101%
EFA103295	SeqID IDENTITY COVERAGE	10319 66% 77%	10633 100% 101%	11140 58% 85%	11493 58% 85%		12029 70% 77%	12640 79% 100%	13320 86% 96%	13771 60% 92%
EFA103348	SeqID IDENTITY COVERAGE		10873 100% 103%	10983 39% 82%	11402 59% 85%		11946 39% 82%			
EFA103365	SeqID IDENTITY COVERAGE	10360 57% 100%	10533 100% 101%	11096 58% 100%	11443 53% 97%	11643 58% 100%	5177 58% 100%	12224 82% 88%	13196 82% 101%	13975 58% 100%
EFA103375	SeqID IDENTITY COVERAGE	10177 50% 82%	10660 100% 102%	11222 52% 82%	11296 36% 97%		5120 50% 94%	12628 66% 102%	13302 78% 102%	
EFA103504	SeqID IDENTITY COVERAGE	10320 42% 97%	10671 100% 101%	11141 45% 97%	11492 41% 96%		12030 48% 97%	12638 63% 98%	13322 81% 100%	13766 41% 100%
EFA103508	SeqID IDENTITY COVERAGE		10672 100% 100%						13321 30% 80%	
EFA103571	SeqID IDENTITY COVERAGE	10335 45% 102%	10879 100% 100%	11121 47% 102%	11425 48% 103%		11988 47% 102%	12578 67% 99%	13240 68% 100%	14095 45% 102%
EFA103786	SeqID IDENTITY COVERAGE		10806 100% 100%					12361 59% 94%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100040	SeqID IDENTITY COVERAGE							12533 100% 101%		
SAU100053	SeqID IDENTITY COVERAGE	10366 32% 97%	10504 46% 100%	11075 30% 99%	11376 32% 81%	11723 33% 84%	11855 33% 81%	12143 100% 100%	13318 48% 100%	13814 32% 97%
SAU100056	SeqID IDENTITY COVERAGE		10930 39% 98%					12577 100% 100%	13477 33% 100%	
SAU100059	SeqID IDENTITY COVERAGE	10213 28% 71%	10598 70% 97%	11161 26% 95%	11528 26% 95%	11750 27% 71%	12064 28% 96%	12652 100% 100%	13433 25% 95%	13929 28% 71%
SAU100062	SeqID IDENTITY COVERAGE	10430 27% 103%	10618 52% 96%	10998 29% 103%	11603 29% 77%	11739 31% 76%		12309 100% 100%	13294 53% 97%	14040 28% 102%
SAU100077	SeqID IDENTITY COVERAGE		10565 64% 102%					12520 100% 100%	13464 62% 102%	
SAU100112	SeqID IDENTITY COVERAGE	10059 49% 97%			11477 52% 100%	11702 53% 77%	12096 46% 100%	12634 100% 100%		13895 49% 97%
SAU100114	SeqID IDENTITY COVERAGE	10152 44% 98%	10515 51% 98%	11279 43% 98%	11302 45% 98%		11851 43% 98%	12535 100% 100%	13387 25% 102%	13824 43% 98%
SAU100118	SeqID IDENTITY COVERAGE		10903 41% 101%				11828 27% 100%	12125 100% 100%	13262 37% 101%	
SAU100123	SeqID IDENTITY COVERAGE	10258 52% 98%	10628 43% 100%	11134 53% 97%	11489 47% 96%		5192 52% 98%	12526 100% 100%	13421 45% 82%	14088 52% 98%
SAU100131	SeqID IDENTITY COVERAGE	10466 35% 71%		11274 33% 97%			11960 40% 70%	12517 100% 100%		13854 35% 71%

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TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100133	SeqID IDENTITY COVERAGE	10311 34% 79%	10493 44% 99%	10990 34% 80%	11308 33% 78%	11703 30% 82%	11885 31% 79%	12574 100% 100%	13412 43% 99%	13769 34% 79%
SAU100139	SeqID IDENTITY COVERAGE	10355 65% 85%	10557 84% 86%	11101 66% 81%	11594 64% 83%		5174 63% 84%	12255 100% 101%	13201 86% 85%	
SAU100140	SeqID IDENTITY COVERAGE	10354 54% 93%	10558 66% 91%	11102 54% 93%	11440 40% 94%		5173 48% 93%	12258 100% 101%	13202 63% 91%	13970 54% 93%
SAU100141	SeqID IDENTITY COVERAGE	10353 55% 96%	10559 78% 101%	11103 58% 96%	11592 54% 96%		5172 57% 96%	12259 100% 100%	13203 74% 100%	13969 55% 96%
SAU100157	SeqID IDENTITY COVERAGE	10364 60% 100%	10480 78% 101%	11061 60% 100%	11408 55% 99%	11659 62% 88%	11996 57% 100%	12444 100% 101%	13232 77% 101%	13966 60% 101%
SAU100158	SeqID IDENTITY COVERAGE	10363 60% 98%	10481 75% 97%	11060 59% 98%	11568 63% 97%		11858 59% 98%	12443 100% 100%	13233 77% 97%	13965 58% 99%
SAU100162	SeqID IDENTITY COVERAGE	10069 43% 92%	10630 49% 89%	11239 44% 88%	11382 37% 80%		11971 43% 83%	12583 100% 100%	13597 46% 89%	14084 43% 93%
SAU100175	SeqID IDENTITY COVERAGE	10250 34% 98%	10651 42% 100%	11012 38% 93%			11954 34% 93%	12582 100% 100%	13272 42% 102%	13705 35% 99%
SAU100182	SeqID IDENTITY COVERAGE							12362 100% 101%		
SAU100186	SeqID IDENTITY COVERAGE	10043 46% 99%	10489 61% 99%	11124 44% 99%	11423 46% 98%		11939 45% 100%	12317 100% 101%	13355 54% 99%	13909 45% 101%
SAU100198	SeqID IDENTITY COVERAGE				11445 29% 78%			12120 100% 101%	13414 29% 79%	
SAU100227	SeqID IDENTITY COVERAGE		10765 36% 100%					12525 100% 100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100242	SeqID IDENTITY COVERAGE	10097 65% 94%		11201 62% 96%			11836 65% 95%	12336 100% 100%		14056 65% 94%
SAU100246	SeqID IDENTITY COVERAGE		10821 35% 101%					12496 100% 101%	13490 38% 93%	
SAU100251	SeqID IDENTITY COVERAGE							12363 100% 100%		
SAU100265	SeqID IDENTITY COVERAGE	10469 37% 88%						12122 100% 100%		
SAU100266	SeqID IDENTITY COVERAGE							12256 100% 101%		
SAU100272	SeqID IDENTITY COVERAGE		10617 26% 104%					12141 100% 100%		
SAU100275	SeqID IDENTITY COVERAGE	10041 52% 88%	10487 73% 94%	11149 47% 93%	11621 51% 98%		11941 51% 90%	12314 100% 100%	13438 65% 98%	13907 51% 88%
SAU100300	SeqID IDENTITY COVERAGE	10434 67% 99%	10612 86% 99%	11039 68% 99%	11413 63% 97%		11999 65% 99%	12451 100% 101%	13517 82% 97%	
SAU100301	SeqID IDENTITY COVERAGE	10433 41% 99%	10624 58% 98%	11083 41% 102%	11414 35% 96%		12000 42% 98%	12452 100% 101%	13168 51% 97%	
SAU100302	SeqID IDENTITY COVERAGE	10432 25% 92%		11082 34% 93%			12001 31% 103%	12453 100% 102%		
SAU100305	SeqID IDENTITY COVERAGE	10311 40% 94%	10774 50% 99%	10990 38% 94%			11885 40% 92%	12397 100% 100%	13491 49% 101%	13769 40% 94%
SAU100307	SeqID IDENTITY COVERAGE	10392 28% 99%	10725 32% 100%	10954 29% 99%		11685 28% 99%		12313 100% 100%	13252 29% 99%	13919 28% 99%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100308	SeqID IDENTITY COVERAGE	10013 26% 90%	10814 44% 86%	10963 30% 86%				12312 100% 100%	13244 40% 92%	13711 27% 90%
SAU100313	SeqID IDENTITY COVERAGE		10757 46% 99%					12661 100% 100%	13293 43% 100%	
SAU100315	SeqID IDENTITY COVERAGE	10419 54% 96%	10802 73% 96%	11136 53% 96%	11326 53% 96%	11727 55% 82%	12087 53% 97%	12358 100% 100%	13521 74% 91%	13791 54% 96%
SAU100323	SeqID IDENTITY COVERAGE	10216 32% 88%	10855 71% 99%					12575 100% 100%		13933 34% 88%
SAU100347	SeqID IDENTITY COVERAGE		10895 44% 106%	10961 30% 84%			12077 30% 100%	12334 100% 100%	13206 42% 100%	
SAU100355	SeqID IDENTITY COVERAGE		10683 42% 93%					12155 100% 100%	13300 31% 109%	
SAU100359	SeqID IDENTITY COVERAGE		10757 52% 97%					12239 100% 100%	13293 43% 99%	
SAU100381	SeqID IDENTITY COVERAGE	10411 28% 101%	10674 29% 99%				11903 33% 92%	12276 100% 100%		14031 28% 101%
SAU100389	SeqID IDENTITY COVERAGE	10473 27% 75%	10737 50% 95%		11374 41% 99%			12279 100% 100%	13344 27% 71%	
SAU100401	SeqID IDENTITY COVERAGE	10090 31% 95%	10706 30% 99%	10980 27% 95%		11641 33% 95%		12576 100% 101%		14053 31% 99%
SAU100412	SeqID IDENTITY COVERAGE	10102 31% 74%	10563 42% 100%	11194 30% 80%	11360 33% 74%		5150 35% 73%	12197 100% 100%	13468 40% 97%	
SAU100414	SeqID IDENTITY COVERAGE	10453 60% 96%	10556 80% 99%	11205 61% 98%	11300 60% 99%		11943 67% 91%	12148 100% 101%	13401 76% 96%	13872 60% 96%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100432	SeqID IDENTITY COVERAGE	10436 34% 98%	10614 60% 98%	11071 33% 100%	11411 31% 95%		5181 39% 99%	12450 100% 101%	13246 55% 98%	14045 31% 98%
SAU100433	SeqID IDENTITY COVERAGE	10437 58% 97%	10615 64% 99%	11072 63% 98%	11572 57% 99%		5180 58% 98%	12449 100% 101%	13247 69% 99%	14044 58% 98%
SAU100436	SeqID IDENTITY COVERAGE		10569 27% 100%					12154 100% 100%	13393 27% 100%	
SAU100443	SeqID IDENTITY COVERAGE	10272 40% 92%	10894 52% 100%	11081 39% 96%			11930 38% 92%	12333 100% 100%	13515 45% 100%	13869 40% 92%
SAU100444	SeqID IDENTITY COVERAGE	10440 29% 75%	10583 30% 88%	11016 41% 94%	11540 41% 90%		11967 28% 81%	12392 100% 100%	13403 52% 91%	14041 29% 75%
SAU100475	SeqID IDENTITY COVERAGE		10927 33% 101%				11911 30% 101%	12337 100% 100%		
SAU100478	SeqID IDENTITY COVERAGE			11273 25% 96%				12605 100% 100%		
SAU100489	SeqID IDENTITY COVERAGE	10332 33% 101%	10685 33% 102%	11074 31% 99%	11580 34% 94%	11729 34% 101%	11778 29% 99%	12566 100% 100%	13298 34% 97%	14100 33% 94%
SAU100496	SeqID IDENTITY COVERAGE		10744 40% 80%					12484 100% 100%		
SAU100497	SeqID IDENTITY COVERAGE	10245 46% 99%	10709 59% 101%	11171 49% 99%	11395 44% 100%		11792 48% 99%	12140 100% 100%		13740 45% 100%
SAU100514	SeqID IDENTITY COVERAGE	10215 52% 93%			11388 34% 95%		12036 51% 98%	12626 100% 100%		13932 51% 95%
SAU100521	SeqID IDENTITY COVERAGE	10251 43% 104%		10969 39% 108%	11370 34% 103%		11955 39% 103%	12600 100% 100%		13703 42% 104%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100522	SeqID IDENTITY COVERAGE	10114 36% 91%		11206 34% 89%		11680 30% 80%	11904 36% 90%	12599 100% 100%		14007 35% 91%
SAU100527	SeqID IDENTITY COVERAGE	10298 44% 98%	10721 48% 97%	10996 42% 99%			11782 41% 98%	12341 100% 101%	13452 43% 98%	13736 45% 97%
SAU100528	SeqID IDENTITY COVERAGE		10521 30% 83%					12507 100% 101%	13470 33% 71%	
SAU100532	SeqID IDENTITY COVERAGE	10235 39% 101%	10645 47% 100%	11128 29% 72%	11389 34% 90%			12580 100% 100%	13193 40% 97%	13744 31% 72%
SAU100542	SeqID IDENTITY COVERAGE	10371 52% 100%		11070 51% 98%	11422 46% 98%		12017 31% 102%	12532 100% 100%	13444 35% 102%	13806 52% 100%
SAU100546	SeqID IDENTITY COVERAGE	10359 43% 97%		11097 46% 97%	11596 34% 90%		5176 47% 99%	12235 100% 100%	13197 66% 99%	13974 46% 91%
SAU100547	SeqID IDENTITY COVERAGE	10358 41% 92%	10549 62% 100%	11098 39% 97%	11595 40% 96%		5175 46% 97%	12240 100% 100%	13198 63% 100%	13973 41% 93%
SAU100557	SeqID IDENTITY COVERAGE		10928 50% 99%					12565 100% 100%	13651 49% 99%	
SAU100582	SeqID IDENTITY COVERAGE							12503 100% 100%		
SAU100590	SeqID IDENTITY COVERAGE							12121 100% 100%		
SAU100595	SeqID IDENTITY COVERAGE	10051 47% 88%	10832 66% 89%		11464 42% 89%		12109 50% 93%	12547 100% 100%	13174 46% 90%	13722 42% 91%
SAU100596	SeqID IDENTITY COVERAGE	10050 36% 99%	10833 50% 99%	11067 31% 100%	11624 41% 92%	11656 38% 89%	12110 42% 95%	12548 100% 100%	13173 30% 106%	13720 32% 95%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100601	SeqID IDENTITY COVERAGE							12616 100% 100%		
SAU100608	SeqID IDENTITY COVERAGE	10032 30% 102%	10870 61% 96%	11190 29% 100%	11349 29% 98%		12008 34% 87%	12293 100% 100%	13507 50% 96%	14079 28% 104%
SAU100610	SeqID IDENTITY COVERAGE							12294 100% 100%		
SAU100613	SeqID IDENTITY COVERAGE	10378 44% 91%	10904 54% 88%	11094 43% 93%			11781 46% 73%	12126 100% 100%	13589 49% 89%	
SAU100617	SeqID IDENTITY COVERAGE		10502 26% 91%					12295 100% 100%	13314 25% 91%	
SAU100633	SeqID IDENTITY COVERAGE	10079 27% 92%	10589 42% 103%			11698 25% 89%	5107 29% 101%	12515 100% 100%	13644 35% 105%	13724 26% 103%
SAU100646	SeqID IDENTITY COVERAGE	10051 50% 95%	10570 48% 94%		11464 46% 97%		12109 49% 95%	12168 100% 100%	13174 42% 95%	14109 50% 96%
SAU100658	SeqID IDENTITY COVERAGE	10322 49% 100%	10813 59% 100%	11177 49% 100%	11351 46% 100%		12018 48% 100%	12388 100% 100%	13186 58% 100%	13733 49% 100%
SAU100659	SeqID IDENTITY COVERAGE	10045 47% 92%	10923 54% 92%	11174 45% 95%	11601 40% 103%		11937 46% 97%	12390 100% 101%	13616 56% 95%	13911 44% 81%
SAU100679	SeqID IDENTITY COVERAGE	10303 32% 96%		10997 31% 99%	11453 32% 106%	11713 33% 96%	11799 35% 97%	12137 100% 100%	13329 42% 104%	13757 35% 96%
SAU100684	SeqID IDENTITY COVERAGE	10412 46% 97%			11486 40% 99%		12097 46% 99%	12632 100% 100%		13749 46% 97%
SAU100685	SeqID IDENTITY COVERAGE							12633 100% 100%		

TABLE VIIA (Continued)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100689	SeqID IDENTITY COVERAGE		10694 55% 98%					12323 100% 100%	13311 46% 96%	
SAU100702	SeqID IDENTITY COVERAGE		10655 46% 97%					12196 100% 100%	13671 41% 91%	
SAU100710	SeqID IDENTITY COVERAGE						11908 27% 73%	12546 100% 101%		
SAU100714	SeqID IDENTITY COVERAGE	10465 48% 108%	10675 66% 100%	11238 41% 110%	11563 41% 102%		11961 44% 108%	12635 100% 103%	13382 60% 101%	13853 48% 108%
SAU100731	SeqID IDENTITY COVERAGE	10071 62% 99%	10688 79% 100%	11019 67% 100%	11371 40% 101%		11850 63% 99%	12601 100% 101%	13319 76% 100%	13945 60% 101%
SAU100733	SeqID IDENTITY COVERAGE	10415 41% 95%			11611 33% 92%	11636 42% 74%	12084 42% 95%	12602 100% 100%		13746 39% 95%
SAU100734	SeqID IDENTITY COVERAGE	10321 28% 98%	10573 36% 95%	11142 29% 97%	11306 27% 90%		12031 28% 93%	12603 100% 100%	13273 31% 72%	13734 29% 101%
SAU100736	SeqID IDENTITY COVERAGE		10585 27% 97%					12391 100% 100%	13404 26% 97%	
SAU100738	SeqID IDENTITY COVERAGE	10188 48% 97%	10847 45% 98%	10953 46% 98%	11600 42% 97%	11634 48% 94%	11907 51% 97%	12624 100% 100%	13169 45% 97%	13981 49% 97%
SAU100741	SeqID IDENTITY COVERAGE	10081 65% 100%	10591 50% 101%		11459 35% 82%		11776 54% 100%	12409 100% 101%		13714 66% 101%
SAU100745	SeqID IDENTITY COVERAGE	10442 34% 98%	10484 53% 97%	11202 35% 100%	11607 31% 99%	11733 35% 101%	11906 34% 98%	12596 100% 100%	13453 49% 98%	13847 35% 101%
SAU100747	SeqID IDENTITY COVERAGE		10749 32% 74%					12597 100% 100%	13266 31% 73%	

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100751	SeqID	10425	10866	11080		11747	11927	12335	13431	13788
	IDENTITY	62%	64%	59%		62%	62%	100%	63%	61%
	COVERAGE	99%	99%	98%		87%	99%	100%	99%	99%
SAU100752	SeqID	10140					11976	12524		14022
	IDENTITY	31%					35%	100%		38%
	COVERAGE	71%					82%	100%		72%
SAU100767	SeqID	10290					12094	12579		13875
	IDENTITY	43%					42%	100%		42%
	COVERAGE	100%					90%	100%		100%
SAU100771	SeqID	10084					11821	12545	13306	13710
	IDENTITY	30%					29%	100%	28%	26%
	COVERAGE	88%					80%	101%	90%	94%
SAU100773	SeqID	10055	10758	11093	11336	11763	11928	12377	13250	
	IDENTITY	47%	70%	41%	41%	46%	51%	100%	70%	
	COVERAGE	94%	100%	98%	96%	94%	93%	101%	96%	
SAU100776	SeqID							12482		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100778	SeqID	10083		10957			11970	12514		14062
	IDENTITY	52%		52%			45%	100%		47%
	COVERAGE	89%		89%			88%	100%		89%
SAU100793	SeqID							12188	13392	
	IDENTITY							100%	27%	
	COVERAGE							100%	103%	
SAU100794	SeqID	10203						12189		
	IDENTITY	25%						100%		
	COVERAGE	101%						100%		
SAU100799	SeqID							12682		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100808	SeqID							12345		14081
	IDENTITY							100%		35%
	COVERAGE							100%		70%
SAU100810	SeqID	10070					11824	12343		14080
	IDENTITY	51%					49%	100%		50%
	COVERAGE	94%					96%	100%		96%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100813	SeqID IDENTITY COVERAGE	10314 47% 98%	10764 63% 94%	11216 47% 100%	11501 45% 91%		5198 48% 92%	12322 100% 100%	13381 58% 95%	13765 50% 92%
SAU100831	SeqID IDENTITY COVERAGE	10376 42% 97%	10741 58% 98%	11058 42% 102%			12093 42% 98%	12403 100% 100%	13349 51% 98%	13811 42% 101%
SAU100836	SeqID IDENTITY COVERAGE							12212 100% 100%		
SAU100838	SeqID IDENTITY COVERAGE							12211 100% 100%		
SAU100839	SeqID IDENTITY COVERAGE		10794 42% 100%					12210 100% 100%	13183 44% 100%	
SAU100843	SeqID IDENTITY COVERAGE	10126 26% 101%	10921 28% 73%	10974 28% 101%	11342 28% 102%			12328 100% 100%	13601 26% 100%	14092 26% 104%
SAU100845	SeqID IDENTITY COVERAGE							12329 100% 100%		
SAU100858	SeqID IDENTITY COVERAGE	10256 37% 106%	10776 48% 98%		11367 35% 103%	11719 37% 106%		12401 100% 101%	13472 39% 100%	13796 39% 106%
SAU100859	SeqID IDENTITY COVERAGE	10446 33% 94%	10777 38% 94%	11254 33% 95%	11548 35% 96%		12071 34% 94%	12402 100% 100%	13473 38% 92%	14026 32% 95%
SAU100865	SeqID IDENTITY COVERAGE	10252 39% 100%	10877 49% 99%	11010 41% 100%	11406 28% 101%		11956 44% 99%	12648 100% 100%	13506 48% 99%	13704 38% 100%
SAU100866	SeqID IDENTITY COVERAGE	10191 54% 100%	10878 64% 100%	11005 51% 100%	11347 51% 100%		11815 53% 100%	12553 100% 100%	13492 57% 99%	13754 55% 100%
SAU100879	SeqID IDENTITY COVERAGE							12483 100% 100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100880	SeqID	10429	10720		11335		12039	12340	13451	14072
	IDENTITY	31%	51%		35%		36%	100%	45%	32%
	COVERAGE	81%	95%		97%		81%	100%	99%	85%
SAU100882	SeqID	10322	10750	11177	11351		12018	12374	13330	13733
	IDENTITY	43%	54%	42%	40%		45%	100%	52%	43%
	COVERAGE	98%	98%	98%	99%		98%	100%	98%	98%
SAU100885	SeqID	10410	10754	11001	11509		12095	12376		14032
	IDENTITY	52%	67%	53%	52%		53%	100%		52%
	COVERAGE	93%	74%	94%	96%		92%	100%		93%
SAU100886	SeqID	10224	10701	11213	11357		11905	12139	13348	13957
	IDENTITY	38%	60%	38%	36%		36%	100%	52%	38%
	COVERAGE	97%	83%	93%	99%		104%	100%	102%	98%
SAU100887	SeqID	10393	10952	11057	11330		11774	12138	13342	13920
	IDENTITY	50%	51%	50%	49%		48%	100%	70%	50%
	COVERAGE	85%	96%	82%	83%		83%	100%	96%	85%
SAU100899	SeqID							12277		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100901	SeqID							12278		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100916	SeqID	10209	10887					12394		13876
	IDENTITY	32%	34%					100%		32%
	COVERAGE	75%	72%					101%		75%
SAU100920	SeqID	10060	10772	11191	11530	11756	11983	12395		13896
	IDENTITY	43%	48%	31%	28%	40%	30%	100%		43%
	COVERAGE	91%	86%	87%	91%	86%	90%	100%		91%
SAU100921	SeqID	10027	10773	11185			12012	12396	13478	14074
	IDENTITY	32%	43%	33%			33%	100%	34%	32%
	COVERAGE	101%	96%	96%			96%	100%	98%	101%
SAU100932	SeqID	10095		11271			11834	12615		14055
	IDENTITY	39%		36%			39%	100%		39%
	COVERAGE	101%		101%			102%	100%		101%
SAU100944	SeqID	10017	10687	11219	11506		12057	12505	13498	14012
	IDENTITY	37%	26%	36%	36%		39%	100%	27%	39%
	COVERAGE	80%	108%	79%	79%		83%	100%	83%	80%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100952	SeqID IDENTITY COVERAGE		10717 33% 104%					12523 100% 100%	13312 31% 102%	
SAU100959	SeqID IDENTITY COVERAGE		10704 58% 99%					12485 100% 100%	13504 49% 101%	
SAU100961	SeqID IDENTITY COVERAGE	10320 42% 98%	10671 63% 99%	11141 47% 98%	11312 40% 97%		12030 50% 98%	12638 100% 101%	13322 57% 101%	13766 42% 99%
SAU100962	SeqID IDENTITY COVERAGE				11299 28% 80%			12639 100% 101%	13577 26% 92%	
SAU100963	SeqID IDENTITY COVERAGE	10319 60% 84%	10633 79% 96%	11140 59% 81%	11493 61% 81%		12029 63% 84%	12640 100% 101%	13320 81% 92%	13771 60% 88%
SAU100964	SeqID IDENTITY COVERAGE		10501 61% 101%	11139 45% 76%			12028 47% 77%	12641 100% 100%	13331 60% 101%	
SAU100965	SeqID IDENTITY COVERAGE							12642 100% 101%		
SAU100970	SeqID IDENTITY COVERAGE	10128 52% 99%	10516 54% 99%	11247 39% 100%	11512 47% 100%		11891 52% 99%	12529 100% 100%	13362 46% 99%	
SAU100996	SeqID IDENTITY COVERAGE		10686 38% 97%		11350 34% 73%			12606 100% 100%	13600 39% 96%	
SAU101006	SeqID IDENTITY COVERAGE	10185 29% 84%	10572 40% 98%	11022 31% 87%	11473 26% 94%		5122 26% 79%	12190 100% 100%		13820 30% 91%
SAU101020	SeqID IDENTITY COVERAGE							12710 100% 100%		
SAU101024	SeqID IDENTITY COVERAGE							12711 100% 101%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101028	SeqID IDENTITY COVERAGE	10034 46% 106%	10848 57% 101%	11148 43% 107%	11364 46% 100%		12006 46% 108%	12552 100% 100%	13471 55% 100%	13901 45% 106%
SAU101034	SeqID IDENTITY COVERAGE		10578 36% 80%					12608 100% 100%	13654 37% 71%	
SAU101038	SeqID IDENTITY COVERAGE		10716 42% 96%				11822 35% 78%	12521 100% 101%	13428 36% 103%	
SAU101039	SeqID IDENTITY COVERAGE							12522 100% 100%		
SAU101065	SeqID IDENTITY COVERAGE	10221 37% 98%	10681 49% 103%	11210 40% 100%	11607 28% 108%	11668 38% 97%	11801 36% 98%	12289 100% 100%	13191 46% 102%	14027 31% 98%
SAU101067	SeqID IDENTITY COVERAGE		10682 41% 100%					12290 100% 100%	13394 40% 99%	
SAU101070	SeqID IDENTITY COVERAGE		10770 40% 89%					12291 100% 100%	13380 32% 82%	
SAU101084	SeqID IDENTITY COVERAGE	10066 36% 90%		11156 34% 102%			11974 35% 92%	12283 100% 100%		
SAU101085	SeqID IDENTITY COVERAGE	10170 37% 89%		11263 34% 88%	11462 37% 94%		11973 38% 94%	12284 100% 100%	13225 47% 101%	13993 32% 88%
SAU101086	SeqID IDENTITY COVERAGE				11366 42% 74%		11972 34% 94%	12285 100% 100%	13666 49% 101%	
SAU101090	SeqID IDENTITY COVERAGE		10755 36% 97%					12191 100% 100%	13188 31% 97%	
SAU101092	SeqID IDENTITY COVERAGE	10450 35% 71%	10567 33% 96%				11847 30% 72%	12192 100% 100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101104	SeqID	10135	10768	11248	11404	11732	11869	12195	13482	13827
	IDENTITY	38%	45%	39%	37%	37%	42%	100%	38%	37%
	COVERAGE	98%	100%	100%	92%	99%	99%	100%	96%	99%
SAU101143	SeqID	10040		11157	11315		11968	12502		13906
	IDENTITY	47%		27%	43%		44%	100%		47%
	COVERAGE	99%		82%	98%		100%	100%		99%
SAU101145	SeqID		10548				12070	12299		
	IDENTITY		42%				43%	100%		
	COVERAGE		98%				96%	101%		
SAU101155	SeqID	10287	10697	11077	11352	11690	11944	12310	13549	13868
	IDENTITY	43%	49%	40%	30%	42%	42%	100%	37%	43%
	COVERAGE	95%	95%	95%	86%	95%	94%	100%	76%	95%
SAU101156	SeqID	10426	10698	11032	11333		12083	12311		13790
	IDENTITY	56%	63%	60%	52%		58%	100%		55%
	COVERAGE	96%	101%	96%	97%		96%	101%		96%
SAU101159	SeqID		10891		11532			12331	13463	
	IDENTITY		65%		36%			100%	54%	
	COVERAGE		100%		100%			100%	104%	
SAU101175	SeqID							12213		
	IDENTITY							100%		
	COVERAGE							101%		
SAU101180	SeqID	10061	10888				11910	12656		
	IDENTITY	38%	50%				37%	100%		
	COVERAGE	72%	89%				70%	100%		
SAU101183	SeqID		10843					12304		
	IDENTITY		42%					100%		
	COVERAGE		102%					100%		
SAU101184	SeqID	10477	10711	11218	11376	11735	12033	12305	13499	13709
	IDENTITY	37%	46%	36%	30%	38%	35%	100%	44%	38%
	COVERAGE	86%	100%	102%	85%	82%	85%	100%	98%	82%
SAU101189	SeqID							12264		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101197	SeqID	10180	10787	11024			11924	12300	13340	13976
	IDENTITY	31%	44%	31%			27%	100%	46%	30%
	COVERAGE	98%	98%	101%			100%	100%	98%	98%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101198	SeqID IDENTITY COVERAGE	10218 43% 74%	10786 50% 98%	11023 43% 73%			11923 41% 75%	12301 100% 100%	13341 46% 102%	
SAU101199	SeqID IDENTITY COVERAGE	10088 29% 97%	10742 40% 86%	10970 31% 94%			11949 36% 97%	12302 100% 100%	13178 37% 87%	14052 30% 98%
SAU101220	SeqID IDENTITY COVERAGE	10286 32% 74%	10864 37% 81%					12645 100% 100%	13390 39% 99%	13870 31% 74%
SAU101224	SeqID IDENTITY COVERAGE				11533 28% 77%			12647 100% 100%		
SAU101226	SeqID IDENTITY COVERAGE		10837 52% 96%			11658 28% 75%	11825 37% 90%	12298 100% 100%	13296 27% 77%	13721 27% 77%
SAU101231	SeqID IDENTITY COVERAGE	10301 32% 101%	10513 61% 100%				12079 32% 73%	12303 100% 101%		13759 31% 106%
SAU101235	SeqID IDENTITY COVERAGE		10616 37% 84%	11087 27% 90%				12561 100% 100%	13486 35% 97%	
SAU101236	SeqID IDENTITY COVERAGE	10089 42% 101%	10500 55% 77%			11673 29% 108%	11951 39% 100%	12564 100% 100%	13474 35% 103%	
SAU101239	SeqID IDENTITY COVERAGE				11361 33% 98%			12570 100% 100%		
SAU101240	SeqID IDENTITY COVERAGE							12573 100% 101%		
SAU101242	SeqID IDENTITY COVERAGE	10335 48% 104%	10879 67% 101%	11121 47% 104%	11425 48% 105%		11988 47% 104%	12578 100% 101%	13240 55% 101%	14095 47% 105%
SAU101247	SeqID IDENTITY COVERAGE		10919 32% 91%				11984 36% 90%	12512 100% 100%	13359 33% 85%	

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101262	SeqID	10137	10735		11399		11922	12488	13238	13837
	IDENTITY	28%	70%		47%		33%	100%	67%	28%
	COVERAGE	73%	100%		101%		97%	100%	100%	73%
SAU101266	SeqID	10238	10789	11178	11517		11829	12490	13317	13864
	IDENTITY	45%	57%	46%	41%		43%	100%	51%	44%
	COVERAGE	100%	99%	100%	98%		89%	100%	98%	100%
SAU101267	SeqID							12364		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101270	SeqID	10175	10718	11220	11324		11881	12365	13383	13942
	IDENTITY	50%	62%	47%	45%		52%	100%	61%	50%
	COVERAGE	96%	99%	97%	93%		97%	100%	98%	96%
SAU101271	SeqID	10174	10719	11221	11556		11880	12366	13385	13943
	IDENTITY	37%	46%	36%	25%		35%	100%	46%	37%
	COVERAGE	100%	102%	100%	100%		100%	100%	101%	75%
SAU101275	SeqID	10232	10684	10981	11521	11708	11845	12604	13299	13954
	IDENTITY	35%	57%	38%	33%	34%	34%	100%	57%	35%
	COVERAGE	95%	101%	93%	98%	96%	94%	100%	101%	95%
SAU101286	SeqID		10884					12292	13189	
	IDENTITY		47%					100%	40%	
	COVERAGE		100%					101%	99%	
SAU101293	SeqID							12631		
	IDENTITY							100%		
	COVERAGE							101%		
SAU101300	SeqID		10751					12557	13194	
	IDENTITY		57%					100%	54%	
	COVERAGE		93%					101%	90%	
SAU101301	SeqID		10752				11785	12558	13195	
	IDENTITY		57%				27%	100%	54%	
	COVERAGE		96%				94%	101%	99%	
SAU101302	SeqID		10753		11317			12559	13611	
	IDENTITY		49%		33%			100%	26%	
	COVERAGE		101%		86%			101%	72%	
SAU101310	SeqID	10330	10924	11160	11321		12063	12562	13364	13885
	IDENTITY	47%	52%	48%	43%		47%	100%	51%	47%
	COVERAGE	98%	98%	98%	98%		98%	100%	98%	98%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101311	SeqID IDENTITY COVERAGE	10094 46% 98%		11278 46% 98%			11859 42% 96%	12563 100% 100%		13891 46% 95%
SAU101320	SeqID IDENTITY COVERAGE	10263 50% 100%	10861 59% 99%	10965 49% 99%	11562 39% 100%		11948 51% 99%	12128 100% 100%	13254 56% 97%	14089 49% 100%
SAU101327	SeqID IDENTITY COVERAGE	10018 35% 100%	10710 46% 97%	11147 43% 101%			11779 34% 92%	12612 100% 101%	13495 35% 99%	14014 35% 100%
SAU101339	SeqID IDENTITY COVERAGE	10093 55% 99%	10520 30% 74%		11365 26% 74%		11839 54% 97%	12399 100% 100%	13405 27% 76%	13888 45% 99%
SAU101340	SeqID IDENTITY COVERAGE	10092 37% 106%					11840 35% 101%	12400 100% 101%		13889 39% 104%
SAU101341	SeqID IDENTITY COVERAGE	10230 47% 93%	10925 55% 92%	11212 48% 92%	11385 48% 98%		11898 45% 92%	12618 100% 100%	13365 48% 100%	13952 47% 93%
SAU101343	SeqID IDENTITY COVERAGE	10422 50% 99%	10649 55% 100%	11162 49% 99%		11721 50% 99%		12619 100% 100%	13346 58% 92%	13785 51% 99%
SAU101344	SeqID IDENTITY COVERAGE	10171 48% 81%	10650 62% 88%	11252 40% 79%			11826 37% 82%	12620 100% 100%	13347 44% 79%	13755 38% 81%
SAU101346	SeqID IDENTITY COVERAGE	10058 36% 99%			11282 35% 103%		11803 43% 99%	12621 100% 100%		13894 36% 99%
SAU101347	SeqID IDENTITY COVERAGE	10139 63% 100%		11163 29% 96%	11283 62% 101%		11877 62% 100%	12622 100% 100%	13259 30% 91%	13839 62% 100%
SAU101350	SeqID IDENTITY COVERAGE	10184 61% 95%	10508 56% 98%		11318 32% 81%		12069 46% 100%	12487 100% 100%	13286 55% 97%	13982 60% 97%
SAU101351	SeqID IDENTITY COVERAGE		10507 60% 96%					12486 100% 100%	13285 59% 96%	

TABLE VIIA (Continued)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101360	SeqID	10138	10571	10977	11598	11684	11878	12555	13175	13838
	IDENTITY	56%	70%	54%	35%	55%	58%	100%	71%	56%
	COVERAGE	98%	101%	98%	97%	88%	98%	100%	101%	98%
SAU101365	SeqID	10269	10491	11127	11577		11809	12556	13295	13874
	IDENTITY	45%	55%	44%	40%		45%	100%	50%	45%
	COVERAGE	101%	101%	101%	99%		101%	100%	100%	101%
SAU101366	SeqID	10147	10654					12266	13179	13843
	IDENTITY	49%	73%					100%	56%	48%
	COVERAGE	99%	98%					100%	99%	99%
SAU101369	SeqID							12274		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101371	SeqID				11372		11902	12275	13243	
	IDENTITY				40%		32%	100%	34%	
	COVERAGE				86%		79%	100%	77%	
SAU101381	SeqID	10373						12145	13432	
	IDENTITY	26%						100%	41%	
	COVERAGE	98%						100%	99%	
SAU101382	SeqID	10239	10707	11179	11292	11635	11879	12146	13657	13862
	IDENTITY	53%	60%	50%	42%	39%	53%	100%	63%	52%
	COVERAGE	98%	99%	97%	97%	79%	98%	100%	96%	98%
SAU101383	SeqID	10317	10625	11226	11418		12055	12147	13422	13761
	IDENTITY	37%	39%	36%	26%		38%	100%	37%	39%
	COVERAGE	102%	90%	97%	98%		94%	100%	112%	94%
SAU101385	SeqID	10403	10830	11030	11368	11640	12115	12385	13508	14067
	IDENTITY	33%	52%	31%	27%	32%	29%	100%	38%	32%
	COVERAGE	99%	90%	92%	89%	96%	98%	100%	92%	99%
SAU101387	SeqID	10402	10839		11549		12114	12386	13509	14068
	IDENTITY	27%	35%		27%		27%	100%	32%	27%
	COVERAGE	87%	88%		71%		87%	101%	90%	87%
SAU101389	SeqID	10401	10801	11029	11400		12113	12387	13510	14069
	IDENTITY	55%	72%	57%	60%		57%	100%	74%	55%
	COVERAGE	98%	99%	99%	100%		98%	100%	94%	98%
SAU101398	SeqID	10313	10881	11224	11502	11754	12051	12324	13485	13767
	IDENTITY	55%	78%	54%	51%	57%	56%	100%	68%	54%
	COVERAGE	100%	101%	100%	99%	101%	100%	101%	101%	101%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101399	SeqID IDENTITY COVERAGE	10312 50% 99%	10882 63% 100%	10989 48% 98%	11416 38% 97%	11755 51% 85%	12050 51% 97%	12325 100% 100%	13699 58% 99%	13768 49% 99%
SAU101400	SeqID IDENTITY COVERAGE		10743 46% 96%		11448 32% 95%			12326 100% 100%	13391 41% 96%	
SAU101408	SeqID IDENTITY COVERAGE	10267 37% 100%	10509 43% 99%					12308 100% 100%	13278 42% 101%	14050 39% 100%
SAU101421	SeqID IDENTITY COVERAGE		10676 38% 93%					12498 100% 100%		
SAU101427	SeqID IDENTITY COVERAGE							12500 100% 100%	13234 48% 100%	
SAU101432	SeqID IDENTITY COVERAGE			11046 57% 99%	11286 60% 100%	11744 63% 101%	12065 68% 99%	12184 100% 101%	13538 26% 73%	
SAU101436	SeqID IDENTITY COVERAGE	10271 27% 90%		11045 62% 99%	11285 61% 97%		12067 59% 98%	12183 100% 100%		13873 27% 90%
SAU101438	SeqID IDENTITY COVERAGE	10146 30% 88%	10825 29% 94%	11042 29% 89%				12379 100% 100%	13337 27% 94%	13842 30% 88%
SAU101444	SeqID IDENTITY COVERAGE	10254 60% 100%	10827 66% 101%	11144 57% 100%	11301 54% 100%		12034 60% 100%	12381 100% 100%	13335 61% 99%	13792 59% 100%
SAU101445	SeqID IDENTITY COVERAGE	10248 52% 99%	10828 70% 100%	11207 52% 96%			12037 54% 99%	12382 100% 100%	13408 72% 100%	13949 51% 100%
SAU101446	SeqID IDENTITY COVERAGE	10411 50% 98%	10674 59% 100%				11903 33% 97%	12383 100% 100%		14031 50% 99%
SAU101447	SeqID IDENTITY COVERAGE							12683 100% 101%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101452	SeqID IDENTITY COVERAGE							12684 100% 100%		
SAU101455	SeqID IDENTITY COVERAGE							12686 100% 100%		
SAU101461	SeqID IDENTITY COVERAGE		10705 54% 93%				11790 26% 86%	12680 100% 101%		
SAU101463	SeqID IDENTITY COVERAGE	10268 29% 77%	10708 45% 98%				11919 26% 91%	12679 100% 101%	13584 26% 88%	14051 29% 77%
SAU101476	SeqID IDENTITY COVERAGE	10469 38% 84%	10905 29% 94%					12254 100% 100%	13454 25% 95%	13905 26% 73%
SAU101481	SeqID IDENTITY COVERAGE	10125 40% 93%	10920 39% 95%	10975 40% 96%	11290 32% 93%		11894 39% 96%	12130 100% 100%	13580 41% 96%	
SAU101482	SeqID IDENTITY COVERAGE	10126 55% 98%	10921 51% 100%	10974 52% 98%	11342 44% 98%	11738 36% 77%	11893 52% 98%	12123 100% 100%	13360 48% 99%	14092 37% 101%
SAU101483	SeqID IDENTITY COVERAGE	10127 65% 88%	10918 41% 90%	10973 59% 90%	11341 58% 90%		11892 61% 87%	12124 100% 101%	13674 51% 92%	13871 31% 94%
SAU101488	SeqID IDENTITY COVERAGE		10730 28% 95%				11868 25% 74%	12164 100% 100%	13450 33% 98%	13799 28% 73%
SAU101491	SeqID IDENTITY COVERAGE		10580 42% 104%					12165 100% 100%	13315 42% 95%	
SAU101492	SeqID IDENTITY COVERAGE	10073 38% 98%	10581 52% 101%	11020 37% 98%	11284 29% 78%		11831 37% 94%	12166 100% 101%	13323 43% 85%	13715 38% 98%
SAU101493	SeqID IDENTITY COVERAGE	10074 42% 96%		11021 41% 97%	11381 30% 94%		11832 43% 98%	12167 100% 101%	13564 64% 91%	13716 44% 96%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101495	SeqID IDENTITY COVERAGE	10030 32% 92%	10805 34% 92%	11188 36% 90%	11458 29% 86%		5187 33% 90%	12360 100% 100%	13333 32% 94%	14077 32% 92%
SAU101497	SeqID IDENTITY COVERAGE		10806 59% 100%					12361 100% 100%		
SAU101509	SeqID IDENTITY COVERAGE	10121 34% 104%				11712 36% 104%		12418 100% 100%	13249 49% 83%	
SAU101526	SeqID IDENTITY COVERAGE		10901 38% 88%					12179 100% 100%	13465 34% 89%	
SAU101529	SeqID IDENTITY COVERAGE							12544 100% 100%		
SAU101541	SeqID IDENTITY COVERAGE	10024 41% 101%	10631 63% 100%	11182 42% 101%	11526 38% 98%		12014 42% 101%	12344 100% 100%	13647 59% 101%	14019 40% 100%
SAU101543	SeqID IDENTITY COVERAGE	10025 26% 78%	10634 33% 97%	11183 27% 78%			11867 27% 73%	12346 100% 100%	13406 32% 96%	14091 28% 76%
SAU101545	SeqID IDENTITY COVERAGE	10029 31% 98%	10636 50% 99%	11187 32% 97%	11329 27% 83%		12010 28% 97%	12348 100% 100%	13633 47% 97%	14076 30% 98%
SAU101546	SeqID IDENTITY COVERAGE		10638 27% 80%					12349 100% 100%		
SAU101549	SeqID IDENTITY COVERAGE	10443 40% 70%	10762 38% 95%	11228 30% 88%		11767 38% 70%	12049 29% 92%	12549 100% 102%	13460 39% 92%	14030 38% 70%
SAU101551	SeqID IDENTITY COVERAGE	10172 52% 97%	10490 77% 98%	11194 26% 98%	11360 27% 89%		12019 26% 96%	12550 100% 100%	13326 76% 98%	13939 52% 97%
SAU101554	SeqID IDENTITY COVERAGE		10485 48% 83%		11485 26% 81%			12551 100% 101%	13672 46% 91%	

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101561	SeqID IDENTITY COVERAGE	10400 44% 99%	10937 57% 99%	11073 44% 99%	11355 38% 100%	11759 42% 99%	12112 44% 100%	12149 100% 100%	13307 49% 99%	14064 43% 99%
SAU101565	SeqID IDENTITY COVERAGE	10134 37% 93%	10552 50% 96%	11211 35% 94%			11895 36% 92%	12151 100% 100%	13448 44% 99%	13826 36% 92%
SAU101567	SeqID IDENTITY COVERAGE							12144 100% 100%		
SAU101570	SeqID IDENTITY COVERAGE	10037 32% 100%	10690 48% 100%	11208 31% 99%		11700 34% 95%	11835 33% 102%	12584 100% 100%	13563 37% 100%	13900 30% 100%
SAU101571	SeqID IDENTITY COVERAGE		10691 45% 98%				11917 33% 94%	12585 100% 100%	13308 31% 97%	
SAU101572	SeqID IDENTITY COVERAGE	10068 26% 75%	10692 56% 101%			11689 46% 89%	11864 43% 96%	12586 100% 100%	13309 45% 98%	14083 25% 75%
SAU101573	SeqID IDENTITY COVERAGE	10096 31% 98%	10693 49% 103%	11270 35% 98%			11865 30% 101%	12587 100% 100%		14054 31% 98%
SAU101574	SeqID IDENTITY COVERAGE							12588 100% 101%		
SAU101575	SeqID IDENTITY COVERAGE		10869 31% 98%					12589 100% 100%	13638 27% 96%	
SAU101576	SeqID IDENTITY COVERAGE		10762 32% 93%				12049 29% 98%	12554 100% 102%	13460 39% 98%	
SAU101586	SeqID IDENTITY COVERAGE							12598 100% 101%	13487 34% 78%	
SAU101592	SeqID IDENTITY COVERAGE	10249 51% 101%	10605 74% 100%	10987 53% 100%	11555 53% 100%	11741 51% 101%	11952 52% 101%	12406 100% 100%	13283 70% 100%	13950 51% 101%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101599	SeqID IDENTITY COVERAGE							12478 100% 100%		
SAU101610	SeqID IDENTITY COVERAGE	10449 38% 105%			11390 38% 101%		12048 40% 99%	12629 100% 100%		13816 38% 105%
SAU101612	SeqID IDENTITY COVERAGE							12637 100% 100%		
SAU101614	SeqID IDENTITY COVERAGE	10167 49% 100%	10678 55% 98%	11262 29% 93%	11534 29% 94%		11978 39% 95%	12649 100% 100%	13462 53% 99%	13851 48% 100%
SAU101616	SeqID IDENTITY COVERAGE	10186 33% 102%	10667 28% 99%		11407 32% 88%	11695 29% 104%	11872 34% 96%	12432 100% 100%		13903 33% 100%
SAU101622	SeqID IDENTITY COVERAGE	10162 69% 100%			11619 29% 104%	11710 67% 78%	12104 43% 101%	12430 100% 100%		13832 70% 100%
SAU101624	SeqID IDENTITY COVERAGE	10193 26% 101%		11255 27% 106%	11316 38% 97%			12429 100% 100%	13430 26% 103%	13752 26% 107%
SAU101630	SeqID IDENTITY COVERAGE							12410 100% 100%		
SAU101632	SeqID IDENTITY COVERAGE							12407 100% 100%		
SAU101637	SeqID IDENTITY COVERAGE		10886 44% 99%					12201 100% 101%	13384 38% 98%	
SAU101641	SeqID IDENTITY COVERAGE	10223 51% 92%					11918 53% 95%	12193 100% 100%		
SAU101651	SeqID IDENTITY COVERAGE		10790 38% 97%		11552 28% 89%		12021 34% 90%	12491 100% 101%	13369 42% 100%	

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101652	SeqID		10791		11369		12022	12492	13368	
	IDENTITY		62%		49%		50%	100%	56%	
	COVERAGE		97%		91%		95%	100%	98%	
SAU101653	SeqID		10792		11520		12023	12493	13367	
	IDENTITY		73%		46%		49%	100%	63%	
	COVERAGE		100%		100%		100%	100%	100%	
SAU101655	SeqID	10205	10793				11896	12494	13334	
	IDENTITY	31%	50%				30%	100%	33%	
	COVERAGE	84%	97%				83%	100%	93%	
SAU101663	SeqID							12261		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101664	SeqID	10202	10512	11138			11863	12262	13685	13823
	IDENTITY	37%	41%	36%			38%	100%	38%	36%
	COVERAGE	98%	97%	108%			106%	101%	105%	98%
SAU101674	SeqID	10067					11846	12594		14082
	IDENTITY	27%					27%	100%		27%
	COVERAGE	103%					101%	100%		103%
SAU101679	SeqID	10190	10644	11055	11398		12105	12593	13264	13756
	IDENTITY	41%	53%	42%	36%		45%	100%	45%	40%
	COVERAGE	90%	100%	99%	86%		90%	100%	98%	90%
SAU101681	SeqID	10464	10746				11861	12592	13419	13987
	IDENTITY	39%	46%				31%	100%	44%	40%
	COVERAGE	100%	102%				95%	100%	102%	97%
SAU101682	SeqID	10156	10670	11265				12591	13488	13884
	IDENTITY	28%	30%	28%				100%	34%	26%
	COVERAGE	94%	96%	102%				100%	80%	94%
SAU101685	SeqID		10590				11920	12152	13396	
	IDENTITY		26%				37%	100%	56%	
	COVERAGE		88%				97%	100%	100%	
SAU101717	SeqID	10129	10586	11027	11610		11890	12131	13352	14070
	IDENTITY	33%	51%	35%	31%		38%	100%	49%	34%
	COVERAGE	101%	100%	93%	70%		99%	100%	93%	101%
SAU101724	SeqID	10309	10588	11268	11337		12015	12136	13678	13772
	IDENTITY	44%	44%	41%	36%		43%	100%	45%	43%
	COVERAGE	97%	99%	97%	87%		80%	100%	98%	97%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101726	SeqID IDENTITY COVERAGE	10130 37% 101%	10664 50% 100%	11026 42% 101%	11461 36% 101%		11889 40% 100%	12134 100% 100%	13550 48% 100%	14071 41% 77%
SAU101727	SeqID IDENTITY COVERAGE		10665 50% 101%					12133 100% 101%	13551 49% 101%	
SAU101728	SeqID IDENTITY COVERAGE	10019 34% 86%	10666 54% 95%	11053 35% 88%		11734 35% 85%	11800 34% 90%	12132 100% 100%	13182 53% 94%	14015 34% 86%
SAU101736	SeqID IDENTITY COVERAGE	10225 28% 72%					11817 38% 99%	12519 100% 100%		13958 29% 72%
SAU101737	SeqID IDENTITY COVERAGE				11405 32% 78%		11817 30% 96%	12518 100% 101%		
SAU101744	SeqID IDENTITY COVERAGE		10562 44% 101%					12367 100% 100%		
SAU101751	SeqID IDENTITY COVERAGE	10474 30% 85%	10606 46% 100%			11671 30% 82%		12448 100% 100%	13165 45% 99%	13706 31% 79%
SAU101752	SeqID IDENTITY COVERAGE	10438 46% 115%	10626 75% 99%	11037 47% 114%	11410 40% 120%		11997 45% 116%	12447 100% 100%	13187 69% 99%	14043 46% 115%
SAU101754	SeqID IDENTITY COVERAGE	10439 46% 116%	10627 72% 100%	11036 46% 117%	11571 53% 80%		5179 46% 118%	12446 100% 100%	13646 68% 101%	14042 46% 116%
SAU101756	SeqID IDENTITY COVERAGE	10365 65% 91%	10479 83% 93%	11062 66% 91%	11409 65% 91%		5178 68% 91%	12445 100% 101%	13231 82% 93%	13967 65% 93%
SAU101771	SeqID IDENTITY COVERAGE	10220 43% 91%	10784 65% 101%	11276 37% 77%		11765 35% 82%	11950 36% 80%	12350 100% 101%	13280 67% 98%	13934 41% 91%
SAU101772	SeqID IDENTITY COVERAGE	10240 50% 100%	10785 63% 101%	11275 51% 100%	11294 27% 77%		11925 38% 100%	12351 100% 100%	13281 61% 101%	13863 48% 84%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101777	SeqID IDENTITY COVERAGE		10673 64% 97%		11448 43% 88%			12352 100% 100%	13176 62% 98%	
SAU101781	SeqID IDENTITY COVERAGE		10495 67% 99%				11917 38% 93%	12353 100% 100%	13308 28% 85%	
SAU101782	SeqID IDENTITY COVERAGE		10496 75% 100%			11689 44% 89%	11916 41% 99%	12354 100% 100%	13309 40% 96%	
SAU101784	SeqID IDENTITY COVERAGE	10037 44% 97%	10498 65% 100%	11208 45% 97%		11700 35% 92%	11866 42% 99%	12355 100% 100%	13563 37% 99%	13900 44% 97%
SAU101790	SeqID IDENTITY COVERAGE	10350 51% 86%	10524 81% 99%	11106 55% 86%	11437 48% 86%		5170 55% 90%	12215 100% 101%	13207 79% 99%	
SAU101791	SeqID IDENTITY COVERAGE	10349 67% 101%	10525 90% 101%	11107 69% 101%	11436 62% 100%		5169 66% 100%	12216 100% 101%	13208 89% 101%	14108 67% 102%
SAU101792	SeqID IDENTITY COVERAGE	10348 53% 96%	10526 66% 94%	11108 52% 95%			5168 49% 97%	12217 100% 101%	13209 68% 94%	14107 50% 96%
SAU101793	SeqID IDENTITY COVERAGE	10347 64% 100%	10527 85% 101%	11109 65% 99%	11589 51% 99%	11654 64% 101%	5167 63% 99%	12218 100% 101%	13210 79% 100%	14106 64% 101%
SAU101795	SeqID IDENTITY COVERAGE	10345 51% 99%	10528 79% 101%	11111 47% 99%	11435 44% 98%		5165 44% 100%	12219 100% 101%	13212 76% 101%	14104 51% 101%
SAU101797	SeqID IDENTITY COVERAGE	10343 45% 100%	10530 68% 101%	11113 41% 99%	11433 41% 93%		5163 48% 96%	12221 100% 101%	13214 66% 101%	14102 46% 101%
SAU101798	SeqID IDENTITY COVERAGE	10342 55% 99%	10531 72% 95%	11114 55% 99%	11432 62% 87%		5162 52% 99%	12222 100% 101%	13215 66% 96%	14101 55% 99%
SAU101799	SeqID IDENTITY COVERAGE	10341 51% 100%	10532 62% 102%	11115 42% 100%			5161 42% 97%	12223 100% 102%	13216 69% 98%	

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101800	SeqID	10340	10534	11116	11431		5160	12225	13217	14099
	IDENTITY	47%	79%	46%	40%		42%	100%	84%	47%
	COVERAGE	99%	101%	99%	90%		99%	101%	101%	99%
SAU101802	SeqID	10075	10536	11008	11348	11633	11942	12227	13219	13717
	IDENTITY	48%	64%	52%	31%	47%	53%	100%	56%	47%
	COVERAGE	97%	97%	97%	93%	97%	84%	100%	96%	97%
SAU101803	SeqID	10111	10537	11052	11429	11651	11876	12228	13220	14010
	IDENTITY	71%	84%	71%	60%	70%	71%	100%	82%	70%
	COVERAGE	97%	101%	97%	100%	101%	97%	101%	101%	101%
SAU101805	SeqID	10337	10539	11119	11427		11990	12229	13221	14097
	IDENTITY	53%	75%	52%	58%		60%	100%	74%	52%
	COVERAGE	96%	101%	99%	99%		96%	101%	101%	96%
SAU101806	SeqID	10336	10540	11120	11426		11989	12230	13222	14096
	IDENTITY	62%	85%	64%	60%		61%	100%	85%	63%
	COVERAGE	100%	101%	100%	102%		100%	101%	92%	101%
SAU101807	SeqID	10334	10541	11122	11583		11987	12231	13223	14094
	IDENTITY	42%	71%	42%	37%		42%	100%	58%	42%
	COVERAGE	99%	100%	99%	94%		99%	100%	99%	99%
SAU101808	SeqID	10333	10542	11123	11582	11627	5158	12232	13224	14093
	IDENTITY	48%	65%	49%	46%	48%	45%	100%	67%	48%
	COVERAGE	98%	103%	98%	99%	78%	98%	101%	106%	98%
SAU101810	SeqID	10053	10544	11229	11625	11666	11909	12233	13441	14110
	IDENTITY	35%	52%	34%	32%	36%	33%	100%	47%	36%
	COVERAGE	76%	88%	78%	77%	73%	72%	100%	88%	73%
SAU101811	SeqID	10196	10545	11068	11463	11666	11888	12234	13440	13721
	IDENTITY	38%	49%	33%	32%	33%	32%	100%	45%	34%
	COVERAGE	78%	87%	82%	82%	83%	82%	100%	87%	76%
SAU101814	SeqID	10327	10602	11241	11471	11655	5188	12237	13356	13729
	IDENTITY	58%	69%	57%	47%	56%	55%	100%	65%	56%
	COVERAGE	94%	96%	94%	92%	71%	97%	101%	99%	94%
SAU101815	SeqID	10326		11240	11288		12016	12238	13361	13732
	IDENTITY	49%		48%	46%		53%	100%	69%	51%
	COVERAGE	98%		98%	93%		93%	101%	99%	99%
SAU101818	SeqID			11231	11307		11814	12369	13494	
	IDENTITY			32%	33%		31%	100%	35%	
	COVERAGE			95%	90%		96%	101%	93%	

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101824	SeqID IDENTITY COVERAGE	10158 33% 71%					12004 28% 75%	12371 100% 100%		
SAU101833	SeqID IDENTITY COVERAGE	10207 42% 100%	10747 49% 102%	11040 28% 95%	11481 44% 107%		11794 35% 117%	12373 100% 100%	13388 46% 103%	13775 44% 89%
SAU101839	SeqID IDENTITY COVERAGE	10398 30% 94%	10849 33% 78%	11236 32% 90%			12100 25% 98%	12495 100% 100%	13291 32% 83%	13924 28% 94%
SAU101842	SeqID IDENTITY COVERAGE	10105 45% 98%	10942 70% 95%	11075 33% 95%	11376 48% 99%	11723 33% 94%	11855 47% 97%	12510 100% 100%	13445 65% 82%	13999 45% 99%
SAU101845	SeqID IDENTITY COVERAGE	10231 30% 101%	10739 47% 102%		11567 40% 102%		11899 26% 101%	12506 100% 100%	13544 43% 102%	13953 28% 101%
SAU101849	SeqID IDENTITY COVERAGE	10015 56% 103%	10740 77% 99%	11209 54% 103%	11472 56% 101%		12058 56% 103%	12567 100% 100%	13379 75% 98%	13713 56% 104%
SAU101857	SeqID IDENTITY COVERAGE							12569 100% 100%		
SAU101862	SeqID IDENTITY COVERAGE	10257 40% 98%	10817 63% 100%	10955 40% 98%	11334 33% 101%		11802 39% 98%	12571 100% 100%	13305 62% 99%	13797 39% 98%
SAU101864	SeqID IDENTITY COVERAGE							12572 100% 100%		
SAU101865	SeqID IDENTITY COVERAGE	10044 43% 85%	10834 58% 88%	11151 45% 88%	11417 40% 87%		11938 40% 87%	12318 100% 100%	13227 54% 88%	13910 41% 88%
SAU101866	SeqID IDENTITY COVERAGE		10835 42% 102%				11873 29% 99%	12319 100% 100%	13586 40% 100%	
SAU101868	SeqID IDENTITY COVERAGE	10049 45% 101%	10733 56% 99%	11086 45% 101%	11305 42% 96%		11813 48% 100%	12320 100% 100%	13228 49% 108%	13898 45% 99%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101869	SeqID IDENTITY COVERAGE		10734 55% 100%					12321 100% 100%	13668 49% 101%	
SAU101876	SeqID IDENTITY COVERAGE							12169 100% 101%		
SAU101881	SeqID IDENTITY COVERAGE	10325 42% 98%					12081 41% 97%	12162 100% 100%		13728 42% 98%
SAU101882	SeqID IDENTITY COVERAGE	10246 33% 96%	10824 30% 89%			11743 31% 73%	12080 31% 94%	12163 100% 100%		13727 33% 95%
SAU101890	SeqID IDENTITY COVERAGE	10374 53% 91%		11125 49% 92%			12091 47% 93%	12280 100% 100%		13809 53% 91%
SAU101891	SeqID IDENTITY COVERAGE	10295 63% 91%	10766 72% 91%	11196 62% 90%	11483 60% 90%		11791 58% 93%	12281 100% 100%	13413 67% 92%	13739 64% 91%
SAU101893	SeqID IDENTITY COVERAGE	10300 46% 87%	10724 47% 100%			11748 41% 78%	11981 35% 93%	12282 100% 100%	13290 40% 95%	13825 43% 96%
SAU101904	SeqID IDENTITY COVERAGE	10047 34% 98%	10648 38% 101%	11089 33% 102%	11451 31% 105%		11935 31% 104%	12617 100% 100%	13345 34% 93%	13913 33% 98%
SAU101907	SeqID IDENTITY COVERAGE	10362 75% 100%	10482 90% 101%	11059 76% 100%	11415 74% 101%		11995 73% 101%	12442 100% 100%	13171 75% 101%	13964 74% 100%
SAU101909	SeqID IDENTITY COVERAGE	10390 41% 99%		11249 32% 88%	11346 29% 90%		11789 36% 93%	12441 100% 100%		14063 32% 73%
SAU101910	SeqID IDENTITY COVERAGE	10199 56% 97%					11818 60% 97%	12440 100% 100%		
SAU101915	SeqID IDENTITY COVERAGE		10838 26% 90%					12439 100% 100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101922	SeqID IDENTITY COVERAGE							12438 100% 100%		
SAU101948	SeqID IDENTITY COVERAGE							12709 100% 100%		
SAU101966	SeqID IDENTITY COVERAGE	10101 45% 88%	10561 31% 91%	11007 32% 92%	11538 37% 86%	11705 43% 88%	11897 45% 88%	12186 100% 101%		14003 45% 88%
SAU101968	SeqID IDENTITY COVERAGE	10106 30% 90%	10568 31% 92%	11242 33% 90%	11480 27% 88%		11965 30% 83%	12187 100% 100%		13998 31% 76%
SAU101991	SeqID IDENTITY COVERAGE		10938 40% 101%					12454 100% 101%	13500 25% 80%	
SAU101995	SeqID IDENTITY COVERAGE	10388 46% 72%	10939 47% 78%	11066 49% 73%	11575 58% 72%	11646 46% 72%	11957 57% 76%	12455 100% 100%	13386 51% 74%	
SAU101996	SeqID IDENTITY COVERAGE	10237 38% 98%	10940 64% 99%	10999 36% 98%	11325 38% 98%		11901 35% 99%	12456 100% 100%	13455 58% 100%	13956 37% 98%
SAU101999	SeqID IDENTITY COVERAGE	10476 48% 97%	10941 61% 98%	11259 46% 98%	11304 49% 91%		12035 51% 96%	12423 100% 100%	13241 64% 97%	13708 48% 97%
SAU102001	SeqID IDENTITY COVERAGE	10258 47% 105%	10628 58% 98%	11134 47% 106%	11489 43% 105%		11787 49% 98%	12424 100% 100%	13636 46% 98%	14088 47% 105%
SAU102002	SeqID IDENTITY COVERAGE							12425 100% 100%		
SAU102003	SeqID IDENTITY COVERAGE							12426 100% 101%		
SAU102006	SeqID IDENTITY COVERAGE			11267 44% 92%	11555 28% 74%			12427 100% 101%	13260 47% 105%	

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102007	SeqID IDENTITY COVERAGE			11266 60% 97%				12428 100% 100%	13258 61% 97%	
SAU102032	SeqID IDENTITY COVERAGE						12086 62% 99%	12198 100% 100%		13989 58% 75%
SAU102035	SeqID IDENTITY COVERAGE	10299 60% 98%	10933 50% 99%	10974 26% 85%	11514 29% 84%		11860 41% 97%	12199 100% 100%	13360 31% 86%	13763 56% 99%
SAU102044	SeqID IDENTITY COVERAGE	10141 56% 100%	10916 67% 102%	11011 59% 100%	11344 50% 101%		12041 58% 101%	12414 100% 100%	13447 69% 102%	13977 56% 100%
SAU102046	SeqID IDENTITY COVERAGE	10103 32% 74%	10723 28% 86%				12089 29% 90%	12415 100% 100%		14001 29% 89%
SAU102049	SeqID IDENTITY COVERAGE	10427 36% 101%	10518 39% 99%	10962 49% 97%	11291 40% 99%		11784 41% 100%	12416 100% 100%	13652 46% 98%	13781 36% 101%
SAU102054	SeqID IDENTITY COVERAGE	10280 53% 100%	10494 50% 79%	11095 55% 100%	11356 51% 100%	11676 53% 70%	11856 55% 100%	12417 100% 100%		13877 53% 100%
SAU102059	SeqID IDENTITY COVERAGE	10085 43% 107%	10771 72% 100%	11152 43% 107%	11622 40% 102%		11969 41% 109%	12286 100% 100%	13226 72% 71%	14059 40% 89%
SAU102067	SeqID IDENTITY COVERAGE	10380 32% 95%	10564 52% 98%	11155 31% 98%			11795 28% 97%	12287 100% 100%	13407 44% 98%	13798 31% 94%
SAU102068	SeqID IDENTITY COVERAGE		10680 29% 101%					12288 100% 100%		
SAU102102	SeqID IDENTITY COVERAGE							12696 100% 100%		
SAU102113	SeqID IDENTITY COVERAGE		10641 34% 110%					12178 100% 101%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102116	SeqID IDENTITY COVERAGE		10642 29% 85%					12180 100% 100%	13480 31% 81%	
SAU102117	SeqID IDENTITY COVERAGE	10016 43% 101%	10643 61% 100%		11604 38% 102%		12027 42% 103%	12181 100% 100%	13481 55% 100%	13947 41% 85%
SAU102129	SeqID IDENTITY COVERAGE		10859 60% 98%					12176 100% 100%	13400 56% 99%	
SAU102132	SeqID IDENTITY COVERAGE		10760 39% 101%					12177 100% 100%	13304 41% 101%	
SAU102142	SeqID IDENTITY COVERAGE	10154 37% 99%						12457 100% 100%		
SAU102143	SeqID IDENTITY COVERAGE	10154 32% 100%						12458 100% 100%		
SAU102144	SeqID IDENTITY COVERAGE							12459 100% 100%		
SAU102162	SeqID IDENTITY COVERAGE							12462 100% 100%		
SAU102165	SeqID IDENTITY COVERAGE							12460 100% 100%		
SAU102200	SeqID IDENTITY COVERAGE							12665 100% 101%		
SAU102201	SeqID IDENTITY COVERAGE							12666 100% 101%		
SAU102222	SeqID IDENTITY COVERAGE	10447 58% 99%	10797 68% 99%	10994 58% 99%	11358 52% 99%		11986 59% 99%	12511 100% 100%	13192 67% 99%	13818 58% 99%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102231	SeqID IDENTITY COVERAGE	10323 41% 94%	10798 50% 93%	11193 42% 89%			12020 38% 94%	12527 100% 100%	13561 46% 99%	13731 41% 94%
SAU102232	SeqID IDENTITY COVERAGE	10100 36% 75%	10799 40% 79%			11687 35% 74%		12530 100% 100%	13562 42% 79%	14004 34% 75%
SAU102233	SeqID IDENTITY COVERAGE		10800 61% 98%					12531 100% 100%	13496 45% 91%	
SAU102241	SeqID IDENTITY COVERAGE	10163 28% 74%	10845 43% 99%					12539 100% 100%		
SAU102242	SeqID IDENTITY COVERAGE	10188 47% 100%	10847 72% 99%	10953 44% 101%	11600 38% 100%	11634 47% 98%	11907 47% 100%	12540 100% 100%	13593 70% 100%	13981 47% 100%
SAU102246	SeqID IDENTITY COVERAGE	10274 59% 99%	10854 74% 100%	11154 60% 97%	11476 54% 96%		11932 62% 100%	12542 100% 100%	13313 81% 101%	13866 58% 99%
SAU102247	SeqID IDENTITY COVERAGE							12543 100% 101%	13180 28% 74%	
SAU102252	SeqID IDENTITY COVERAGE	10300 39% 79%	10677 48% 93%			11748 39% 73%	11981 37% 91%	12241 100% 100%	13290 43% 95%	13825 41% 98%
SAU102256	SeqID IDENTITY COVERAGE	10451 33% 97%			11515 32% 97%			12243 100% 101%	13531 75% 101%	
SAU102257	SeqID IDENTITY COVERAGE	10451 38% 81%			11515 29% 75%			12244 100% 101%	13274 85% 101%	
SAU102259	SeqID IDENTITY COVERAGE		10844 65% 97%					12245 100% 100%	13519 72% 97%	13782 25% 87%
SAU102260	SeqID IDENTITY COVERAGE	10182 34% 96%	10646 37% 87%			11682 32% 96%		12246 100% 101%	13275 83% 100%	13984 32% 87%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102261	SeqID IDENTITY COVERAGE	10183 25% 79%	10731 30% 80%					12247 100% 100%	13276 74% 99%	13983 26% 79%
SAU102262	SeqID IDENTITY COVERAGE	10270 35% 104%	10759 39% 103%			11724 31% 84%		12248 100% 100%	13277 82% 100%	13881 34% 104%
SAU102264	SeqID IDENTITY COVERAGE	10160 45% 100%					5103 44% 100%	12250 100% 100%		13830 43% 101%
SAU102265	SeqID IDENTITY COVERAGE						11926 37% 100%	12251 100% 100%		
SAU102268	SeqID IDENTITY COVERAGE							12252 100% 101%		
SAU102270	SeqID IDENTITY COVERAGE							12253 100% 100%		
SAU102280	SeqID IDENTITY COVERAGE							12378 100% 100%		
SAU102281	SeqID IDENTITY COVERAGE	10316 45% 99%		11227 48% 99%	11469 39% 100%		12054 45% 99%	12384 100% 100%	13497 61% 100%	13762 44% 99%
SAU102283	SeqID IDENTITY COVERAGE	10260 41% 88%	10875 59% 88%	10982 43% 88%	11560 41% 92%		11945 41% 95%	12119 100% 102%	13251 54% 88%	14086 41% 88%
SAU102284	SeqID IDENTITY COVERAGE							12389 100% 100%		
SAU102286	SeqID IDENTITY COVERAGE	10385 37% 104%	10595 42% 99%					12393 100% 100%	13688 39% 101%	
SAU102287	SeqID IDENTITY COVERAGE	10220 42% 81%	10594 45% 95%	11025 40% 88%		11663 39% 89%	11925 41% 84%	12398 100% 101%	13427 41% 94%	13934 39% 83%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102292	SeqID IDENTITY COVERAGE	10399 41% 101%	10579 59% 100%	11018 40% 101%	11455 37% 100%	11758 41% 101%	12111 42% 101%	12368 100% 100%	13230 57% 94%	14065 41% 101%
SAU102294	SeqID IDENTITY COVERAGE							12610 100% 100%		
SAU102297	SeqID IDENTITY COVERAGE	10405 52% 99%	10912 66% 100%	11063 51% 100%	11303 46% 99%		12117 50% 98%	12704 100% 100%	13686 64% 100%	14066 48% 77%
SAU102298	SeqID IDENTITY COVERAGE	10404 36% 72%	10914 62% 99%	11031 33% 87%		11686 35% 89%	12116 28% 87%	12705 100% 100%	13255 54% 100%	
SAU102308	SeqID IDENTITY COVERAGE	10077 38% 88%	10577 46% 100%	11248 37% 86%	11625 33% 87%	11732 39% 88%	12032 38% 90%	12706 100% 100%	13350 45% 100%	13995 39% 95%
SAU102318	SeqID IDENTITY COVERAGE	10122 32% 90%	10795 75% 97%				11806 37% 72%	12707 100% 100%	13242 63% 97%	14039 31% 89%
SAU102333	SeqID IDENTITY COVERAGE	10057 41% 96%	10550 43% 97%				12102 40% 96%	12657 100% 100%	13316 31% 90%	13829 38% 95%
SAU102334	SeqID IDENTITY COVERAGE	10056 50% 91%					12101 50% 92%	12658 100% 100%		
SAU102336	SeqID IDENTITY COVERAGE							12659 100% 101%		
SAU102340	SeqID IDENTITY COVERAGE							12660 100% 100%		
SAU102345	SeqID IDENTITY COVERAGE						11843 37% 86%	12655 100% 101%		
SAU102350	SeqID IDENTITY COVERAGE							12433 100% 101%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102352	SeqID IDENTITY COVERAGE		10657 55% 100%					12434 100% 100%	13426 39% 91%	
SAU102355	SeqID IDENTITY COVERAGE		10726 39% 87%					12435 100% 100%		
SAU102356	SeqID IDENTITY COVERAGE	10227 43% 95%	10669 60% 100%	11203 45% 95%	11546 48% 98%		11805 43% 95%	12436 100% 100%	13324 56% 99%	13960 43% 95%
SAU102378	SeqID IDENTITY COVERAGE							12437 100% 100%		
SAU102380	SeqID IDENTITY COVERAGE						11870 32% 71%	12265 100% 100%		
SAU102388	SeqID IDENTITY COVERAGE	10367 36% 96%		11157 33% 90%	11386 27% 101%		11808 39% 99%	12267 100% 100%		13802 36% 96%
SAU102389	SeqID IDENTITY COVERAGE	10063 33% 99%	10547 59% 97%	10988 31% 97%			11837 36% 95%	12268 100% 100%	13395 35% 98%	13917 33% 99%
SAU102390	SeqID IDENTITY COVERAGE	10192 41% 100%				11678 26% 97%		12269 100% 101%		13753 42% 100%
SAU102392	SeqID IDENTITY COVERAGE	10131 50% 73%	10500 42% 80%			11673 32% 80%	11951 42% 74%	12270 100% 100%	13474 42% 76%	
SAU102394	SeqID IDENTITY COVERAGE		10807 32% 102%					12271 100% 100%		
SAU102396	SeqID IDENTITY COVERAGE	10243 37% 101%	10809 62% 99%					12272 100% 100%	13467 27% 98%	13794 37% 98%
SAU102401	SeqID IDENTITY COVERAGE							12209 100% 100%		

TABLE VIIA (*Continued)*

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102417	SeqID IDENTITY COVERAGE		10934 31% 79%				12068 25% 72%	12204 100% 100%		
SAU102418	SeqID IDENTITY COVERAGE					11760 25% 89%		12205 100% 100%		
SAU102420	SeqID IDENTITY COVERAGE							12206 100% 100%		
SAU102422	SeqID IDENTITY COVERAGE	10308 30% 92%				11665 30% 72%	11977 27% 93%	12207 100% 100%		13776 31% 92%
SAU102423	SeqID IDENTITY COVERAGE			11084 27% 94%	11491 25% 92%		12099 27% 93%	12208 100% 100%		
SAU102433	SeqID IDENTITY COVERAGE	10395 42% 101%	10908 51% 100%	11167 39% 100%	11616 37% 73%		11772 52% 72%	12701 100% 100%	13552 44% 98%	
SAU102434	SeqID IDENTITY COVERAGE	10394 26% 99%	10907 44% 100%	11166 28% 99%			11773 26% 100%	12700 100% 100%	13446 40% 101%	13921 27% 99%
SAU102437	SeqID IDENTITY COVERAGE	10393 55% 86%	10952 67% 99%	11057 57% 88%	11330 51% 86%		11774 55% 87%	12695 100% 100%	13420 64% 99%	13920 56% 86%
SAU102440	SeqID IDENTITY COVERAGE						12085 41% 98%	12692 100% 100%		13990 39% 99%
SAU102447	SeqID IDENTITY COVERAGE		10947 38% 98%					12685 100% 100%	13436 32% 98%	
SAU102448	SeqID IDENTITY COVERAGE	10460 32% 101%	10946 55% 102%	11049 31% 101%	11332 35% 101%		12073 34% 101%	12681 100% 101%	13435 46% 102%	13860 32% 102%
SAU102449	SeqID IDENTITY COVERAGE	10445 45% 97%	10945 55% 98%	11253 43% 98%	11444 35% 99%	11731 43% 76%	12072 44% 97%	12677 100% 100%	13434 51% 100%	14028 45% 97%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102450	SeqID IDENTITY COVERAGE	10456 47% 100%	10943 70% 100%	11264 46% 100%	11487 43% 99%		12076 47% 99%	12675 100% 100%	13237 68% 100%	13857 47% 100%
SAU102452	SeqID IDENTITY COVERAGE	10420 41% 97%	10748 70% 98%	11143 37% 97%	11478 32% 97%	11629 40% 94%	11820 40% 97%	12674 100% 100%	13265 62% 100%	13783 38% 99%
SAU102453	SeqID IDENTITY COVERAGE		10749 43% 101%				12107 29% 70%	12669 100% 100%	13266 41% 71%	
SAU102460	SeqID IDENTITY COVERAGE	10063 34% 98%	10547 35% 100%	10988 34% 100%			11837 34% 100%	12171 100% 100%	13395 34% 101%	13917 34% 98%
SAU102469	SeqID IDENTITY COVERAGE	10217 58% 98%						12172 100% 100%		
SAU102473	SeqID IDENTITY COVERAGE		10868 28% 88%					12173 100% 100%	13475 35% 83%	
SAU102474	SeqID IDENTITY COVERAGE		10713 26% 96%	10971 26% 105%				12174 100% 100%	13476 26% 89%	14025 27% 97%
SAU102476	SeqID IDENTITY COVERAGE							12175 100% 100%		
SAU102479	SeqID IDENTITY COVERAGE	10306 26% 84%						12405 100% 100%		
SAU102480	SeqID IDENTITY COVERAGE	10310 28% 100%	10935 33% 88%				11871 30% 100%	12404 100% 100%		13770 27% 100%
SAU102481	SeqID IDENTITY COVERAGE	10289 26% 102%	10831 29% 94%					12422 100% 101%		13879 26% 102%
SAU102485	SeqID IDENTITY COVERAGE	10457 28% 86%	10890 53% 100%					12421 100% 100%	13512 56% 99%	13961 60% 93%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102486	SeqID IDENTITY COVERAGE	10294 36% 95%	10889 38% 97%	11025 27% 95%				12420 100% 101%	13513 42% 93%	13962 37% 95%
SAU102487	SeqID IDENTITY COVERAGE							12419 100% 100%		
SAU102498	SeqID IDENTITY COVERAGE	10241 36% 93%	10597 35% 94%	10974 35% 93%	11342 33% 92%	11706 37% 94%	11842 38% 94%	12688 100% 100%	13387 35% 93%	14092 36% 93%
SAU102502	SeqID IDENTITY COVERAGE						12060 26% 85%	12689 100% 100%		
SAU102503	SeqID IDENTITY COVERAGE						12059 32% 92%	12690 100% 100%		
SAU102526	SeqID IDENTITY COVERAGE							12691 100% 100%		
SAU102527	SeqID IDENTITY COVERAGE	10352 54% 93%	10560 74% 101%	11104 55% 93%	11439 56% 94%		5171 58% 93%	12260 100% 101%	13204 75% 94%	13968 54% 93%
SAU102531	SeqID IDENTITY COVERAGE		10765 34% 102%					12667 100% 100%		
SAU102541	SeqID IDENTITY COVERAGE	10076 41% 93%	10520 49% 102%	11000 38% 91%	11498 37% 93%		11966 44% 100%	12668 100% 100%	13405 45% 81%	13718 41% 93%
SAU102551	SeqID IDENTITY COVERAGE			11013 47% 87%	11353 38% 84%		11816 39% 84%	12672 100% 101%	13271 41% 95%	
SAU102554	SeqID IDENTITY COVERAGE		10494 47% 99%					12673 100% 100%	13466 44% 98%	
SAU102575	SeqID IDENTITY COVERAGE	10166 28% 98%		11232 29% 91%	11618 35% 99%		11777 30% 96%	12609 100% 100%		13836 27% 98%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102578	SeqID IDENTITY COVERAGE	10459 59% 88%	10948 76% 95%	11050 60% 88%	11420 51% 89%		12074 65% 81%	12411 100% 101%	13503 73% 94%	13859 59% 89%
SAU102584	SeqID IDENTITY COVERAGE							12537 100% 100%		
SAU102585	SeqID IDENTITY COVERAGE							12611 100% 100%		
SAU102593	SeqID IDENTITY COVERAGE		10889 27% 87%					12463 100% 100%	13513 27% 88%	
SAU102598	SeqID IDENTITY COVERAGE	10187 30% 102%		10958 32% 85%		11710 27% 75%	11979 31% 92%	12464 100% 100%		13833 31% 86%
SAU102599	SeqID IDENTITY COVERAGE	10206 36% 89%	10944 26% 76%	10958 30% 93%	11619 30% 73%		11975 33% 79%	12466 100% 100%	13653 32% 77%	13773 32% 101%
SAU102601	SeqID IDENTITY COVERAGE	10273 27% 95%		11076 30% 93%		11722 28% 95%	11931 28% 93%	12467 100% 100%	13256 51% 97%	13867 27% 92%
SAU102602	SeqID IDENTITY COVERAGE	10356 58% 100%	10555 78% 100%	11100 61% 100%	11441 57% 100%	11679 59% 100%	11993 60% 99%	12249 100% 100%	13200 77% 100%	13971 58% 99%
SAU102603	SeqID IDENTITY COVERAGE							12469 100% 100%		
SAU102605	SeqID IDENTITY COVERAGE		10836 47% 96%					12470 100% 100%		
SAU102606	SeqID IDENTITY COVERAGE	10273 27% 95%		11076 30% 92%		11722 27% 95%	11931 25% 93%	12471 100% 100%	13256 50% 97%	13867 26% 94%
SAU102607	SeqID IDENTITY COVERAGE							12472 100% 100%	13579 43% 98%	

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102609	SeqID IDENTITY COVERAGE							12473 100% 100%		
SAU102610	SeqID IDENTITY COVERAGE							12474 100% 100%		
SAU102613	SeqID IDENTITY COVERAGE	10461 26% 97%		11272 28% 95%				12475 100% 100%		13988 26% 97%
SAU102614	SeqID IDENTITY COVERAGE	10211 33% 89%	10600 55% 100%					12476 100% 100%		13927 32% 89%
SAU102615	SeqID IDENTITY COVERAGE	10234 32% 98%	10601 40% 100%			11720 32% 92%	12098 26% 87%	12477 100% 100%		13926 31% 100%
SAU102620	SeqID IDENTITY COVERAGE							12479 100% 100%		
SAU102621	SeqID IDENTITY COVERAGE	10288 61% 100%	10519 62% 101%			11724 58% 81%		12480 100% 100%	13370 59% 101%	13881 61% 100%
SAU102629	SeqID IDENTITY COVERAGE		10885 26% 108%					12481 100% 100%		
SAU102631	SeqID IDENTITY COVERAGE		10522 27% 83%			11657 44% 83%	11841 32% 81%	12712 100% 100%		
SAU102636	SeqID IDENTITY COVERAGE							12650 100% 100%	13696 29% 102%	
SAU102637	SeqID IDENTITY COVERAGE							12651 100% 100%	13697 39% 98%	
SAU102652	SeqID IDENTITY COVERAGE							12653 100% 101%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102658	SeqID IDENTITY COVERAGE	10283 45% 97%	10910 54% 92%	11064 42% 97%			12090 39% 97%	12654 100% 100%	13514 49% 96%	13855 41% 100%
SAU102663	SeqID IDENTITY COVERAGE	10304 43% 99%	10840 58% 99%	11043 44% 96%	11626 34% 95%		11798 45% 91%	12158 100% 100%	13172 56% 97%	13780 41% 99%
SAU102669	SeqID IDENTITY COVERAGE	10022 42% 96%	10756 26% 91%	11257 43% 95%			12045 41% 94%	12160 100% 100%	13371 54% 95%	14035 41% 93%
SAU102671	SeqID IDENTITY COVERAGE	10409 34% 91%		11079 32% 91%	11319 44% 96%	11683 35% 74%	12043 56% 99%	12161 100% 100%	13373 69% 96%	14033 33% 91%
SAU102674	SeqID IDENTITY COVERAGE	10020 55% 102%		11164 54% 103%		11648 46% 101%	5127 55% 105%	12156 100% 101%		14016 53% 102%
SAU102693	SeqID IDENTITY COVERAGE	10178 53% 82%	10659 74% 87%		11474 38% 86%		11883 49% 86%	12627 100% 101%	13301 61% 90%	13940 49% 72%
SAU102694	SeqID IDENTITY COVERAGE	10177 48% 97%	10660 66% 102%	11222 50% 97%	11296 44% 94%		5120 55% 94%	12628 100% 102%	13302 60% 102%	
SAU102725	SeqID IDENTITY COVERAGE	10418 40% 96%	10514 72% 100%	11137 39% 96%	11507 38% 103%		12088 37% 104%	12338 100% 100%	13378 66% 100%	13789 40% 96%
SAU102764	SeqID IDENTITY COVERAGE	10179 44% 99%	10929 67% 99%	11234 42% 99%	11295 41% 90%		11884 42% 97%	12625 100% 100%	13484 63% 99%	13938 43% 99%
SAU102812	SeqID IDENTITY COVERAGE		10860 48% 100%					12127 100% 101%	13253 49% 96%	
SAU102870	SeqID IDENTITY COVERAGE	10113 29% 92%	10880 35% 83%					12170 100% 100%	13270 29% 93%	14008 28% 87%
SAU102880	SeqID IDENTITY COVERAGE	10360 60% 100%	10533 82% 101%	11096 61% 100%	11443 57% 97%	11643 61% 100%	5177 58% 100%	12224 100% 101%	13196 85% 101%	13975 61% 100%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102881	SeqID	10357	10551	11099			11994	12242	13199	13972
	IDENTITY	38%	69%	37%			38%	100%	54%	38%
	COVERAGE	89%	98%	89%			89%	101%	102%	89%
SAU102883	SeqID	10396		11168	11449		12118	12702	13181	
	IDENTITY	63%		70%	60%		65%	100%	76%	
	COVERAGE	86%		88%	86%		86%	102%	90%	
SAU102905	SeqID		10732	11217	11373			12273		
	IDENTITY		31%	26%	38%			100%		
	COVERAGE		92%	80%	87%			100%		
SAU102909	SeqID	10042	10488	11150	11457	11637	11940	12315	13437	13908
	IDENTITY	59%	68%	60%	69%	59%	60%	100%	73%	59%
	COVERAGE	95%	95%	95%	130%	95%	98%	101%	124%	95%
SAU102933	SeqID	10448	10949	10995	11579	11762	11985	12412	13502	13817
	IDENTITY	33%	53%	35%	32%	31%	29%	100%	50%	31%
	COVERAGE	104%	113%	101%	108%	107%	101%	101%	101%	103%
SAU102936	SeqID	10236	10872				11804	12356		13955
	IDENTITY	33%	66%				60%	100%		33%
	COVERAGE	97%	100%				96%	101%		98%
SAU102942	SeqID	10136	10492	11230		11696		12296	13339	13834
	IDENTITY	52%	55%	43%		50%		100%	51%	51%
	COVERAGE	100%	100%	99%		99%		100%	99%	99%
SAU102944	SeqID							12468	13257	
	IDENTITY							100%	42%	
	COVERAGE							100%	99%	
SAU102979	SeqID	10014		10979	11384		11936	12536	13429	13712
	IDENTITY	33%		37%	32%		41%	100%	33%	33%
	COVERAGE	88%		87%	87%		87%	100%	87%	90%
SAU102983	SeqID		10883					12676	13269	
	IDENTITY		28%					100%	27%	
	COVERAGE		70%					100%	76%	
SAU102992	SeqID	10176	10661	11223	11297		11882	12630	13303	13941
	IDENTITY	62%	70%	62%	48%		59%	100%	63%	61%
	COVERAGE	99%	92%	99%	97%		99%	101%	99%	101%
SAU103010	SeqID							12194		
	IDENTITY							100%		
	COVERAGE							100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU103024	SeqID IDENTITY COVERAGE					11670 44% 89%	12042 26% 72%	12200 100% 101%		
SAU103025	SeqID IDENTITY COVERAGE							12202 100% 100%		
SAU103037	SeqID IDENTITY COVERAGE		10867 27% 99%					12613 100% 101%	13267 26% 86%	
SAU103077	SeqID IDENTITY COVERAGE							12408 100% 100%		
SAU103115	SeqID IDENTITY COVERAGE							12508 100% 101%	13469 32% 101%	
SAU103144	SeqID IDENTITY COVERAGE		10936 42% 84%					12663 100% 100%		
SAU103159	SeqID IDENTITY COVERAGE	10110 43% 115%	10783 48% 100%	11134 38% 112%	11489 48% 117%		11787 48% 98%	12670 100% 100%	13411 63% 101%	13994 43% 116%
SAU103169	SeqID IDENTITY COVERAGE							12678 100% 100%	13239 34% 84%	
SAU103175	SeqID IDENTITY COVERAGE	10157 36% 96%						12687 100% 100%		
SAU103191	SeqID IDENTITY COVERAGE							12465 100% 102%	13332 42% 75%	
SAU103204	SeqID IDENTITY COVERAGE							12499 100% 101%		
SAU103226	SeqID IDENTITY COVERAGE							12713 100% 100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU103232	SeqID IDENTITY COVERAGE	10368 36% 102%				11704 35% 98%	11848 48% 101%	12697 100% 101%		13803 35% 102%
SAU200006	SeqID IDENTITY COVERAGE	10033 53% 78%	10639 70% 80%	11192 47% 84%	11553 43% 82%		12007 50% 89%	12723 100% 100%	13479 65% 77%	
SAU200028	SeqID IDENTITY COVERAGE							12694 100% 100%		
SAU200030	SeqID IDENTITY COVERAGE	10372 42% 84%	10553 74% 98%	11056 39% 84%	11447 43% 93%	11672 41% 86%	12092 35% 93%	12745 100% 102%	13449 73% 95%	13807 42% 84%
SAU200058	SeqID IDENTITY COVERAGE		10621 39% 79%					12719 100% 101%	13327 37% 78%	
SAU200059	SeqID IDENTITY COVERAGE	10259 31% 73%	10622 33% 97%	10978 32% 73%			12026 36% 74%	12720 100% 100%	13325 40% 96%	14087 31% 73%
SAU200088	SeqID IDENTITY COVERAGE	10262 51% 82%		10984 56% 91%	11403 57% 93%		11947 45% 93%	12724 100% 102%	13415 68% 100%	14090 49% 82%
SAU200242	SeqID IDENTITY COVERAGE		10712 28% 99%					12734 100% 100%		
SAU200297	SeqID IDENTITY COVERAGE	10109 33% 95%	10756 64% 100%	11257 34% 98%			11982 33% 95%	12739 100% 100%	13371 33% 95%	13996 32% 95%
SAU200345	SeqID IDENTITY COVERAGE							12751 100% 100%		
SAU200392	SeqID IDENTITY COVERAGE	10164 26% 97%	10584 30% 80%	10968 25% 96%	11566 27% 98%		11912 33% 93%	12755 100% 100%		13892 26% 98%
SAU200468	SeqID IDENTITY COVERAGE	10201 78% 74%	10478 75% 75%	11054 62% 74%			12061 36% 81%	12937 100% 101%	13425 76% 75%	13822 78% 74%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU200558	SeqID IDENTITY COVERAGE	10039 28% 72%	10728 31% 102%	11277 26% 80%			12046 30% 75%	12777 100% 100%	13423 32% 99%	13904 29% 72%
SAU200561	SeqID IDENTITY COVERAGE							12693 100% 100%		
SAU200564	SeqID IDENTITY COVERAGE	10099 33% 87%		11170 31% 87%	11602 31% 82%	11645 34% 86%	11788 32% 93%	12780 100% 100%		13992 34% 87%
SAU200565	SeqID IDENTITY COVERAGE	10098 32% 97%		11250 34% 96%	11386 35% 98%		11786 39% 97%	12781 100% 100%		13991 33% 97%
SAU200593	SeqID IDENTITY COVERAGE	10435 53% 99%	10613 73% 100%	11038 50% 99%	11412 53% 98%		11998 52% 100%	12784 100% 100%	13397 64% 99%	14046 52% 99%
SAU200628	SeqID IDENTITY COVERAGE	10173 32% 92%	10856 31% 97%					12790 100% 100%	13297 29% 97%	13937 34% 94%
SAU200685	SeqID IDENTITY COVERAGE							12801 100% 100%	13185 31% 94%	
SAU200721	SeqID IDENTITY COVERAGE	10208 40% 92%	10582 33% 79%	11015 41% 99%	11541 36% 94%			12797 100% 100%	13681 42% 100%	13922 41% 94%
SAU200725	SeqID IDENTITY COVERAGE	10118 30% 98%	10761 46% 100%	10966 30% 97%			11780 25% 98%	12933 100% 100%	13632 47% 100%	14020 29% 98%
SAU200731	SeqID IDENTITY COVERAGE	10283 55% 99%	10822 54% 100%	11064 44% 98%			12090 43% 98%	12342 100% 100%	13514 51% 100%	13855 46% 99%
SAU200740	SeqID IDENTITY COVERAGE	10318 48% 86%	10554 56% 102%	11225 48% 86%	11393 49% 73%		12056 50% 87%	12798 100% 100%	13695 55% 93%	13760 48% 86%
SAU200752	SeqID IDENTITY COVERAGE							12809 100% 100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU200914	SeqID IDENTITY COVERAGE	10383 26% 96%	10714 28% 98%			11747 27% 79%	11927 27% 90%	12837 100% 100%	13431 25% 91%	13788 25% 90%
SAU200916	SeqID IDENTITY COVERAGE							12838 100% 100%		
SAU200928	SeqID IDENTITY COVERAGE	10439 54% 86%	10627 73% 99%	11036 55% 87%	11571 53% 86%		5179 49% 102%	12815 100% 100%	13646 69% 100%	14042 54% 86%
SAU200934	SeqID IDENTITY COVERAGE	10212 44% 72%	10780 60% 93%				11964 42% 82%	12842 100% 100%		13835 42% 88%
SAU200949	SeqID IDENTITY COVERAGE							12846 100% 100%		
SAU200960	SeqID IDENTITY COVERAGE				11500 42% 70%		11886 33% 91%	12431 100% 102%		
SAU200994	SeqID IDENTITY COVERAGE	10036 36% 100%	10497 62% 101%	11270 32% 100%			11865 37% 102%	12935 100% 100%	13310 35% 73%	14054 33% 99%
SAU201167	SeqID IDENTITY COVERAGE		10779 37% 98%					12887 100% 100%		
SAU201168	SeqID IDENTITY COVERAGE		10819 53% 102%					12889 100% 100%	13626 56% 100%	
SAU201184	SeqID IDENTITY COVERAGE	10448 40% 70%	10715 52% 108%	10995 35% 97%	11579 37% 82%		11985 37% 70%	12807 100% 101%	13502 53% 111%	13819 32% 111%
SAU201197	SeqID IDENTITY COVERAGE	10330 58% 99%	10924 66% 99%	11160 60% 99%	11321 53% 98%		5215 58% 99%	12938 100% 101%	13364 63% 96%	13885 58% 99%
SAU201225	SeqID IDENTITY COVERAGE		10812 41% 93%	11090 33% 80%				12896 100% 100%	13170 38% 87%	

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU201236	SeqID IDENTITY COVERAGE	10026 32% 92%	10679 29% 96%	11184 33% 93%	11613 33% 89%		12013 34% 95%	12891 100% 100%	13505 30% 95%	14073 32% 90%
SAU201301	SeqID IDENTITY COVERAGE							12899 100% 100%		
SAU201333	SeqID IDENTITY COVERAGE	10192 41% 100%				11678 28% 96%		12905 100% 101%		13753 41% 100%
SAU201375	SeqID IDENTITY COVERAGE						11929 36% 95%	12926 100% 100%		
SAU201380	SeqID IDENTITY COVERAGE	10379 34% 94%	10499 25% 93%		11313 26% 95%		12024 25% 89%	12922 100% 100%		13801 25% 101%
SAU201381	SeqID IDENTITY COVERAGE	10241 68% 89%	10597 59% 96%	10974 46% 90%	11387 44% 91%	11706 56% 89%	11833 57% 100%	12923 100% 104%	13387 52% 92%	13878 64% 89%
SAU201403	SeqID IDENTITY COVERAGE							12913 100% 100%		
SAU201469	SeqID IDENTITY COVERAGE							12967 100% 100%		
SAU201486	SeqID IDENTITY COVERAGE							13023 100% 100%		
SAU201506	SeqID IDENTITY COVERAGE	10145 49% 101%					11963 49% 102%	12946 100% 100%		13841 50% 100%
SAU201508	SeqID IDENTITY COVERAGE	10370 37% 73%					11874 42% 72%	12947 100% 100%		13805 36% 73%
SAU201513	SeqID IDENTITY COVERAGE	10229 29% 71%						12944 100% 101%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU201539	SeqID IDENTITY COVERAGE	10109 33% 95%		11257 28% 96%			5099 34% 96%	12943 100% 100%	13625 32% 97%	13996 33% 95%
SAU201541	SeqID IDENTITY COVERAGE	10131 50% 71%	10500 39% 74%			11673 33% 77%	11951 41% 73%	12942 100% 100%	13474 41% 73%	
SAU201558	SeqID IDENTITY COVERAGE	10112 51% 96%		11258 51% 94%	11396 43% 94%		11875 49% 99%	12954 100% 101%	13598 46% 96%	14009 51% 96%
SAU201571	SeqID IDENTITY COVERAGE	10224 50% 98%	10951 61% 94%	11213 47% 99%	11357 50% 92%		11905 45% 103%	12997 100% 100%	13268 54% 70%	13957 49% 98%
SAU201611	SeqID IDENTITY COVERAGE				11539 38% 73%		11902 48% 99%	12973 100% 100%	13243 58% 95%	
SAU201615	SeqID IDENTITY COVERAGE						11962 40% 72%	12972 100% 100%		
SAU201621	SeqID IDENTITY COVERAGE	10038 49% 91%	10842 53% 91%		11392 42% 91%	11707 49% 91%	12047 47% 91%	12662 100% 101%		13902 46% 91%
SAU201654	SeqID IDENTITY COVERAGE							12982 100% 101%		
SAU201666	SeqID IDENTITY COVERAGE	10291 33% 71%	10900 29% 80%	11028 35% 71%	11557 31% 76%	11761 32% 79%	11811 34% 73%	12981 100% 100%		13743 33% 71%
SAU201752	SeqID IDENTITY COVERAGE		10623 45% 89%					12963 100% 100%	13689 40% 92%	
SAU201765	SeqID IDENTITY COVERAGE							12770 100% 100%		
SAU201773	SeqID IDENTITY COVERAGE							12996 100% 100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU201775	SeqID IDENTITY COVERAGE							12996 100% 100%		
SAU201810	SeqID IDENTITY COVERAGE							12769 100% 100%		
SAU201827	SeqID IDENTITY COVERAGE	10258 38% 108%	10783 46% 100%	11134 41% 100%	11310 41% 104%		11787 45% 88%	13002 100% 100%	13411 63% 101%	14088 39% 108%
SAU201929	SeqID IDENTITY COVERAGE							13008 100% 100%		
SAU201952	SeqID IDENTITY COVERAGE							13020 100% 100%		
SAU201971	SeqID IDENTITY COVERAGE							13015 100% 101%		
SAU202006	SeqID IDENTITY COVERAGE							13018 100% 100%		
SAU202039	SeqID IDENTITY COVERAGE				11359 44% 96%			13009 100% 101%	13374 48% 98%	
SAU202126	SeqID IDENTITY COVERAGE	10261 51% 94%	10874 50% 94%	10983 52% 91%	11561 33% 84%		11946 46% 93%	12714 100% 101%	13417 58% 94%	14085 52% 94%
SAU202174	SeqID IDENTITY COVERAGE							12895 100% 101%		
SAU202176	SeqID IDENTITY COVERAGE							12895 100% 101%		
SAU202186	SeqID IDENTITY COVERAGE	10062 28% 73%						12731 100% 101%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU202267	SeqID IDENTITY COVERAGE							12727 100% 100%		
SAU202708	SeqID IDENTITY COVERAGE	10428 25% 86%	10913 28% 84%					12855 100% 100%		13735 25% 86%
SAU202736	SeqID IDENTITY COVERAGE	10148 39% 95%	10902 40% 93%	11181 37% 98%	11494 40% 91%	11677 37% 80%	11857 38% 93%	12927 100% 100%	13248 38% 103%	13844 39% 95%
SAU202756	SeqID IDENTITY COVERAGE	10436 44% 97%	10614 63% 92%	11071 47% 86%			5181 44% 92%	13027 100% 100%	13246 53% 91%	14045 40% 97%
SAU202781	SeqID IDENTITY COVERAGE							12718 100% 100%		
SAU202872	SeqID IDENTITY COVERAGE		10656 45% 101%					12866 100% 100%	13670 28% 98%	
SAU202882	SeqID IDENTITY COVERAGE							12848 100% 101%		
SAU202930	SeqID IDENTITY COVERAGE							12871 100% 100%		
SAU202945	SeqID IDENTITY COVERAGE							12868 100% 100%		
SAU202968	SeqID IDENTITY COVERAGE							12886 100% 100%		
SAU203001	SeqID IDENTITY COVERAGE							12894 100% 100%		
SAU203007	SeqID IDENTITY COVERAGE							12893 100% 100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU203196	SeqID IDENTITY COVERAGE							12945 100% 101%		
SAU203293	SeqID IDENTITY COVERAGE							12979 100% 101%		
SAU203296	SeqID IDENTITY COVERAGE				11330 29% 88%			12263 100% 101%		
SAU203524	SeqID IDENTITY COVERAGE							12957 100% 100%		
SAU300110	SeqID IDENTITY COVERAGE	10054 33% 82%	10544 38% 109%			11662 33% 73%		13031 100% 102%	13441 30% 109%	
SAU300131	SeqID IDENTITY COVERAGE	10344 45% 100%	10529 71% 99%	11112 44% 100%	11434 52% 99%		5164 47% 99%	13034 100% 101%	13213 60% 99%	14103 44% 100%
SAU300156	SeqID IDENTITY COVERAGE							13036 100% 100%		
SAU300191	SeqID IDENTITY COVERAGE		10562 43% 103%		11519 39% 91%		11844 32% 72%	12367 100% 101%	13522 41% 104%	
SAU300572	SeqID IDENTITY COVERAGE				11522 32% 108%			12717 100% 100%		
SAU300617	SeqID IDENTITY COVERAGE		10851 50% 97%					12513 100% 100%	13289 49% 97%	
SAU300713	SeqID IDENTITY COVERAGE		10767 26% 83%				11823 30% 93%	13058 100% 100%		
SAU300719	SeqID IDENTITY COVERAGE	10468 46% 100%	10611 34% 87%	11246 34% 101%	11380 30% 94%	11644 30% 101%	11887 40% 100%	12987 100% 101%	13456 33% 96%	13726 34% 100%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU300732	SeqID IDENTITY COVERAGE	10282 26% 71%	10682 51% 88%					13061 100% 100%	13394 49% 86%	
SAU300825	SeqID IDENTITY COVERAGE		10655 52% 97%					13068 100% 100%	13671 41% 97%	
SAU300975	SeqID IDENTITY COVERAGE		10604 30% 72%					12203 100% 102%		
SAU300998	SeqID IDENTITY COVERAGE		10820 40% 99%					13077 100% 102%	13489 40% 99%	
SAU301004	SeqID IDENTITY COVERAGE		10744 40% 101%					13079 100% 100%		
SAU301030	SeqID IDENTITY COVERAGE							13080 100% 100%		
SAU301080	SeqID IDENTITY COVERAGE							13083 100% 100%		
SAU301118	SeqID IDENTITY COVERAGE	10242 47% 98%	10808 58% 98%	11092 48% 91%		11653 53% 78%		12904 100% 100%		13795 48% 96%
SAU301133	SeqID IDENTITY COVERAGE		10898 39% 96%					13087 100% 100%	13443 30% 93%	
SAU301223	SeqID IDENTITY COVERAGE	10297 31% 104%	10640 50% 99%	10964 31% 102%	11323 32% 90%		11783 34% 102%	13090 100% 100%	13664 48% 98%	13737 32% 104%
SAU301230	SeqID IDENTITY COVERAGE	10252 52% 95%	10877 52% 92%	11010 63% 74%		11669 52% 95%	11956 59% 77%	13092 100% 100%	13506 59% 92%	13704 52% 95%
SAU301268	SeqID IDENTITY COVERAGE							13102 100% 100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU301275	SeqID IDENTITY COVERAGE	10048 54% 99%	10926 47% 84%	11014 55% 97%	11511 50% 97%		11934 53% 97%	13103 100% 101%	13366 46% 84%	13897 54% 99%
SAU301357	SeqID IDENTITY COVERAGE		10696 74% 98%	11063 32% 80%		11766 33% 93%		12859 100% 101%	13354 76% 100%	
SAU301433	SeqID IDENTITY COVERAGE							12845 100% 100%	13393 26% 91%	
SAU301465	SeqID IDENTITY COVERAGE	10210 29% 100%	10663 54% 104%	11214 32% 104%	11554 37% 100%		11921 28% 101%	13013 100% 100%	13418 52% 103%	13925 29% 102%
SAU301472	SeqID IDENTITY COVERAGE	10157 36% 85%						12925 100% 100%		
SAU301592	SeqID IDENTITY COVERAGE							13137 100% 100%		
SAU301620	SeqID IDENTITY COVERAGE							13140 100% 100%		
SAU301758	SeqID IDENTITY COVERAGE							13156 100% 100%		
SAU301773	SeqID IDENTITY COVERAGE							12729 100% 100%		
SAU301829	SeqID IDENTITY COVERAGE	10107 45% 98%			11309 40% 97%		11857 42% 96%	13162 100% 100%	13248 38% 106%	13935 41% 99%
SAU301869	SeqID IDENTITY COVERAGE		10732 30% 80%		11373 36% 95%			12903 100% 100%		
SAU301898	SeqID IDENTITY COVERAGE		10932 27% 71%					13057 100% 100%		

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU302060	SeqID IDENTITY COVERAGE							13042 100% 100%		
SAU302513	SeqID IDENTITY COVERAGE							12851 100% 100%		
SAU302626	SeqID IDENTITY COVERAGE							13105 100% 100%		
SAU302685	SeqID IDENTITY COVERAGE							13113 100% 100%		
SAU302698	SeqID IDENTITY COVERAGE							12725 100% 100%		
SAU302699	SeqID IDENTITY COVERAGE							13115 100% 100%		
SAU302805	SeqID IDENTITY COVERAGE				11345 33% 75%			13133 100% 101%		
SAU302901	SeqID IDENTITY COVERAGE							12872 100% 100%		
SAU302931	SeqID IDENTITY COVERAGE							13155 100% 100%		
SAU302950	SeqID IDENTITY COVERAGE							12664 100% 101%		
SAU302956	SeqID IDENTITY COVERAGE	10023 32% 88%		11256 28% 88%		11742 31% 88%	12044 26% 86%	12930 100% 101%	13372 31% 88%	14018 32% 88%

TABLE VIIA (*Continued*)

LOCUSID	**Data**	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
ECO100078	Seq ID IDENTITY COVERAGE	10023 100% 100%		11256 66% 98%		11742 95% 100%	12044 65% 99%		13595 41% 97%	14018 97% 100%
ECO100252	Seq ID IDENTITY COVERAGE	10052 100% 100%			11503 41% 99%		12078 48% 96%	12626 38% 93%		13932 40% 93%
ECO100397	Seq ID IDENTITY COVERAGE	10064 100% 100%	10781 50% 96%	10993 71% 100%	11499 38% 97%		11959 71% 97%	12884 45% 97%	13614 47% 97%	13915 94% 99%
ECO100398	Seq ID IDENTITY COVERAGE	10065 100% 100%	10653 53% 95%	10992 81% 101%	11311 46% 98%		11958 71% 99%	12883 57% 95%	13177 50% 95%	13916 98% 100%
ECO100990	Seq ID IDENTITY COVERAGE	10120 100% 100%				11768 72% 82%				
ECO102108	Seq ID IDENTITY COVERAGE	10214 100% 100%	10608 36% 96%	11129 74% 100%		11757 94% 100%	11852 36% 97%		13627 36% 97%	13931 96% 73%
ECO102262	Seq ID IDENTITY COVERAGE	10228 100% 100%		11204 42% 100%		11631 86% 81%	12038 51% 100%	13132 35% 100%		13963 87% 100%
ECO102447	Seq ID IDENTITY COVERAGE	10247 100% 100%					11812 47% 93%			13948 99% 96%
ECO102539	Seq ID IDENTITY COVERAGE	10258 100% 100%	10628 46% 101%	11134 77% 100%	11489 48% 100%		5192 71% 100%	12526 52% 100%	13636 47% 82%	14088 97% 100%
ECO102620	Seq ID IDENTITY COVERAGE	10266 100% 100%	10510 51% 93%	11269 26% 80%	11524 30% 94%		11819 28% 91%	12915 42% 96%	13279 49% 101%	14049 89% 99%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
ECO103101	Seq ID IDENTITY COVERAGE	10315 100% 100%	10763 37% 74%	11215 73% 100%	11615 26% 76%	11716 96% 100%	12052 64% 100%		13662 33% 74%	13764 94% 101%
ECO104120	Seq ID IDENTITY COVERAGE	10462 100% 100%	10609 29% 79%	11034 34% 89%		11726 87% 100%	11853 28% 89%			13887 37% 92%
ECO104268	Seq ID IDENTITY COVERAGE	10475 100% 100%	10607 43% 92%					12370 43% 99%	13166 38% 92%	13707 95% 100%
KPN100432	Seq ID IDENTITY COVERAGE	10258 90% 100%	10736 37% 97%	11134 62% 100%	11310 37% 93%	11628 100% 101%	5192 62% 97%	12789 41% 86%	13636 47% 87%	14088 92% 101%
KPN100854	Seq ID IDENTITY COVERAGE	10086 35% 74%	10652 29% 72%	11197 26% 72%	11565 27% 85%	11630 100% 100%	11862 42% 77%		13389 32% 71%	14060 35% 74%
KPN101022	Seq ID IDENTITY COVERAGE	10475 90% 100%	10607 29% 77%			11642 100% 101%		12370 27% 101%	13166 26% 79%	13707 91% 101%
KPN101026	Seq ID IDENTITY COVERAGE	10228 86% 99%		11204 44% 97%		11631 100% 100%	12038 54% 98%	13132 37% 99%		13963 85% 99%
KPN101729	Seq ID IDENTITY COVERAGE			11045 50% 96%	11467 50% 96%	11647 100% 102%	12067 63% 96%	13032 63% 96%		
KPN101750	Seq ID IDENTITY COVERAGE	10052 94% 100%			11503 38% 103%	11652 100% 100%	12078 47% 100%	12626 37% 96%		13918 34% 100%
KPN102057	Seq ID IDENTITY COVERAGE	10406 29% 96%	10892 30% 96%	11035 30% 84%		11661 100% 100%	11854 27% 97%	13153 28% 85%		13883 29% 96%
KPN102638	Seq ID IDENTITY COVERAGE	10266 77% 79%	10510 51% 79%		11524 29% 83%	11667 100% 100%		12915 44% 80%	13557 50% 79%	14049 77% 79%
KPN103882	Seq ID IDENTITY COVERAGE	10315 96% 100%	10763 38% 74%	11215 73% 100%	11454 26% 77%	11716 100% 100%	12052 65% 100%		13662 33% 74%	13764 93% 101%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
KPN104183	Seq ID IDENTITY COVERAGE	10065 97% 85%	10653 56% 74%	10992 80% 89%	11490 46% 86%	11650 100% 100%	11958 80% 85%	12883 60% 74%	13177 55% 74%	13916 98% 85%
KPN104281	Seq ID IDENTITY COVERAGE	10023 95% 94%		11256 68% 92%		11742 100% 101%	12044 66% 94%		13595 41% 91%	14018 95% 101%
KPN104538	Seq ID IDENTITY COVERAGE	10462 87% 100%	10609 27% 87%	11034 35% 89%		11726 100% 100%	11853 29% 89%			13887 38% 94%
KPN104716	Seq ID IDENTITY COVERAGE	10214 94% 100%	10608 36% 96%	11129 75% 100%		11757 100% 100%	11852 36% 97%		13627 35% 97%	13931 94% 73%
KPN105779	Seq ID IDENTITY COVERAGE					11770 100% 101%	12103 28% 99%			
KPN106659	Seq ID IDENTITY COVERAGE	10064 90% 80%	10781 58% 70%	10993 72% 75%		11649 100% 101%	11959 74% 74%	12884 51% 72%	13614 58% 70%	13915 91% 81%
KPN106840	Seq ID IDENTITY COVERAGE	10259 91% 100%	10857 44% 101%	10978 74% 98%		11664 100% 100%	12026 55% 99%	12182 38% 94%	13691 42% 92%	14087 91% 100%
KPN107776	Seq ID IDENTITY COVERAGE	10222 78% 98%		11132 37% 89%		11771 100% 102%	11810 35% 87%			13936 80% 98%
SAU100968	Seq ID IDENTITY COVERAGE	10064 45% 97%	10781 62% 97%	10993 44% 100%	11499 36% 99%		11959 46% 97%	12643 100% 100%	13614 62% 98%	13915 46% 97%
SAU201145	Seq ID IDENTITY COVERAGE	10064 45% 97%	10781 62% 97%	10993 44% 100%	11499 36% 99%		11959 46% 97%	12884 100% 100%	13614 62% 98%	13915 46% 97%
SPN101971	Seq ID IDENTITY COVERAGE	10064 46% 100%	10781 77% 99%	10993 42% 102%	11499 36% 100%		11959 48% 100%	12884 62% 99%	13287 100% 100%	13915 46% 100%
SPN201024	Seq ID IDENTITY COVERAGE	10064 46% 99%	10781 77% 99%	10993 43% 102%	11499 36% 101%		11959 49% 99%	12884 62% 99%	13614 100% 100%	13915 46% 99%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
STY000277	Seq ID IDENTITY COVERAGE	10475 95% 100%	10607 44% 91%					12370 42% 99%	13166 38% 96%	13707 100% 100%
STY000625	Seq ID IDENTITY COVERAGE	10421 93% 100%								13784 100% 101%
STY000773	Seq ID IDENTITY COVERAGE	10315 94% 100%	10763 36% 74%	11215 71% 100%	11454 26% 77%	11716 93% 100%	12052 62% 100%		13662 31% 74%	13764 100% 100%
STY001430	Seq ID IDENTITY COVERAGE	10064 94% 100%	10781 49% 96%	10993 70% 101%	11499 37% 98%		11959 70% 98%	12884 46% 97%	13614 47% 98%	13915 100% 100%
STY001433	Seq ID IDENTITY COVERAGE	10065 98% 99%	10653 53% 94%	10992 82% 100%	11311 46% 97%		11958 72% 99%	12883 58% 94%	13177 50% 94%	13916 100% 100%
STY001867	Seq ID IDENTITY COVERAGE	10247 99% 98%					11812 47% 96%			13948 100% 100%
STY002995	Seq ID IDENTITY COVERAGE	10023 97% 94%		11256 67% 92%		11742 95% 101%	12044 65% 94%		13595 40% 91%	14018 100% 101%
STY003357	Seq ID IDENTITY COVERAGE	10228 87% 100%		11204 42% 100%		11631 85% 81%	12038 49% 101%	13132 36% 100%		13963 100% 100%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA0028	SeqID COVERAGE IDENTITY						5053 100% 100%			
PA0120	SeqID COVERAGE IDENTITY	10386 96% 28%		10959 94% 28%			5054 100% 100%			13899 95% 28%
PA0129	SeqID COVERAGE IDENTITY	10265 93% 67%			11388 91% 32%		5055 100% 100%	12844 94% 36%		14048 91% 67%
PA0141	SeqID COVERAGE IDENTITY						5056 100% 100%			
PA0221	SeqID COVERAGE IDENTITY			11250 73% 32%	11386 77% 26%	11701 83% 28%	5057 100% 100%	12781 96% 28%		13778 77% 29%
PA0265	SeqID COVERAGE IDENTITY	10264 100% 81%	10550 97% 35%		11466 99% 26%		5058 100% 100%	12375 96% 38%	13316 91% 34%	14047 100% 80%
PA0321	SeqID COVERAGE IDENTITY						5059 100% 100%			
PA0337	SeqID COVERAGE IDENTITY	10278 99% 43%	10785 73% 35%	11275 72% 37%			5060 100% 100%	12351 72% 36%	13281 73% 35%	13880 99% 42%
PA0353	SeqID COVERAGE IDENTITY	10408 97% 74%		11088 100% 75%	11397 88% 28%	11749 101% 74%	5061 100% 100%	12159 100% 45%	13511 96% 38%	14034 101% 74%
PA0378	SeqID COVERAGE IDENTITY	10324 94% 52%		11130 80% 49%			5062 100% 100%			13730 95% 53%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA0401	SeqID COVERAGE IDENTITY	10078 99% 26%	10858 100% 31%				5063 100% 100%	12993 96% 33%	13560 100% 33%	13723 99% 26%
PA0413	SeqID COVERAGE IDENTITY						5064 100% 100%			
PA0414	SeqID COVERAGE IDENTITY						5065 100% 100%			
PA0419	SeqID COVERAGE IDENTITY	10296 100% 46%	10871 93% 29%	11003 102% 45%		11660 78% 47%	5066 100% 100%	12971 100% 27%	13461 91% 29%	13738 100% 47%
PA0423	SeqID COVERAGE IDENTITY	10123 99% 75%			11424 97% 32%		5067 100% 100%	12708 75% 32%		14038 99% 76%
PA0469	SeqID COVERAGE IDENTITY						5068 100% 100%			
PA0472	SeqID COVERAGE IDENTITY	10471 88% 47%					5069 100% 100%			
PA0506	SeqID COVERAGE IDENTITY						5070 100% 100%			
PA0600	SeqID COVERAGE IDENTITY						5071 100% 100%			
PA0642	SeqID COVERAGE IDENTITY						5072 100% 100%			
PA0650	SeqID COVERAGE IDENTITY	10150 95% 38%		11237 83% 38%	11581 93% 35%		5073 100% 100%	12153 76% 34%	13459 95% 38%	13846 95% 39%
PA0715	SeqID COVERAGE IDENTITY						5074 100% 100%			

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA0788	SeqID COVERAGE IDENTITY						5075 100% 100%			
PA0882	SeqID COVERAGE IDENTITY	10233 85% 33%					5076 100% 100%			14013 101% 28%
PA0934	SeqID COVERAGE IDENTITY	10276 101% 47%	10876 93% 40%	11006 101% 46%		11753 80% 37%	5077 100% 100%	12646 92% 39%	13483 94% 38%	
PA0938	SeqID COVERAGE IDENTITY						5078 100% 100%			
PA1019	SeqID COVERAGE IDENTITY	10467 88% 26%	10592 84% 25%	11180 88% 28%			5079 100% 100%			
PA1072	SeqID COVERAGE IDENTITY	10377 100% 62%					5080 100% 100%		13410 71% 36%	13813 100% 61%
PA1115	SeqID COVERAGE IDENTITY						5081 100% 100%			
PA1270	SeqID COVERAGE IDENTITY	10328 76% 26%				11751 79% 25%	5082 100% 100%			13946 76% 26%
PA1301	SeqID COVERAGE IDENTITY	10470 96% 28%					5083 100% 100%			
PA1360	SeqID COVERAGE IDENTITY	10104 92% 63%					5084 100% 100%		13282 97% 25%	14000 92% 63%
PA1365	SeqID COVERAGE IDENTITY						5085 100% 100%			
PA1398	SeqID COVERAGE IDENTITY						5086 100% 100%			

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA1462	SeqID COVERAGE IDENTITY		10915 98% 29%		11559 101% 30%		5087 100% 100%			
PA1493	SeqID COVERAGE IDENTITY	10423 92% 56%				11718 97% 49%	5088 100% 100%			13786 92% 56%
PA1547	SeqID COVERAGE IDENTITY				11377 88% 28%		5089 100% 100%			
PA1636	SeqID COVERAGE IDENTITY	10091 101% 37%					5090 100% 100%	12990 96% 26%		13890 81% 32%
PA1684	SeqID COVERAGE IDENTITY					11693 99% 59%	5091 100% 100%			
PA1868	SeqID COVERAGE IDENTITY	10361 82% 35%					5092 100% 100%			
PA1876	SeqID COVERAGE IDENTITY					11746 76% 40%	5093 100% 100%			14036 93% 39%
PA1918	SeqID COVERAGE IDENTITY	10153 79% 31%		11033 82% 28%			5094 100% 100%			13745 79% 28%
PA1986	SeqID COVERAGE IDENTITY						5095 100% 100%			
PA2009	SeqID COVERAGE IDENTITY						5096 100% 100%			
PA2083	SeqID COVERAGE IDENTITY	10253 87% 31%				11692 85% 35%	5097 100% 100%			
PA2101	SeqID COVERAGE IDENTITY	10198 92% 30%					5098 100% 100%		13282 88% 25%	13861 95% 28%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA2108	SeqID COVERAGE IDENTITY	10109 96% 37%		11257 95% 27%			5099 100% 100%	12943 94% 34%	13625 90% 29%	13996 96% 37%
PA2128	SeqID COVERAGE IDENTITY	10472 97% 27%	10865 96% 26%			11752 86% 25%	5100 100% 100%		13683 80% 27%	13893 97% 33%
PA2147	SeqID COVERAGE IDENTITY	10181 98% 60%					5101 100% 100%			13985 98% 59%
PA2196	SeqID COVERAGE IDENTITY	10169 99% 43%					5102 100% 100%			13852 99% 43%
PA2197	SeqID COVERAGE IDENTITY	10160 100% 74%					5103 100% 100%	12917 97% 44%		13830 100% 73%
PA2222	SeqID COVERAGE IDENTITY						5104 100% 100%			
PA2313	SeqID COVERAGE IDENTITY						5105 100% 100%			
PA2398	SeqID COVERAGE IDENTITY	10132 86% 35%					5106 100% 100%			
PA2424	SeqID COVERAGE IDENTITY						5107 100% 100%			
PA2461	SeqID COVERAGE IDENTITY						5108 100% 100%			
PA2470	SeqID COVERAGE IDENTITY						5109 100% 100%			13930 98% 60%
PA2488	SeqID COVERAGE IDENTITY	10189 89% 32%		11172 70% 28%			5110 100% 100%			13980 87% 29%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA2494	SeqID COVERAGE IDENTITY	10331 99% 42%		11145 98% 31%	11516 100% 26%		5111 100% 100%			13719 98% 41%
PA2584	SeqID COVERAGE IDENTITY	10195 94% 60%	10899 99% 37%	10967 94% 57%	11504 97% 38%		5112 100% 100%	12330 99% 41%	13442 92% 42%	14058 94% 58%
PA2594	SeqID COVERAGE IDENTITY	10116 97% 41%				11714 80% 45%	5113 100% 100%			
PA2634	SeqID COVERAGE IDENTITY	10441 74% 28%					5114 100% 100%			
PA2641	SeqID COVERAGE IDENTITY	10226 95% 80%	10566 89% 37%				5115 100% 100%			13959 95% 80%
PA2671	SeqID COVERAGE IDENTITY						5116 100% 100%			
PA2680	SeqID COVERAGE IDENTITY	10444 101% 42%	10703 74% 30%			11730 90% 43%	5117 100% 100%			14029 101% 42%
PA2684	SeqID COVERAGE IDENTITY	10384 99% 33%					5118 100% 100%			
PA2726	SeqID COVERAGE IDENTITY						5119 100% 100%			
PA2742	SeqID COVERAGE IDENTITY	10177 91% 64%	10660 97% 50%	11222 84% 67%	11296 89% 47%		5120 100% 100%	12628 97% 55%	13302 97% 45%	
PA3006	SeqID COVERAGE IDENTITY						5121 100% 100%			
PA3011	SeqID COVERAGE IDENTITY	10151 100% 68%	10695 79% 40%	11233 100% 64%	11293 86% 39%		5122 100% 100%	12339 75% 42%		13848 100% 66%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA3013	SeqID COVERAGE IDENTITY	10416 98% 64%	10494 80% 39%	11095 102% 43%	11525 102% 41%		5123 100% 100%	12461 102% 40%		13750 98% 64%
PA3041	SeqID COVERAGE IDENTITY	10307 88% 32%					5124 100% 100%			13777 88% 32%
PA3048	SeqID COVERAGE IDENTITY	10117 99% 47%		10966 75% 45%			5125 100% 100%			14005 99% 47%
PA3068	SeqID COVERAGE IDENTITY						5126 100% 100%			
PA3121	SeqID COVERAGE IDENTITY	10021 99% 63%		11164 99% 59%	11363 81% 26%		5127 100% 100%	12156 99% 56%		14017 99% 62%
PA3153	SeqID COVERAGE IDENTITY						5128 100% 100%			
PA3154	SeqID COVERAGE IDENTITY						5129 100% 100%			
PA3160	SeqID COVERAGE IDENTITY						5130 100% 100%			
PA3279	SeqID COVERAGE IDENTITY						5131 100% 100%			
PA3280	SeqID COVERAGE IDENTITY						5132 100% 100%			
PA3374	SeqID COVERAGE IDENTITY	10452 99% 55%					5133 100% 100%			
PA3479	SeqID COVERAGE IDENTITY						5134 100% 100%			

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA3484	SeqID						5135			
	COVERAGE						100%			
	IDENTITY						100%			
PA3522	SeqID	10331		11145	11516		5136			13719
	COVERAGE	98%		99%	99%		100%			99%
	IDENTITY	41%		30%	26%		100%			40%
PA3643	SeqID	10046		11173	11378		5137			13912
	COVERAGE	99%		100%	79%		100%			99%
	IDENTITY	53%		51%	30%		100%			52%
PA3703	SeqID	10194					5138			13751
	COVERAGE	100%					100%			100%
	IDENTITY	30%					100%			31%
PA3709	SeqID						5139			
	COVERAGE						100%			
	IDENTITY						100%			
PA3716	SeqID						5140			
	COVERAGE						100%			
	IDENTITY						100%			
PA3764	SeqID	10255		10991			5141			13793
	COVERAGE	94%		91%			100%			82%
	IDENTITY	38%		41%			100%			39%
PA3845	SeqID	10277		11200			5142			13882
	COVERAGE	98%		98%			100%			98%
	IDENTITY	34%		30%			100%			35%
PA3866	SeqID						5143			
	COVERAGE						100%			
	IDENTITY						100%			
PA3876	SeqID	10144					5144			13840
	COVERAGE	97%					100%			97%
	IDENTITY	61%					100%			58%
PA3877	SeqID	10161					5145	12699		13831
	COVERAGE	98%					100%	92%		98%
	IDENTITY	28%					100%	27%		27%
PA3931	SeqID	10050	10833	11067	11460	11656	5146	12548	13173	13720
	COVERAGE	82%	92%	103%	92%	82%	100%	96%	109%	95%
	IDENTITY	50%	43%	41%	49%	48%	100%	44%	36%	35%

TABLE VIIA (*Continued*)

LOCUSID	**Data**	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA3984	SeqID COVERAGE IDENTITY	10087 97% 40%		11002 98% 37%		11674 91% 39%	5147 100% 100%			14061 99% 40%
PA4024	SeqID COVERAGE IDENTITY	10244 95% 50%	10700 95% 50%			11736 71% 72%	5148 100% 100%			13951 95% 50%
PA4027	SeqID COVERAGE IDENTITY						5149 100% 100%			
PA4037	SeqID COVERAGE IDENTITY	10102 72% 35%	10563 83% 30%	11194 72% 33%	11527 72% 34%	11725 72% 33%	5150 100% 100%	12958 70% 35%	13296 71% 31%	14002 72% 34%
PA4067	SeqID COVERAGE IDENTITY	10149 98% 44%					5151 100% 100%			13845 99% 43%
PA4070	SeqID COVERAGE IDENTITY	10159 96% 28%					5152 100% 100%			
PA4081	SeqID COVERAGE IDENTITY						5153 100% 100%			
PA4105	SeqID COVERAGE IDENTITY						5154 100% 100%			
PA4124	SeqID COVERAGE IDENTITY						5155 100% 100%			14023 93% 64%
PA4125	SeqID COVERAGE IDENTITY						5156 100% 100%			14024 94% 67%
PA4158	SeqID COVERAGE IDENTITY	10080 98% 61%	10610 95% 38%	11009 88% 31%	11379 83% 28%	11769 74% 61%	5157 100% 100%	12297 96% 50%		13725 97% 61%
PA4237	SeqID COVERAGE IDENTITY	10333 91% 79%	10542 97% 43%	11123 98% 76%	11582 90% 43%		5158 100% 100%	12232 92% 45%	13224 97% 42%	14093 91% 79%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA4242	SeqID	10338	10538	11117	11428		5159			
	COVERAGE	100%	100%	100%	100%		100%			
	IDENTITY	87%	68%	76%	74%		100%			
PA4244	SeqID	10340	10534	11116			5160	12225	13217	14099
	COVERAGE	100%	100%	100%			100%	100%	100%	100%
	IDENTITY	65%	46%	63%			100%	42%	43%	65%
PA4245	SeqID	10341	10532	11115			5161	12223	13216	13812
	COVERAGE	95%	98%	95%			100%	98%	98%	78%
	IDENTITY	56%	42%	58%			100%	42%	40%	33%
PA4246	SeqID	10342	10531	11114	11432		5162	12222	13215	14101
	COVERAGE	100%	92%	99%	88%		100%	99%	92%	100%
	IDENTITY	77%	52%	74%	49%		100%	52%	53%	77%
PA4247	SeqID	10343	10530	11113	11433		5163	12221	13214	14102
	COVERAGE	99%	98%	99%	97%		100%	98%	98%	99%
	IDENTITY	59%	52%	63%	37%		100%	48%	54%	59%
PA4248	SeqID	10344	10529	11112	11434		5164	12220	13571	14103
	COVERAGE	100%	99%	100%	99%		100%	99%	99%	100%
	IDENTITY	62%	49%	66%	50%		100%	43%	47%	62%
PA4249	SeqID	10345	10528	11111	11435		5165	13033	13212	14104
	COVERAGE	99%	102%	99%	100%		100%	102%	102%	99%
	IDENTITY	64%	46%	64%	40%		100%	44%	47%	64%
PA4250	SeqID	10346	10599	11110			5166	12737	13211	14105
	COVERAGE	100%	100%	100%			100%	100%	100%	100%
	IDENTITY	69%	43%	63%			100%	46%	53%	67%
PA4251	SeqID	10347	10527	11109	11589	11654	5167	12218	13210	14106
	COVERAGE	99%	99%	99%	99%	99%	100%	90%	98%	99%
	IDENTITY	69%	58%	68%	48%	69%	100%	63%	61%	68%
PA4252	SeqID	10348	10526	11108			5168	12217	13209	14107
	COVERAGE	97%	92%	94%			100%	98%	92%	96%
	IDENTITY	65%	49%	62%			100%	49%	46%	64%
PA4253	SeqID	10349	10525	11107	11436		5169	12216	13208	14108
	COVERAGE	101%	100%	101%	100%		100%	100%	100%	101%
	IDENTITY	85%	66%	85%	65%		100%	66%	66%	84%
PA4254	SeqID	10350	10524	11106	11437		5170	12215	13207	
	COVERAGE	90%	98%	90%	84%		100%	89%	89%	
	IDENTITY	71%	53%	62%	45%		100%	55%	56%	

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA4256	SeqID COVERAGE IDENTITY	10352 100% 77%	10560 100% 54%	11104 100% 77%	11439 96% 65%		5171 100% 100%	12260 98% 58%	13204 98% 57%	13968 100% 77%
PA4257	SeqID COVERAGE IDENTITY	10353 99% 74%	10559 91% 61%	11103 100% 72%	11592 99% 55%		5172 100% 100%	12259 91% 57%	13203 93% 59%	13969 99% 74%
PA4258	SeqID COVERAGE IDENTITY	10354 100% 69%	10558 91% 57%	11102 100% 70%	11593 95% 41%		5173 100% 100%	12258 99% 48%	13202 91% 58%	13970 100% 69%
PA4259	SeqID COVERAGE IDENTITY	10355 100% 82%	10557 101% 70%	11101 100% 84%	11594 99% 61%		5174 100% 100%	12255 100% 63%	13201 100% 67%	
PA4262	SeqID COVERAGE IDENTITY	10358 100% 68%	10549 95% 45%	11098 100% 72%	11595 96% 36%		5175 100% 100%	12240 101% 46%	13198 97% 44%	13973 100% 68%
PA4263	SeqID COVERAGE IDENTITY	10359 99% 75%		11097 98% 73%	11442 91% 35%		5176 100% 100%	12235 103% 46%	13197 99% 51%	13974 99% 75%
PA4264	SeqID COVERAGE IDENTITY	10360 100% 90%	10533 75% 58%	11096 100% 92%	11443 95% 57%	11643 100% 92%	5177 100% 100%		13196 99% 61%	13975 100% 91%
PA4268	SeqID COVERAGE IDENTITY	10365 100% 89%	10479 111% 70%	11062 100% 89%	11409 100% 75%		5178 100% 100%	12445 111% 68%	13231 111% 70%	13967 100% 89%
PA4269	SeqID COVERAGE IDENTITY	10439 100% 76%	10627 100% 46%	11036 100% 73%	11410 109% 47%		5179 100% 100%	12446 101% 46%	13646 99% 45%	14042 100% 75%
PA4271	SeqID COVERAGE IDENTITY	10437 100% 66%	10615 101% 65%	11072 101% 66%	11572 102% 54%		5180 100% 100%	12449 98% 58%	13247 100% 58%	14044 100% 64%
PA4272	SeqID COVERAGE IDENTITY	10436 99% 68%	10614 95% 40%	11071 100% 66%			5181 100% 100%	12450 99% 39%	13246 95% 42%	14045 99% 65%
PA4316	SeqID COVERAGE IDENTITY	10200 88% 51%		11235 90% 47%			5182 100% 100%			13821 91% 51%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA4332	SeqID COVERAGE IDENTITY						5183 100% 100%			
PA4347	SeqID COVERAGE IDENTITY					11699 86% 27%	5184 100% 100%			
PA4363	SeqID COVERAGE IDENTITY	10292 95% 40%				11740 81% 36%	5185 100% 100%			13742 95% 41%
PA4375	SeqID COVERAGE IDENTITY	10072 101% 33%		11145 100% 45%	11516 100% 28%		5186 100% 100%			13719 101% 33%
PA4413	SeqID COVERAGE IDENTITY	10030 90% 45%	10805 94% 33%	11188 92% 41%	11458 93% 30%		5187 100% 100%	12360 93% 33%	13333 98% 32%	14077 90% 44%
PA4433	SeqID COVERAGE IDENTITY	10327 100% 75%	10602 99% 59%	11241 100% 73%	11289 94% 54%	11655 72% 76%	5188 100% 100%	12237 99% 55%	13356 99% 56%	13729 100% 72%
PA4473	SeqID COVERAGE IDENTITY	10463 84% 39%		11195 81% 37%			5189 100% 100%			13986 84% 39%
PA4506	SeqID COVERAGE IDENTITY	10381 99% 58%	10658 77% 48%	11198 98% 60%	11314 79% 51%	11717 91% 59%	5190 100% 100%	12850 99% 46%	13248 81% 42%	13800 99% 58%
PA4512	SeqID COVERAGE IDENTITY						5191 100% 100%			13815 99% 57%
PA4542	SeqID COVERAGE IDENTITY	10258 100% 71%	10628 101% 47%	11134 100% 70%	11489 100% 49%		5192 100% 100%	12526 101% 52%	13421 80% 46%	14088 100% 71%
PA4576	SeqID COVERAGE IDENTITY						5193 100% 100%			
PA4598	SeqID COVERAGE IDENTITY	10072 100% 50%		11145 100% 29%	11516 99% 28%		5194 100% 100%			13719 100% 50%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA4665	SeqID	10143	10826	11251	11287	11675	5195	12380	13336	13979
	COVERAGE	100%	97%	101%	97%	100%	100%	98%	99%	100%
	IDENTITY	66%	54%	64%	52%	65%	100%	53%	50%	66%
PA4681	SeqID						5196			
	COVERAGE						100%			
	IDENTITY						100%			
PA4709	SeqID						5197			
	COVERAGE						100%			
	IDENTITY						100%			
PA4744	SeqID	10314		11216	11501		5198	12322	13663	13765
	COVERAGE	107%		98%	93%		100%	78%	91%	107%
	IDENTITY	58%		58%	39%		100%	48%	43%	58%
PA4771	SeqID	10387		11280			5199		13402	13828
	COVERAGE	100%		99%			100%		96%	97%
	IDENTITY	87%		75%			100%		33%	33%
PA4888	SeqID						5200			
	COVERAGE						100%			
	IDENTITY						100%			
PA4942	SeqID	10455		10972			5201			13856
	COVERAGE	93%		91%			100%			95%
	IDENTITY	48%		41%			100%			48%
PA4997	SeqID	10115	10619	10960	11394		5202	12501	13458	14006
	COVERAGE	86%	82%	97%	83%		100%	96%	97%	86%
	IDENTITY	43%	36%	44%	31%		100%	37%	32%	44%
PA5030	SeqID	10165					5203			
	COVERAGE	90%					100%			
	IDENTITY	64%					100%			
PA5076	SeqID	10197	10796	11176	11383	11694	5204		13292	14057
	COVERAGE	94%	82%	97%	97%	90%	100%		98%	94%
	IDENTITY	29%	33%	27%	26%	29%	100%		30%	30%
PA5088	SeqID						5205			
	COVERAGE						100%			
	IDENTITY						100%			
PA5193	SeqID	10373		11126		11709	5206			13808
	COVERAGE	100%		96%		77%	100%			100%
	IDENTITY	41%		39%		42%	100%			41%

TABLE VIIA (*Continued*)

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA5199	SeqID	10375	10596			11711	5207			13810
	COVERAGE	102%	71%			102%	100%			103%
	IDENTITY	33%	26%			34%	100%			32%
PA5207	SeqID			11260	11612		5208	12730		
	COVERAGE			100%	88%		100%	100%		
	IDENTITY			54%	39%		100%	28%		
PA5209	SeqID	10302					5209			13758
	COVERAGE	90%					100%			89%
	IDENTITY	29%					100%			28%
PA5248	SeqID						5210			
	COVERAGE						100%			
	IDENTITY						100%			
PA5299	SeqID						5211			
	COVERAGE						100%			
	IDENTITY						100%			
PA5316	SeqID	10391		11158	11327		5212	12129		
	COVERAGE	100%		99%	78%		100%	73%		
	IDENTITY	82%		79%	39%		100%	40%		
PA5388	SeqID		10503				5213			
	COVERAGE		85%				100%			
	IDENTITY		28%				100%			
PA5393	SeqID						5214			
	COVERAGE						100%			
	IDENTITY						100%			
PA5436	SeqID	10330	10924	11160	11321		5215	13127	13617	13885
	COVERAGE	94%	94%	94%	94%		100%	94%	94%	94%
	IDENTITY	52%	51%	52%	46%		100%	55%	54%	52%
PA5443	SeqID	10413	10788	11199	11452		5216	12489	13643	13748
	COVERAGE	100%	103%	100%	96%		100%	100%	105%	100%
	IDENTITY	64%	38%	56%	35%		100%	38%	39%	64%
PA5490	SeqID						5217			
	COVERAGE						100%			
	IDENTITY						100%			
PA5493	SeqID	10417	10668	11133	11609		5218	12623	13236	
	COVERAGE	102%	102%	102%	102%		100%	100%	101%	
	IDENTITY	62%	37%	58%	31%		100%	38%	37%	

TABLE VIIA (*Continued*)

LOCUSID	**Data**	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA5507	SeqID COVERAGE IDENTITY	10119 99% 31%					5219 100% 100%			
PA5567	SeqID COVERAGE IDENTITY	10397 99% 67%	10911 103% 39%	11169 99% 64%	11450 100% 33%		5220 100% 100%	12703 102% 34%	13338 101% 37%	13923 99% 67%

<u>TABLE VIIB</u>

PathoSeq Cluster ID	Enterococcus faecalis	Escherichia coli	Pseudomonas aeruginosa	Staphylococcus aureus
15	EFA102326	ECO101796	PAE100280	SAU102515
55	EFA100151	ECO104157	PAE100416	SAU100633
57	EFA100617	ECO102690	PAE105434	SAU100158
1443	EFA100689	ECO103692	PAE101987	SAU100952
1861	EFA101412	ECO103231	PAE104331	SAU101793
2286	EFA103268	ECO103265	PAE104314	SAU101756
2362	EFA101425	ECO100662	PAE101537	SAU101236
2367	EFA101417	ECO103226	PAE103206	SAU101798
2549	EFA101410	ECO103233	PAE104329	SAU101791
3816	EFA101159	ECO103243	PAE104319	SAU100546
3857	EFA101415	ECO103228	PAE103204	SAU101796
4322	EFA101165	ECO103237	PAE104325	SAU100141
4569	EFA100955	ECO103217	PAE103215	SAU101808
4948	EFA101160	ECO103242	PAE104320	SAU100547
5818	EFA100742	ECO103224	PAE103208	SAU101800
8159	EFA101163	ECO103239	PAE104323	SAU100139
8296	EFA101164	ECO103238	PAE104324	SAU100140
8316	EFA101409	ECO103234	PAE104328	SAU101790
8494	EFA103062	ECO103884	PAE104311	SAU100433
8498	EFA101411	ECO103232	PAE104330	SAU101792
8499	EFA101416	ECO103227	PAE103205	SAU101797
7		ECO100071	PAE100837	SAU102674
8	EFA101340		PAE106580	SAU100118
28	EFA101403		PAE102647	SAU100514
41	EFA101753	ECO100148		SAU101565
63	EFA101685		PAE103857	SAU100331
147		ECO100645	PAE100543	SAU100053
548		ECO100377	PAE100604	SAU100747
730		ECO103592	PAE103108	SAU100061
1721	EFA101686	ECO100663		SAU101996
1749	EFA101477	ECO102557		SAU100613
2153	EFA102656	ECO100184		SAU101869
2790	EFA102764	ECO100500		SAU101578
3164	EFA101162	ECO103240		SAU102602
3312	EFA103174		PAE105008	SAU100521
3926	EFA100194	ECO103220		SAU101806
4441	EFA102541		PAE105364	SAU101814
5685	EFA100190	ECO103264		SAU100157
7417	EFA102788	ECO101684		SAU102992
7437	EFA102351	ECO100084		SAU100056
7579		ECO102470	PAE102641	SAU100607
7726	EFA102551	ECO103221		SAU101805
7727	EFA100978	ECO103218		SAU101807
8092		ECO102035	PAE102964	SAU100794
8158	EFA103365		PAE104318	SAU102880

PathoSeq Cluster ID	Enterococcus faecalis	Escherichia coli	Pseudomonas aeruginosa	Staphylococcus aureus
8161	EFA100210		PAE104326	SAU102527
8162	EFA101414		PAE103203	SAU101795
8164	EFA100741	ECO103223		SAU101801
8493	EFA101141		PAE104310	SAU100432
10185	EFA102728	ECO104092		SAU102578
35		ECO102870		SAU100497
44			PAE101061	SAU101143
54			PAE100225	SAU100123
85		ECO101104		SAU101262
184			PAE104901	SAU101366
362	EFA102736			SAU100414
575	EFA101790			SAU100133
579	EFA102110			SAU101624
911			PAE105432	SAU102054
941		ECO101365		SAU102162
952	EFA100615			SAU100964
1084	EFA100289	ECO102819		
1141		ECO102255		SAU102356
1232		ECO100703		SAU101346
1274			PAE103655	SAU102264
1337		ECO102562		SAU100567
1350		ECO100930	PAE103901	
1374		ECO103659		SAU101385
1427	EFA100394			SAU100714
1535		ECO101207		SAU101561
1653	EFA102655			SAU101868
1849	EFA100642			SAU101653
1932	EFA100919			SAU101365
2156	EFA101150			SAU101271
2189		ECO102827	PAE100476	
2238		ECO101436		SAU101092
2338	EFA103038			SAU100518
2411	EFA102802			SAU102246
2501	EFA101121			SAU100996
2974			PAE102537	SAU102125
3027		ECO103959		SAU200242
3239	EFA103021			SAU100300
3244	EFA100399			SAU101891
3386	EFA100426			SAU100886
3447	EFA102915			SAU102112
3460	EFA102023			SAU101399
3682	EFA100740			SAU101802
3771	EFA101540			SAU100275
4424	EFA102542			SAU101815
4654		ECO100488	PAE106184	
5148	EFA100065			SAU100658
7227	EFA100023			SAU100436

PathoSeq Cluster ID	Enterococcus faecalis	Escherichia coli	Pseudomonas aeruginosa	Staphylococcus aureus
7240		ECO103672		SAU101682
7278			PAE101620	SAU301370
7374			PAE106765	SAU103042
7375	EFA102051			SAU103038
7402		ECO103572	PAE106044	
7419		ECO101686		SAU102693
7436	EFA101792			SAU101495
7504	EFA101670			SAU102603
7653	EFA100397			SAU100246
7660	EFA102352	ECO103698		
7719	EFA100756			SAU100496
7725	EFA100739			SAU101803
8040	EFA101736			SAU101197
8058	EFA103571			SAU101242
8077	EFA100200			SAU102231
8082	EFA101080			SAU100199
8116	EFA101963			SAU101028
8122	EFA101737			SAU101198
8141	EFA102780			SAU102433
8177	EFA103348			SAU202126
8178	EFA101022			SAU102283
8181	EFA101541			SAU102909
8191	EFA102022			SAU101398
8234	EFA103033			SAU100745
8237	EFA101682			SAU101266
8238	EFA103295			SAU100963
8251			PAE100662	SAU100596
8300	EFA101120			SAU100944
8539	EFA101339			SAU101400
8610		ECO103661		SAU102298
8874	EFA100748			SAU101155
9028	EFA103210			SAU100731
9996	EFA102338			SAU100175
10234	EFA102186			SAU102933
10248		ECO102828		SAU101220
10297			PAE105229	SAU101381
10328	EFA101079			SAU101547
10345	EFA100295			SAU100659
10365	EFA100641			SAU101655
10393	EFA103504			SAU100961
10402	EFA101833			SAU100880
12426	EFA101413			SAU101794
14277	EFA103081			SAU200088
14330	EFA101161			SAU102881
14455	EFA101424			SAU101771
14520	EFA100211			SAU101789
15660	EFA103375			SAU102694

EXAMPLE 13

Use of Identified Nucleic Acid Sequences as Probes

The sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids can be used as probes to obtain the sequence of additional genes of interest from a second cell or microorganism. For example, probes to genes encoding potential bacterial target proteins may be hybridized to nucleic acids from other organisms including other bacteria and higher organisms, to identify homologous sequences in these other organisms. For example, the identified sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* , homologous coding nucleic acids, or homologous antisense nucleic acids may be used to identify homologous sequences in *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia*

enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species. In some embodiments of the present invention, the nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids may be used to identify homologous nucleic acids from a heterologous organism other than *E. coli.*

Hybridization between the nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids and nucleic acids from humans might indicate that the protein encoded by the gene to which the probe corresponds is found in humans and therefore not necessarily an optimal drug target. Alternatively, the gene can be conserved only in bacteria and therefore would be a good drug target for a broad spectrum antibiotic or antimicrobial. These probes can also be used in a known manner to isolate homologous nucleic acids from *Staphylococcus, Salmonella, Klebsiella, Pseudomonas, Enterococcus* or other cells or microorganisms, e.g. by screening a genomic or cDNA library.

Probes derived from the nucleic acid sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids, or portions thereof, can be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe can be single stranded or double stranded and can be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it can be denatured prior to contacting the probe. In some applications, the nucleic acid sample can be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid

sample can comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe can be cloned into vectors such as expression vectors, sequencing vectors, or in vitro transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques can be used to isolate, purify and clone sequences from a genomic library, made from a variety of bacterial species, which are capable of hybridizing to probes made from the sequences identified in Examples 5 and 6.

EXAMPLE 14

Preparation of PCR Primers and Amplification of DNA

The identified *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* genes corresponding directly to or located within the operon of nucleic acid sequences required for proliferation, homologous coding nucleic acids, or homologous antisense nucleic acids or portions thereof can be used to prepare PCR primers for a variety of applications, including the identification or isolation of homologous sequences from other species. For example, the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* genes may be used to prepare PCR primers to identify or isolate homologous sequences from *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus*

faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the PCR primers may be used to identify or isolate homologous nucleic acids from an organism other than *E. coli.*

The identified or isolated nucleic acids obtained using the PCR primers may contain part or all of the homologous nucleic acids. Because homologous nucleic acids are related but not identical in sequence, those skilled in the art will often employ degenerate sequence PCR primers. Such degenerate sequence primers are designed based on sequence regions that are either known to be conserved or suspected to be conserved such as conserved coding regions. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. The PCR primers are at least 10 nucleotides, and preferably at least 20 nucleotides in length. More preferably, the PCR primers are at least 20-30 nucleotides in length. In some embodiments, the PCR primers can be more than 30 nucleotides in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in **Methods in Molecular Biology** 67: Humana Press, Totowa 1997. When the entire coding sequence of the target gene is known, the 5' and 3' regions of the target gene can be used as the sequence source for PCR probe generation. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable

polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 15

Inverse PCR

The technique of inverse polymerase chain reaction can be used to extend the known nucleic acid sequence identified in Examples 5 and 6. The inverse PCR reaction is described generally by Ochman et al., in Ch. 10 of **PCR Technology: Principles and Applications for DNA Amplification**, (Henry A. Erlich, Ed.) W.H. Freeman and Co. (1992). Traditional PCR requires two primers that are used to prime the synthesis of complementary strands of DNA. In inverse PCR, only a core sequence need be known.

Using the sequences identified as relevant from the techniques taught in Examples 5 and 6 and applied to other species of bacteria, a subset of nucleic sequences are identified that correspond to genes or operons that are required for bacterial proliferation. In species for which a genome sequence is not known, the technique of inverse PCR provides a method for obtaining the gene in order to determine the sequence or to place the probe sequences in full context to the target sequence to which the identified nucleic acid sequence binds.

To practice this technique, the genome of the target organism is digested with an appropriate restriction enzyme so as to create fragments of nucleic acid that contain the identified sequence as well as unknown sequences that flank the identified sequence. These fragments are then circularized and become the template for the PCR reaction. PCR primers are designed in accordance with the teachings of Example 15 and directed to the ends of the identified sequence.. The primers direct nucleic acid synthesis away from the known sequence and toward the unknown sequence contained within the circularized template. After the PCR reaction is complete, the resulting PCR products can be sequenced so as to extend the sequence of the identified gene past the core sequence of the identified exogenous nucleic acid sequence identified. In this manner, the full sequence of

each novel gene can be identified. Additionally the sequences of adjacent coding and noncoding regions can be identified.

EXAMPLE 16

Identification of Genes Required for *Escherichia coli* Proliferation

Genes required for proliferation in *Escherichia coli* are identified according to the methods described above.

EXAMPLE 17

Identification of Genes Required for *Neisseria gonorrhoeae* Proliferation

Genes required for proliferation in *Neisseria gonorrhoeae* are identified according to the methods described above.

EXAMPLE 18

Identification of Genes Required for *Salmonella enterica* Proliferation

Genes required for proliferation in *Salmonella enterica* are identified according to the methods described above.

EXAMPLE 19

Identification of Genes Required for *Enterococcus faecium* Proliferation

Genes required for proliferation in *Enterococcus faecium* are identified according to the methods described above.

EXAMPLE 20

Identification of Genes Required for *Haemophilus influenzae* Proliferation

Genes required for proliferation in *Haemophilus influenzae* are identified according to the methods described above.

EXAMPLE 21

Identification of Genes Required for *Aspergillus fumigatus* Proliferation

Genes required for proliferation in *Aspergillus fumigatus* are identified according to the methods described above.

EXAMPLE 22

Identification of Genes Required for *Helicobacter pylori* Proliferation

Genes required for proliferation in *Helicobacter pylori* are identified according to the methods described above.

EXAMPLE 23

Identification of Genes Required for *Mycoplasma pneumoniae* Proliferation

Genes required for proliferation in *Mycoplasma pneumoniae* are identified according to the methods described above.

EXAMPLE 24

Identification of Genes Required for *Plasmodium ovale* Proliferation

Genes required for proliferation in *Plasmodium ovale* are identified according to the methods described above.

EXAMPLE 25

Identification of Genes Required for *Entamoeba histolytica* Proliferation

Genes required for proliferation in *Entamoeba histolytica* are identified according to the methods described above.

EXAMPLE 26

Identification of Genes Required for *Candida albicans* Proliferation

Genes required for proliferation in *Candida albicans* are identified according to the methods described above.

EXAMPLE 27

Identification of Genes Required for *Histoplasma capsulatum* Proliferation

Genes required for proliferation in *Histoplasma capsulatum* are identified according to the methods described above.

EXAMPLE 28

Identification of Genes Required for *Salmonella typhi* Proliferation

Genes required for proliferation in *Salmonella typhi* are identified according to the methods described above.

EXAMPLE 29

Identification of Genes Required for *Salmonella paratyphi* Proliferation

Genes required for proliferation in *Salmonella paratyphi* are identified according to the methods described above.

EXAMPLE 30

Identification of Genes Required for *Salmonella cholerasuis* Proliferation

Genes required for proliferation in *Salmonella cholerasuis* are identified according to the methods described above.

EXAMPLE 31

Identification of Genes Required for *Staphylococcus epidermis* Proliferation

Genes required for proliferation in *Staphylococcus epidermis* are identified according to the methods described above.

EXAMPLE 32

Identification of Genes Required for *Mycobacterium tuberculosis* Proliferation

Genes required for proliferation in *Mycobacterium tuberculosis* are identified according to the methods described above.

EXAMPLE 33

Identification of Genes Required for *Mycobacterium leprae* Proliferation

Genes required for proliferation in *Mycobacterium leprae* are identified according to the methods described above.

EXAMPLE 34

Identification of Genes Required for *Treponema pallidum* Proliferation

Genes required for proliferation in *Treponema pallidum* are identified according to the methods described above.

EXAMPLE 35

Identification of Genes Required for *Bacillus anthracis* Proliferation

Genes required for proliferation in *Bacillus anthracis* are identified according to the methods described above.

EXAMPLE 36

Identification of Genes Required for *Yersinia pestis* Proliferation

Genes required for proliferation in *Yersinia pestis* are identified according to the methods described above.

EXAMPLE 37

Identification of Genes Required for *Clostridium botulinum* Proliferation

Genes required for proliferation in *Clostridium botulinum* are identified according to the methods described above.

EXAMPLE 38

Identification of Genes Required for *Campylobacter jejuni* Proliferation

Genes required for proliferation in *Campylobacter jejuni* are identified according to the methods described above.

EXAMPLE 39

Identification of Genes Required for *Chlamydia trachomatis* Proliferation

Genes required for proliferation in *Chlamydia trachomatis* are identified according to the methods described above.

EXAMPLE 40

Identification of Genes Required for *Staphylococcus aureus* Proliferation

Genes required for proliferation in *Staphylococcus aureus* are identified according to the methods described above.

EXAMPLE 41

Identification of Genes Required for *Salmonella typhimurium* Proliferation

Genes required for proliferation in *Salmonella typhimurium* are identified according to the methods described above.

EXAMPLE 42

Identification of Genes Required for *Klebsiella Pneumoniae* Proliferation

Genes required for proliferation in *Klebsiella Pneumoniae* are identified according to the methods described above.

EXAMPLE 43

Identification of Genes Required for *Pseudomonas aeruginosa* Proliferation

Genes required for proliferation in *Pseudomonas aeruginosa* are identified according to the methods described above.

EXAMPLE 44

Identification of Genes Required for *Enterococcus faecalis* Proliferation

Genes required for proliferation in *Enterococcus faecalis* are identified according to the methods described above.

Use of Isolated Exogenous Nucleic Acid Fragments as Antisense Antibiotics

In addition to using the identified sequences to enable screening of molecule libraries to identify compounds useful to identify antibiotics, antisense nucleic acids complementary to the proliferation-required sequences or portions thereof, antisense

nucleic acids complementary to homologous coding nucleic acids, or homologous antisense nucleic acids can be used as therapeutic agents. Specifically, the proliferation-required sequences or homolgous coding nucleic acids, or portions therof, in an antisense orientation or homologous antisense nucleic acids can be provided to an individual to inhibit the translation of a bacterial target gene or the processing, folding, or assembly into a protein/RNA complex of a nontranslated RNA.

EXAMPLE 45

<u>Generation of Antisense Therapeutics from Identified Exogenous Sequences</u>

Antisense nucleic acids complementary to the proliferation-required sequences described herein, or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids, or portions thereof, or homologous antisense nucleic acids or portions thereof can be used as antisense therapeutics for the treatment of bacterial infections or simply for inhibition of bacterial growth *in vitro* or *in vivo*. For example, the antisense therapeutics may be used to treat bacterial infections caused by *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or to inhibit the growth of these organisms. The antisense therapeutics may also be used to treat infections caused by or to inhibit the growth of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas*

aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the antisense therapeutics may be used to treat infection by or inhibit the growth of an organism other than *E. coli*.

The therapy exploits the biological process in cells where genes are transcribed into messenger RNA (mRNA) that is then translated into proteins. Antisense RNA technology contemplates the use of antisense nucleic acids, including antisense oligonucleotides, complementary to a target gene that will bind to its target nucleic acid and decrease or inhibit the expression of the target gene. For example, the antisense nucleic acid may inhibit the translation or transcription of the target nucleic acid. In one embodiment, antisense oligonucleotides can be used to treat and control a bacterial infection of a cell culture containing a population of desired cells contaminated with bacteria. In another embodiment, the antisense oligonucleotides can be used to treat an organism with a bacterial infection.

Antisense oligonucleotides can be synthesized from any of the sequences of the present invention using methods well known in the art. In a preferred embodiment, antisense oligonucleotides are synthesized using artificial means. Uhlmann & Peymann, Chemical Rev. 90:543-584 (1990) review antisense oligonucleotide technology in detail. Modified or unmodified antisense oligonucleotides can be used as therapeutic agents. Modified antisense oligonucleotides are preferred. Modification of the phosphate backbones of the antisense oligonucleotides can be achieved by substituting the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate brides, thioester bridges, as well as many others known in the art may also be used. The preparation of certain antisense oligonucleotides with modified internucleotide linkages is described in U.S. Patent No. 5,142,047, hereby incorporated by reference.

Modifications to the nucleoside units of the antisense oligonucleotides are also contemplated. These modifications can increase the half-life and increase cellular rates of uptake for the oligonucleotides *in vivo*. For example, α-anomeric nucleotide units and modified nucleotides such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenylribofuranose, and N^4, N^4-ethano-5-methyl-cytosine are contemplated for use in the present invention.

An additional form of modified antisense molecules is found in peptide nucleic acids. Peptide nucleic acids (PNA) have been developed to hybridize to single and double stranded nucleic acids. PNA are nucleic acid analogs in which the entire deoxyribose-phosphate backbone has been exchanged with a chemically different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units. Unlike DNA, which is highly negatively charged, the PNA backbone is neutral. Therefore, there is much less repulsive energy between complementary strands in a PNA-DNA hybrid than in the comparable DNA-DNA hybrid, and consequently they are much more stable. PNA can hybridize to DNA in either a Watson/Crick or Hoogsteen fashion (Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:2637-2641, 1995; Egholm, *Nature* **365**:566-568, 1993; Nielsen et al., *Science* **254**:1497-1500, 1991; Dueholm et al., *New J. Chem.* **21**:19-31, 1997).

Molecules called PNA "clamps" have been synthesized which have two identical PNA sequences joined by a flexible hairpin linker containing three 8-amino-3,6-dioxaoctanoic acid units. When a PNA clamp is mixed with a complementary homopurine or homopyrimidine DNA target sequence, a PNA-DNA-PNA triplex hybrid can form which has been shown to be extremely stable (Bentin et al., *Biochemistry* **35**:8863-8869, 1996; Egholm et al., *Nucleic Acids Res.* **23**:217-222, 1995; Griffith et al., *J. Am. Chem. Soc.* **117**:831-832, 1995).

The sequence-specific and high affinity duplex and triplex binding of PNA have been extensively described (Nielsen et al., *Science* **254**:1497-1500, 1991; Egholm et al., *J. Am. Chem. Soc.* **114**:9677-9678, 1992; Egholm et al., *Nature* **365**:566-568, 1993; Almarsson et al., *Proc. Natl. Acad. Sci. U.S.A.* **90**:9542-9546, 1993; Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:2637-2641, 1995). They have also been shown to be resistant to nuclease and protease digestion (Demidov et al., *Biochem. Pharm.* **48**:1010-1313, 1994). PNA has been used to inhibit gene expression (Hanvey et al., *Science* **258**:1481-

1485,1992; Nielsen et al., *Nucl. Acids. Res.*, **21**:197-200, 1993; Nielsen et al., *Gene* **149**:139-145, 1994; Good & Nielsen, **Science**, 95: 2073-2076, 1998; all of which are hereby incorporated by reference), to block restriction enzyme activity (Nielsen et al., *supra.*, 1993), to act as an artificial transcription promoter (Mollegaard, *Proc. Natl. Acad. Sci. U.S.A.* **91**:3892-3895, 1994) and as a pseudo restriction endonuclease (Demidov et al., *Nucl. Acids. Res.* **21**:2103-2107, 1993). Recently, PNA has also been shown to have antiviral and antitumoral activity mediated through an antisense mechanism (Norton, *Nature Biotechnol.*, **14**:615-619, 1996; Hirschman et al., *J. Investig. Med.* **44**:347-351, 1996). PNAs have been linked to various peptides in order to promote PNA entry into cells (Basu et al., *Bioconj. Chem.* **8**:481-488, 1997; Pardridge et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:5592-5596, 1995).

The antisense oligonucleotides contemplated by the present invention can be administered by direct application of oligonucleotides to a target using standard techniques well known in the art. The antisense oligonucleotides can be generated within the target using a plasmid, or a phage. Alternatively, the antisense nucleic acid may be expressed from a sequence in the chromosome of the target cell. For example, a promoter may be introduced into the chromosome of the target cell near the target gene such that the promoter directs the transcription of the antisense nucleic acid. Alternatively, a nucleic acid containing the antisense sequence operably linked to a promoter may be introduced into the chromosome of the target cell. It is further contemplated that the antisense oligonucleotides are incorporated in a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi et al., **Pharmacol. Ther. 50(2)**:245-254, (1991), which is hereby incorporated by reference. The present invention also contemplates using a retron to introduce an antisense oligonucleotide to a cell. Retron technology is exemplified by U.S. Patent No. 5,405,775, which is hereby incorporated by reference. Antisense oligonucleotides can also be delivered using liposomes or by electroporation techniques which are well known in the art.

The antisense nucleic acids described above can also be used to design antibiotic compounds comprising nucleic acids which function by intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. The antisense nucleic acids can be used to inhibit cell or microorganism gene expression in

individuals infected with such microorganisms or containing such cells. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences based on the sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or homologous nucleic acids that are required for proliferation are contemplated for use as antibiotic compound templates.

The antisense nucleic acids, such as antisense oligonucleotides, which are complementary to the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or to homologous coding nucleic acids, or portions thereof, may be used to induce bacterial cell death or at least bacterial stasis by inhibiting target nucleic acid transcription or translation. Antisense oligonucleotides complementary to about 8 to 40 nucleotides of the proliferation-required nucleic acids described herein or homologous coding nucleic acids have sufficient complementarity to form a duplex with the target sequence under physiological conditions.

To kill bacterial cells or inhibit their growth, the antisense oligonucleotides are applied to the bacteria or to the target cells under conditions that facilitate their uptake. These conditions include sufficient incubation times of cells and oligonucleotides so that the antisense oligonucleotides are taken up by the cells. In one embodiment, an incubation period of 7-10 days is sufficient to kill bacteria in a sample. An optimum concentration of antisense oligonucleotides is selected for use.

The concentration of antisense oligonucleotides to be used can vary depending on the type of bacteria sought to be controlled, the nature of the antisense oligonucleotide to be used, and the relative toxicity of the antisense oligonucleotide to the desired cells in the treated culture. Antisense oligonucleotides can be introduced to cell samples at a number of different concentrations preferably between 1×10^{-10}M to

$1x10^{-4}M$. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of $1x10^{-7}$ translates into a dose of approximately 0.6 mg/kg body weight. Levels of oligonucleotide approaching 100 mg/kg body weight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the subject are removed, treated with the antisense oligonucleotide, and reintroduced into the subject. This range is merely illustrative and one of skill in the art are able to determine the optimal concentration to be used in a given case.

After the bacterial cells have been killed or controlled in a desired culture, the desired cell population may be used for other purposes.

EXAMPLE 46

Use of Antisense Oligonucleotides to Treat Contaminated Cell Cultures

The following example demonstrates the ability of an *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* antisense oligonucleotide or an antisense oligonucleotide complementary to a homologous coding nucleic acid, or portions thereof, to act as a bacteriocidal or bacteriostatic agent to treat a contaminated cell culture system. The application of the antisense oligonucleotides of the present invention are thought to inhibit the translation of bacterial gene products required for proliferation. The antisense nucleic acids may also inhibit the transcription, folding or processing of the target RNA.

In one embodiment of the present invention, the antisense oligonucleotide may comprise a phosphorothioate modified nucleic acid comprising at least about 15, at least about 20, at least about 25, at least about 30, at least about 35, at least about 40, or more than 40 consecutive nucleotides of an antisense nucleic acid listed in Table IA. A sense oligodeoxynucleotide complementary to the antisense sequence is synthesized and used as a control. The oligonucleotides are synthesized and purified according to the procedures of Matsukura, et al., Gene 72:343 (1988). The test oligonucleotides are dissolved in a small volume of autoclaved water and added to culture medium to make a 100 micromolar stock solution.

Human bone marrow cells are obtained from the peripheral blood of two patients and cultured according standard procedures well known in the art. The culture is contaminated with *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or an organism containing a homologous nucleic acid and incubated at 37°C overnight to establish bacterial infection.

The control and antisense oligonucleotide containing solutions are added to the contaminated cultures and monitored for bacterial growth. After a 10 hour incubation of culture and oligonucleotides, samples from the control and experimental cultures are drawn and analyzed for the translation of the target bacterial gene using standard microbiological techniques well known in the art. The target *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* gene or an organism containing the homologous coding nucleic acid is found to be translated in the control culture treated with the control oligonucleotide, however, translation of the target gene in the experimental culture treated with the antisense oligonucleotide of the present invention is not detected or reduced, indicating that the culture is no longer contaminated or is contaminated at a reduced level.

EXAMPLE 47

Use of Antisense Oligonucleotides to Treat Infections

A subject suffering from a *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* infection or an infection with an organism containing a homologous coding nucleic acid is treated with the antisense oligonucleotide preparation above. The antisense oligonucleotide is provided in a pharmaceutically acceptable carrier at a concentration effective to inhibit the transcription or translation of the target nucleic acid. The present subject is treated with a concentration of antisense oligonucleotide sufficient to achieve a blood concentration of about 0.1-100 micromolar. The patient receives daily injections of antisense oligonucleotide to maintain this concentration for

a period of 1 week. At the end of the week a blood sample is drawn and analyzed for the presence or absence of the organism using standard techniques well known in the art. There is no detectable evidence of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or an organim containing a homologous coding nucleic acid and the treatment is terminated.

Antisense nucleic acids complementary to a homologous coding nucleic acid or a portion thereof may be used in the preceding method to treat individuals infected with an organism containing the homologous coding nucleic acid.

EXAMPLE 48

Preparation and Use of Triple Helix Forming Oligonucleotides

The sequences of proliferation-required nucleic acids, homologous coding nucleic acids, or homologous antisense nucleic acids are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches that could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into a population of bacterial cells that normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis.

The oligonucleotides can be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for a reduction in proliferation using techniques such as monitoring growth levels as compared to untreated cells using optical density measurements. The oligonucleotides that are effective in inhibiting gene expression in cultured cells can then be introduced *in vivo* using the techniques well known in that art at a dosage level shown to be effective.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases.

Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin et al. (**Science** **245**:967-971 (1989), which is hereby incorporated by this reference).

EXAMPLE 49

Identification of Bacterial Strains from Isolated Specimens by PCR

Classical bacteriological methods for the detection of various bacterial species are time consuming and costly. These methods include growing the bacteria isolated from a subject in specialized medium, cultivation on selective agar medium, followed by a set of confirmation assays that can take from 8 to 10 days or longer to complete. Use of the identified sequences of the present invention provides a method to dramatically reduce the time necessary to detect and identify specific bacterial species present in a sample.

In one exemplary method, bacteria are grown in enriched medium and DNA samples are isolated from specimens of, for example, blood, urine, stool, saliva or central nervous system fluid by conventional methods. A panel of PCR primers based on identified sequences unique to various species or types of cells or microorganisms are then utilized in accordance with Example 12 to amplify DNA of approximately 100-200 nucleotides in length from the specimen. A separate PCR reaction is set up for each pair of PCR primers and after the PCR reaction is complete, the reaction mixtures are assayed for the presence of PCR product. The presence or absence of bacteria from the species to which the PCR primer pairs belong is determined by the presence or absence of a PCR product in the various test PCR reaction tubes.

Although the PCR reaction is used to assay the isolated sample for the presence of various bacterial species, other assays such as the Southern blot hybridization are also contemplated.

Compounds which inhibit the activity or reduce the amount of gene products required for proliferation may be identified using rational drug design. These methods may be used with the proliferation-required polypeptides described herein or homologous polypeptides. In such methods, the structure of the gene product is determined using methods such as x-ray crystallography, NMR, or computer modelling. Compounds are screened to identify those which have a structure which allows them to interact with the

gene product. In some embodiments, the compounds are screened to identify those which have structures which allow them to interact with regions of the gene product which are important for its activity. For example, the compounds may be screened to identify those which have structures which allow them to bind to the active site of the gene product to inhibit its activity. For example, the compound may be a suicide substrate which binds to the active site with high affinity, thereby preventing the gene product from acting on its natural substrate. Alternatively, the compound may bind to a region of the gene product which is involved in complex formation with other biomolecules. In such instances, the activity of the gene product is inhibited by blocking the interaction between the gene product and other members of the complex.

Thus, one embodiment of the present invention comprises a method of using a crystal of the gene products of the present invention and/or a dataset comprising the three-dimensional coordinates obtained from the crystal in a drug-screening assay. The present invention also includes agents (modulators or drugs) that are identified by the methods of the present invention, along with the method of using agents (modulators or drugs) identified by a method of the present invention, for inhibiting the activity of or modulating the amount of an essential gene product. The present invention also includes crystals comprising the gene products of the present invention or portions thereof.

In some embodiments of the present invention, the three-dimensional structure of the polypeptides required for proliferation is determined using X-ray crystallography or NMR. The coordinates of the determined structure are used in computer-assisted modeling programs to identify compounds that bind to and/or modulate the activity or amount of the encoded polypeptide. The method may include the following steps: 1) the generation of high-purity crystals of the encoded recombinant (or endogenous) polypeptide for analysis; 2) determination of the three-dimensional structure of the polypeptide; and, 3) the use of computer-assisted "docking" programs to analyze the molecular interaction of compound structure and the polypeptide (i.e., drug screening).

General methods for performing each of the above steps are described below and are also well known to those of skill in the art. Any method known to those of skill in the art, including those described herein, may be employed for generating the three-

dimensional structure for each identified essential gene product and its use in the drug-screening assays.

Crystals of the gene products required for proliferation may be obtained as follows. Under certain conditions, molecules condense from solution into a highly-ordered crystalline lattice, which is defined by a unit cell, the smallest repeating volume of the crystalline array. The contents of such a cell can interact with and diffract certain electromagnetic and particle waves (e.g., X-rays, neutron beams, electron beams etc.). Due to the symmetry of the lattice, the diffracted waves interact to create a diffraction pattern. By measuring the diffraction pattern, crystallographers are able to reconstruct the three-dimensional structure of the atoms in the crystal.

Any method known to those of skill in the art, including those set forth below, may be employed to prepare high-purity crystals. For example, crystals of the product of the identified essential gene can be grown by a number of techniques including batch crystallization, vapor diffusion (either by sitting drop or hanging drop) and by microdialysis. Seeding of the crystals in some instances is required to obtain X-ray quality crystals. Standard micro and/or macro seeding of crystals may therefore be used. Exemplified below is the hanging-drop vapor diffusion procedure. Hanging drops of an essential gene product (2.5 μl, 10 mg/ml) in 20 mM Tris, pH=8.0, 100 mM NaCl are mixed with an equal amount of reservoir buffer containing 2.7-3.2 M sodium formate and 100 mM Tris buffer, pH=8.0, and kept at 4°C. Crystal showers may appear after 1-2 days with large single crystals growing to full size (0.3 X 0.3 X 0.15 mm^3) within 2-3 weeks. Crystals are harvested in 3.5 M sodium formate and 100 mM Tris buffer, pH=8.0 and cryoprotected in 3.5 M sodium formate, 100 mM Tris buffer, pH=8.0, 10% (w/v) sucrose, and 10% (v/v) ethylene glycol before flash freezing in liquid propane.

In some embodiments, the crystal may be obtained using the methods described in U.S. Patent No. 5,869,604, the disclosure of which is incorporated herein by reference in its entirety. The method involves (a) contacting a mixture containing uncrystallized polypeptides with an exogenous nucleating agent that has an areal lattice match of at least 90.4% to the polypeptide,(b) crystallizing the polypeptides, thereby forming at least one crystal of the polypeptide attached to the nucleating agent, the attached crystal being of a high purity, and at least one polypeptide crystal unattached to the nucleating agent, the unattached crystal being of a lower purity than the attached

crystal, and (c) separating the crystal attached to the nucleating agent from the crystal unattached to the nucleating agent. The crystallized polypeptide may also be purified from contaminants by (a) contacting a mixture containing uncrystallized polypeptides and a contaminant with an exogenous nucleating agent that has an areal lattice match of at least 90.4% to the polypeptide, (b) crystallizing the polypeptides, thereby forming at least one crystal of the polypeptide attached to the nucleating agent, the attached crystal being of a high purity and produced in a high yield, and at least one crystal unattached to the nucleating agent, the unattached crystal being of a lower purity than the attached crystal, and (c) separating the crystal attached to the nucleating agent from the crystal unattached to the nucleating agent.

Once a crystal of the present invention is grown, X-ray diffraction data can be collected using methods familiar to those skilled in the art. Therefore, any person with skill in the art of protein crystallization having the present teachings and without undue experimentation can crystallize a large number of alternative forms of the essential gene products from a variety of different organisms, or polypeptides having conservative substitutions in their amino acid sequence.

A crystal lattice is defined by the symmetry of its unit cell and any structural motifs the unit cell contains. For example, there are 230 possible symmetry groups for an arbitrary crystal lattice, while the unit cell of the crystal lattice group may have an arbitrary dimension that depends on the molecules making up the lattice. Biological macromolecules, however, have asymmetric centers and are limited to 65 of the 230 symmetry groups. See Cantor et al., Biophysical Chemistry, Vol. III, W. H. Freeman & Company (1980), the disclosure of which is incorporated herein by reference in its entirety.

A crystal lattice interacts with electromagnetic or particle waves, such as X-rays or electron beams respectively, that have a wavelength with the same order of magnitude as the spacing between atoms in the unit cell. The diffracted waves are measured as an array of spots on a detection surface positioned adjacent to the crystal. Each spot has a three-dimensional position, hkl, and an intensity, I(hkl), both of which are used to reconstruct the three-dimensional electron density of the crystal with the so-called Electron Density Equation. The Electron Density Equation states that the three-dimensional electron density of the unit cell is the Fourier transform of the structure

factors. Thus, in theory, if the structure factors are known for a sufficient number of spots in the detection space, then the three-dimensional electron density of the unit cell could be calculated using the Electron Density Equation.

In some embodiments of the present invention, an image of a crystal of a gene product required for proliferation or a portion thereof is obtained with the aid of a digital computer and the crystal's diffraction pattern as described in U.S. Patent No. 5,353,236, the disclosure of which is incorporated herein by reference in its entirety. The diffraction pattern contains a plurality of reflections, each having an associated resolution. The image is obtained by (a) converting the diffraction pattern of the crystal into computer usable normalized amplitudes, the pattern being produced with a diffractometer; (b) determining from the diffraction pattern a dimension of a unit cell of the crystal; (c) providing an envelope defining the region of the unit cell occupied by the gene product or portion thereof in the crystal; (d) distributing a collection of scattering bodies within said envelope, the collection of scattering bodies having various arrangements, each of which has an associated pattern of Fourier amplitudes; (e) condensing the collection of scattering bodies to a condensed arrangement that results in a high correlation between a diffraction pattern and the pattern of Fourier amplitudes for said collection of scattering bodies; (f) determining the phase associated with at least one of the reflections of said diffraction pattern from the condensed arrangement of scattering bodies; (g) calculating an electron density distribution of the gene product or portion thereof within the unit cell from the phase determined in procedure f; and (h) displaying a graphical image of the gene product or portion thereof constructed from said electron density distribution.

The crystals of the gene products required for proliferation may be used in drug screening methods such as those described in U.S. Patent Number 6,156,526, the disclosure of which is incorporated herein by reference in its entirety. Briefly, in such methods, a compound which inhibits the formation of a complex comprising the gene product or a portion thereof is identified as follows. A set of atomic coordinates defining the three-dimensional structure of a complex including the gene product of interest or a portion thereof are determined. A potential compound that binds to the gene product or a portion thereof involved in complex formation is selected using the atomic coordinates obtained above. The compound is contacted with the gene product

or portion thereof and its binding partner(s) in the complex under conditions which would permit the complex to form in the absence of the potential compound. The binding affinity of the gene product or portion thereof for its binding partner(s) is determined and a potential compound is identified as a compound that inhibits the formation of the complex when there is a decrease in the binding affinity of the gene product or portion thereof for its binding partner(s).

In some embodiments of the present invention, the three dimensional structure of the essential gene product is determined and potential agonists and/or potential antagonists are designed with the aid of computer modeling [Bugg et al., Scientific American, Dec.:92-98 (1993); West et al., TIPS, 16:67-74 (1995); Dunbrack et al., Folding & Design, 2:27-42 (1997), the disclosures of which are incorporated herein by reference in their entireties].

Computer analysis may be performed with one or more of the computer programs including: QUANTA, CHARMM, INSIGHT, SYBYL, MACROMODEL and ICM [Dunbrack et al., Folding & Design, 2:27-42 (1997), the disclosure of which is incorporated herein by reference in its entirety]. In a further embodiment of this aspect of the invention, an initial drug-screening assay is performed using the three-dimensional structure so obtained, preferably along with a docking computer program. Such computer modeling can be performed with one or more Docking programs such as FlexX, DOC, GRAM and AUTO DOCK [Dunbrack et al., Folding & Design, 2:27-42 (1997)].

It should be understood that for each drug screening assay provided herein, a number of iterative cycles of any or all of the steps may be performed to optimize the selection. The drug screening assays of the present invention may use any of a number of means for determining the interaction between an agent or drug and an essential gene product.

In some embodiments of the present invention, a drug can be specifically designed to bind to an essential gene product of the present invention through NMR based methodology. [Shuker et al., pi Science 274:1531-1534 (1996) the disclosure of which is incorporated herein by reference herein in its entirety.] NMR spectra may be recorded using devices familiar to those skilled in the art, such as the Varian Unity Plus 500 and unity 600 spectrometers, each equipped with a pulsed-field gradient triple

resonance probe as analyzed as described in Bagby et al., [Cell 82:857-867 (1995), the disclosure of which is incorporated herein by reference in its entirety]. Sequential resonance assignments of backbone ^{1}H, .^{15}N, and .^{13}C atoms may be made using a combination of triple resonance experiments similar to those previously described [Bagby et al., Biochemistry, 33:2409-2421 (1994a), the disclosure of which is incorporated herein by reference in its entirety], except with enhanced sensitivity [Muhandiram and Kay, J. Magn. Reson., 103: 203-216 (1994), the disclosure of which is incorporated herein by reference in its entirety] and minimal H_2O saturation [Kay et al., J. Magn. Reson., 109:129-133 (1994), the disclosure of which is incorporated herein by reference in its entirety]. Side chain ^{1}H and ^{13}C assignments may be made using HCCH-TOCSY [Bax et al., J. Magn. Reson., 87:620-627 (1990), the disclosure of which is incorporated herein by reference in its entirety] experiments with mixing times of 8 ms and 16 ms.in solution but need not be included in structure calculations. Nuclear Overhauser effect (NOE) cross peaks in two-dimensional ^{1}H--^{1}H NOE spectroscopy (NOESY), three-dimensional ^{15}N-edited NOESY-HSQC [Zhang et al., J. Biomol, NMR, 4:845-858 (1994), the disclosure of which is incorporated herein by reference in its entirety] and three-dimensional simultaneous acquisition ^{15}N/^{13}C-edited NOE [Pascal et al., J. Magn. Reson., 103:197-201 (1994), the disclosure of which is incorporated herein by reference in its entirety] spectra may be obtained with 100 ms NOE mixing times. Standard pseudo-atom distance corrections [Wuthrich et al., J. Mol. Biol., 169:949-961 (1983), the disclosure of which is incorporated herein by reference in its entirety] may be incorporated to account for center averaging. An additional 0.5 .ANG. may be added to the upper limits for distances involving methyl groups [Wagner et al., J. Mol. Biol., 196:611-639 (1987); Clore et al., Biochemistry, 26:8012-8023 (1987), the disclosures of which are incorporated herein by reference in their entireties].

The structures can be calculated using a simulated annealing protocol [Nilges et al., In computational Aspects of the Study of Biological Macromolecules by Nuclear Magnetic Resonance Spectroscopy, J. C. Hoch, F. M. Poulsen, and C. Redfield, eds., New York: Plenum Press, pp. 451-455 (1991, the disclosures of which are incorporated herein by reference in their entireties] within X-PLOR [Brunger, X-PLOR Manual, Version 3.1, New Haven, Conn.: Department of Molecular Biophysics and Biochemistry, Yale University (1993), the disclosure of which is incorporated herein by

reference in its entirety] using the previously described strategy [Bagby et al., Structure, 2:107-122 (1994b), the disclosure of which is incorporated herein by reference in its entirety]. Interhelical anges may be calculated using a program written by K. Yap. Accessible surface areas were calculated using the program Naccess, available from Prof. J. Thornton, University College, London.

Compounds capable of reducing the activity or amount of gene products required for cellular proliferation may be identified using the methods described in US Pat. No. 6,077,682, the disclosure of which is incorporated herein by reference in its entirety. Briefly, the three-dimensional structure of the gene product or portion thereof may be used in a drug screening assay by (a) selecting a potential drug by performing rational drug design with the three-dimensional structure determined from one or more sets of atomic coordinates of the gene product or portion thereof in conjunction with computer modeling; (b) contacting the potential drug with a polypeptide comprising the gene product or portion thereof and (c) detecting the binding of the potential drug with said polypeptide; wherein a potential drug is selected as a drug if the potential drug binds to the polypeptide. In some methods, the three-dimensional structure of the gene product or portion thereof is used in a drug screening assay involving (a) selecting a potential drug by performing structural based rotational drug design with the three-dimensional structure of the gene product or portion thereof; wherein said selecting is performed in conjunction with computer modeling; (b) contacting the potential drug with a polypeptide comprising the gene product or portion thereof in the presence of a substrate of the gene product; wherein in the absence of the potential drug the substrate is acted upon by the gene product; and (c) determining the extent to which the gene product acted upon the substrate; wherein a drug is selected when a decrease in the action of the gene product on the substrate is determined in the presence of the potential drug relative to in its absence. In some embodiments, the preceding method further involves(d) contacting the potential drug with the gene product or portion thereof for NMR analysis; wherein a binding complex forms between the potential drug and said gene product or portion thereof for NMR analysis; wherein the gene product or portion thereof for NMR analysis comprises a conservative amino acid substitution; (e) determining the three-dimensional structure of the binding complex by NMR; and (f) selecting a candidate drug by performing structural based rational drug design with the

three-dimensional structure determined for the binding complex; wherein said selecting is performed in conjunction with computer modeling; (g) contacting the candidate drug with a second polypeptide comprising the gene product or portion thereof in the presence of a substrate of the gene product or portion thereof; wherein in the absence of the candidate drug the substrate is acted upon by the second polypeptide; and (h) determining the amount of action of the second polypeptide on the substrate; wherein a drug is selected when a decrease in the amount of action of the second polypeptide is determined in the presence of the candidate drug relative to in its absence.

Once the three-dimensional structure of a crystal comprising an essential gene product is determined, a potential modulator of its activity, can be examined through the use of computer modeling using a docking program such as FlexX, GRAM, DOCK, or AUTODOCK [Dunbrack et al., 1997, supra], to identify potential modulators. This procedure can include computer fitting of potential modulators to the polypeptide or fragments thereof to ascertain how well the shape and the chemical structure of the potential modulator will bind. Computer programs can also be employed to estimate the attraction, repulsion, and steric hindrance of the two binding partners (e.g., the essential gene product and a potential modulator). Generally the tighter the fit, the lower the steric hindrances, and the greater the attractive forces, the more potent the potential modulator since these properties are consistent with a tighter binding constant. Furthermore, the more specificity in the design of a potential drug the more likely that the drug will not interact as well with other proteins. This will minimize potential side-effects due to unwanted interactions with other proteins.

Compound and compound analogs can be systematically modified by computer modeling programs until one or more promising potential analogs is identified. In addition systematic modification of selected analogs can then be systematically modified by computer modeling programs until one or more potential analogs are identified. Such analysis has been shown to be effective in the development of HIV protease inhibitors [Lam et al., Science 263:380-384 (1994); Wlodawer et al., Ann. Rev. Biochem. 62:543-585 (1993); Appelt, Perspectives in Drug Discovery and Design 1:23-48 (1993); Erickson, Perspectives in Drug Discovery and Design 1:109-128 (1993), the disclosures of which are incorporated herein by reference in their entireties]. Alternatively a potential modulator could be obtained by initially screening a random

peptide library produced by recombinant bacteriophage for example, [Scott and Smith, Science, 249:386-390 (1990); Cwirla et al., Proc. Natl. Acad. Sci., 87:6378-6382 (1990); Devlin et al., Science, 249:404-406 (1990), the disclosures of which are incorporated herein by reference in their entireties]. A peptide selected in this manner would then be systematically modified by computer modeling programs as described above, and then treated analogously to a structural analog.

Example 45 describes computer modelling of the structures of gene products required for proliferation.

EXAMPLE 50

Determination of the Structure of Gene Products Required for Proliferation Using Computer Modelling

Three dimensional models were built by applying computer modelling methods to some of the gene products required for proliferation of *Staphylococcus aureus* using the amino acid sequences of the encoded proteins as follows. Sir Tom Blundell's program COMPOSER as provided by Tripos Associates in their BIOPOLYMER module to SYBYL was used to build the models. Skolnik's method of topology fingerprinting as implemented in Matchmaker was used to score the average mutation free energy. This number is in Boltzmans (units of kT) and should be negative (the more negative, the better the model.

Composer uses a Needleman Wunsch alignment with jumbling to find significant alignments. The reported parameters are percent identity and significance as measured from the jumbling. Those matches which were 30% identical and had a significance greater that 4 on the scale were judged to be good candidates for model building templates. If no three dimensional structures met these criteria, then a BLAST search was conducted against the most recent PDB sequence database. Any significant hits discovered in this manner were then added to the binary protein structure database and the candidate search was repeated in the manner discussed above.

In the next phase, Composer assigned structurally conserved and structurally variable regions and built the backbone structure and then searched the database for structures of the variable loops. These were then spliced in and a model of the protein resulted. Any loops (variable regions) which were unassignable were manually built and refined with a combination of dynamics.

The structure was then refined. Hydrogen atoms were added and a non-active aggregate was defined. 1000pS of dynamics using AMBER ALL-ATOM and Kollman charges are performed. Next a minimization cycle of up 5000 steepest decent steps were performed and then the aggregate was thawed and the process was repeated on the entire protein.

The resulting structure was then validated in MATCHMAKER. The topologicaly scanned free energy determined from empirically derived protein topologies was computed and the average energy/residue is reported in Boltzamans was reported. As this number represents a free energy the more negative it is the more favorable it is.

Sixty six proteins required for the proliferation of *Staphylococcus aureus* were modelled as described above. MATCHMAKER energies were computed for these. The distribution of the models built by class is shown in the table below.

Classification	Number of Models	Average Matchmaker Energy
Acylases	1	-0.10
Dehydrogenases	3	-0.12
DNA Related	3	-0.12
Heat Shock Protein	2	-0.16
Hydrolases	3	-0.16
Isomerases	1	0.05
Ligases	7	-0.07
Lyases	1	-0.09
Membrane Anchored	1	-0.12
Misc	18	-0.21
Oxidoreductases	6	-0.09
Proteases	1	-0.03
Ribosome	3	-0.11
Synthases	4	-0.14
Transferases	6	-0.12

Table 1. Distribution of models built with their MATCHMAKER energies in kT

The validity of the above method was confirmed using FtsZ. In the case of FtsZ, a crystal structure from M. Janeschi was available. Examination of the gross structural features determined using the above modelling showed all of the folds in the correct place, although there were some minor differences from the structure determined by x-ray crystallography.

EXAMPLE 51

FUNCTIONAL COMPLEMENTATION

In another embodiment, gene products whose activities may be complemented by a proliferation-required gene product from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or homologous polypeptides are identified using merodiploids, created by introducing a plasmid or Bacterial Artificial Chromosome into an organism having a mutation in the essential gene which reduces or eliminates the activity of the gene product. In some embodiments, the mutation may be a conditional mutation, such as a temperature sensitive mutation, such that the organism proliferates under permissive conditions but is unable to proliferate under non-permissive conditions in the absence of complementation by the gene on the plasmid or Bacterial Artificial Chromosome. Alternatively, duplications may be constructed as described in Roth et al. (1987) Biosynthesis of Aromatic Amino Acids in Escherichia coli and Salmonella typhimurium, F. C. ***Neidhardt,*** ed., American Society for Microbiology, publisher, pp. 2269-2270, the disclosure of which is incorporated herein by reference in its entirety. Such methods are familiar to those skilled in the art.

Table VIII provides a cross reference for SEQ ID NOs. of the nucleotide sequences discussed herein and the SEQ ID NOs. of the polypeptides encoded by these nucleotide.

All documents cited herein are incorporated herein by reference in their entireties.

TABLE VIII

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TABLE IA

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12	E3M10000001B05	*Enterococcus faecalis*
13	E3M10000001B06	*Enterococcus faecalis*
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16	E3M10000001C02	*Enterococcus faecalis*
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18	E3M10000001D02	*Enterococcus faecalis*
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37	E3M10000001H03	*Enterococcus faecalis*
38	E3M10000001H04	*Enterococcus faecalis*
39	E3M10000004A04	*Enterococcus faecalis*
40	E3M10000004C03	*Enterococcus faecalis*
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45	E3M10000004F08	*Enterococcus faecalis*
46	E3M10000004F10	*Enterococcus faecalis*
47	E3M10000004G01	*Enterococcus faecalis*
48	E3M10000004H11	*Enterococcus faecalis*
49	E3M10000005A07	*Enterococcus faecalis*
50	E3M10000005B01	*Enterococcus faecalis*
51	E3M10000005B08	*Enterococcus faecalis*
52	E3M10000005C01	*Enterococcus faecalis*

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54	E3M10000005C04	*Enterococcus faecalis*
55	E3M10000005D03	*Enterococcus faecalis*
56	E3M10000005D04	*Enterococcus faecalis*
57	E3M10000005D10	*Enterococcus faecalis*
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59	E3M10000005E02	*Enterococcus faecalis*
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62	E3M10000005F07	*Enterococcus faecalis*
63	E3M10000005F10	*Enterococcus faecalis*
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65	E3M10000005H04	*Enterococcus faecalis*
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81	E3M10000007E05	*Enterococcus faecalis*
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94	E3M10000009C09	*Enterococcus faecalis*
95	E3M10000009D01	*Enterococcus faecalis*
96	E3M10000009E02	*Enterococcus faecalis*
97	E3M10000009E03	*Enterococcus faecalis*
98	E3M10000009E05	*Enterococcus faecalis*
99	E3M10000009G02	*Enterococcus faecalis*

SeqID	Clone name	Organism
100	E3M10000010C08	*Enterococcus faecalis*
101	E3M10000010D05	*Enterococcus faecalis*
102	E3M10000010F01	*Enterococcus faecalis*
103	E3M10000010G05	*Enterococcus faecalis*
104	E3M10000010G07	*Enterococcus faecalis*
105	E3M10000010G09	*Enterococcus faecalis*
106	E3M10000010G10	*Enterococcus faecalis*
107	E3M10000010H02	*Enterococcus faecalis*
108	E3M10000011A09	*Enterococcus faecalis*
109	E3M10000011B03	*Enterococcus faecalis*
110	E3M10000011B09	*Enterococcus faecalis*
111	E3M10000011C07	*Enterococcus faecalis*
112	E3M10000011D03	*Enterococcus faecalis*
113	E3M10000011H02	*Enterococcus faecalis*
114	E3M10000011H05	*Enterococcus faecalis*
115	E3M10000012B01	*Enterococcus faecalis*
116	E3M10000012B02	*Enterococcus faecalis*
117	E3M10000012B07	*Enterococcus faecalis*
118	E3M10000012B08	*Enterococcus faecalis*
119	E3M10000012C01	*Enterococcus faecalis*
120	E3M10000012D10	*Enterococcus faecalis*
121	E3M10000012E08	*Enterococcus faecalis*
122	E3M10000012F05	*Enterococcus faecalis*
123	E3M10000012F06	*Enterococcus faecalis*
124	E3M10000012F07	*Enterococcus faecalis*
125	E3M10000012F10	*Enterococcus faecalis*
126	E3M10000012G02	*Enterococcus faecalis*
127	E3M10000012G07	*Enterococcus faecalis*
128	E3M10000013A06	*Enterococcus faecalis*
129	E3M10000013A07	*Enterococcus faecalis*
130	E3M10000013C05	*Enterococcus faecalis*
131	E3M10000013D02	*Enterococcus faecalis*
132	E3M10000013D08	*Enterococcus faecalis*
133	E3M10000013D10	*Enterococcus faecalis*
134	E3M10000013E02	*Enterococcus faecalis*
135	E3M10000013E08	*Enterococcus faecalis*
136	E3M10000013F05	*Enterococcus faecalis*
137	E3M10000013F12	*Enterococcus faecalis*
138	E3M10000013G10	*Enterococcus faecalis*
139	E3M10000013H03	*Enterococcus faecalis*
140	E3M10000013H05	*Enterococcus faecalis*
141	E3M10000013H10	*Enterococcus faecalis*
142	E3M10000014B12	*Enterococcus faecalis*
143	E3M10000014E12	*Enterococcus faecalis*
144	E3M10000014G09	*Enterococcus faecalis*
145	E3M10000015B04	*Enterococcus faecalis*
146	E3M10000015B12	*Enterococcus faecalis*

SeqID	Clone name	Organism
147	E3M10000015E12	*Enterococcus faecalis*
148	E3M10000016A03	*Enterococcus faecalis*
149	E3M10000016A04	*Enterococcus faecalis*
150	E3M10000016C11	*Enterococcus faecalis*
151	E3M10000016D03	*Enterococcus faecalis*
152	E3M10000016F06	*Enterococcus faecalis*
153	E3M10000016F10	*Enterococcus faecalis*
154	E3M10000016H05	*Enterococcus faecalis*
155	E3M10000016H10	*Enterococcus faecalis*
156	E3M10000017A09	*Enterococcus faecalis*
157	E3M10000017D09	*Enterococcus faecalis*
158	E3M10000018A07	*Enterococcus faecalis*
159	E3M10000018C02	*Enterococcus faecalis*
160	E3M10000018E01	*Enterococcus faecalis*
161	E3M10000018G09	*Enterococcus faecalis*
162	E3M10000018H06	*Enterococcus faecalis*
163	E3M10000019B06	*Enterococcus faecalis*
164	E3M10000019D02	*Enterococcus faecalis*
165	E3M10000019E03	*Enterococcus faecalis*
166	E3M10000019E04	*Enterococcus faecalis*
167	E3M10000020G04	*Enterococcus faecalis*
168	E3M10000020H05	*Enterococcus faecalis*
169	E3M10000021A08	*Enterococcus faecalis*
170	E3M10000021A11	*Enterococcus faecalis*
171	E3M10000021B10	*Enterococcus faecalis*
172	E3M10000021C03	*Enterococcus faecalis*
173	E3M10000021C04	*Enterococcus faecalis*
174	E3M10000021C08	*Enterococcus faecalis*
175	E3M10000021D04	*Enterococcus faecalis*
176	E3M10000021E10	*Enterococcus faecalis*
177	E3M10000021G04	*Enterococcus faecalis*
178	E3M10000021G10	*Enterococcus faecalis*
179	E3M10000021G11	*Enterococcus faecalis*
180	E3M10000021H11	*Enterococcus faecalis*
181	E3M10000022A04	*Enterococcus faecalis*
182	E3M10000022A11	*Enterococcus faecalis*
183	E3M10000022B04	*Enterococcus faecalis*
184	E3M10000022B05	*Enterococcus faecalis*
185	E3M10000022B07	*Enterococcus faecalis*
186	E3M10000022C05	*Enterococcus faecalis*
187	E3M10000022C06	*Enterococcus faecalis*
188	E3M10000022C09	*Enterococcus faecalis*
189	E3M10000022D04	*Enterococcus faecalis*
190	E3M10000022F05	*Enterococcus faecalis*
191	E3M10000022F06	*Enterococcus faecalis*
192	E3M10000022F08	*Enterococcus faecalis*
193	E3M10000022G02	*Enterococcus faecalis*

SeqID	Clone name	Organism
194	E3M10000022G12	*Enterococcus faecalis*
195	E3M10000023A03	*Enterococcus faecalis*
196	E3M10000023A06	*Enterococcus faecalis*
197	E3M10000023A07	*Enterococcus faecalis*
198	E3M10000023A09	*Enterococcus faecalis*
199	E3M10000023B02	*Enterococcus faecalis*
200	E3M10000023B06	*Enterococcus faecalis*
201	E3M10000023C03	*Enterococcus faecalis*
202	E3M10000023C04	*Enterococcus faecalis*
203	E3M10000023C06	*Enterococcus faecalis*
204	E3M10000023C08	*Enterococcus faecalis*
205	E3M10000023C09	*Enterococcus faecalis*
206	E3M10000023D02	*Enterococcus faecalis*
207	E3M10000023D04	*Enterococcus faecalis*
208	E3M10000023D10	*Enterococcus faecalis*
209	E3M10000023E04	*Enterococcus faecalis*
210	E3M10000023E07	*Enterococcus faecalis*
211	E3M10000023E09	*Enterococcus faecalis*
212	E3M10000023F02	*Enterococcus faecalis*
213	E3M10000023F10	*Enterococcus faecalis*
214	E3M10000023G02	*Enterococcus faecalis*
215	E3M10000023G04	*Enterococcus faecalis*
216	E3M10000023G10	*Enterococcus faecalis*
217	E3M10000023H08	*Enterococcus faecalis*
218	E3M10000024A03	*Enterococcus faecalis*
219	E3M10000024A04	*Enterococcus faecalis*
220	E3M10000024A08	*Enterococcus faecalis*
221	E3M10000024C06	*Enterococcus faecalis*
222	E3M10000025A06	*Enterococcus faecalis*
223	E3M10000025B01	*Enterococcus faecalis*
224	E3M10000025B03	*Enterococcus faecalis*
225	E3M10000025B05	*Enterococcus faecalis*
226	E3M10000025B10	*Enterococcus faecalis*
227	E3M10000025C01	*Enterococcus faecalis*
228	E3M10000025C04	*Enterococcus faecalis*
229	E3M10000025C05	*Enterococcus faecalis*
230	E3M10000025C07	*Enterococcus faecalis*
231	E3M10000025C08	*Enterococcus faecalis*
232	E3M10000025C09	*Enterococcus faecalis*
233	E3M10000025C11	*Enterococcus faecalis*
234	E3M10000025D01	*Enterococcus faecalis*
235	E3M10000025D10	*Enterococcus faecalis*
236	E3M10000025E07	*Enterococcus faecalis*
237	E3M10000025E08	*Enterococcus faecalis*
238	E3M10000025E12	*Enterococcus faecalis*
239	E3M10000025F04	*Enterococcus faecalis*
240	E3M10000025F06	*Enterococcus faecalis*

SeqID	Clone name	Organism
241	E3M10000025F08	*Enterococcus faecalis*
242	E3M10000025F09	*Enterococcus faecalis*
243	E3M10000025F10	*Enterococcus faecalis*
244	E3M10000025F11	*Enterococcus faecalis*
245	E3M10000025F12	*Enterococcus faecalis*
246	E3M10000025G02	*Enterococcus faecalis*
247	E3M10000025G07	*Enterococcus faecalis*
248	E3M10000025G09	*Enterococcus faecalis*
249	E3M10000027A02	*Enterococcus faecalis*
250	E3M10000027A07	*Enterococcus faecalis*
251	E3M10000027A09	*Enterococcus faecalis*
252	E3M10000027B07	*Enterococcus faecalis*
253	E3M10000027B08	*Enterococcus faecalis*
254	E3M10000027B09	*Enterococcus faecalis*
255	E3M10000027C02	*Enterococcus faecalis*
256	E3M10000027C03	*Enterococcus faecalis*
257	E3M10000027C08	*Enterococcus faecalis*
258	E3M10000027D03	*Enterococcus faecalis*
259	E3M10000027D05	*Enterococcus faecalis*
260	E3M10000027D08	*Enterococcus faecalis*
261	E3M10000027D10	*Enterococcus faecalis*
262	E3M10000027G01	*Enterococcus faecalis*
263	E3M10000027G08	*Enterococcus faecalis*
264	E3M10000027H04	*Enterococcus faecalis*
265	E3M10000027H07	*Enterococcus faecalis*
266	E3M10000028A02	*Enterococcus faecalis*
267	E3M10000028A03	*Enterococcus faecalis*
268	E3M10000028A04	*Enterococcus faecalis*
269	E3M10000028A05	*Enterococcus faecalis*
270	E3M10000028A06	*Enterococcus faecalis*
271	E3M10000028A08	*Enterococcus faecalis*
272	E3M10000028B01	*Enterococcus faecalis*
273	E3M10000028B02	*Enterococcus faecalis*
274	E3M10000028B03	*Enterococcus faecalis*
275	E3M10000028B04	*Enterococcus faecalis*
276	E3M10000028B05	*Enterococcus faecalis*
277	E3M10000028B06	*Enterococcus faecalis*
278	E3M10000028B07	*Enterococcus faecalis*
279	E3M10000028B08	*Enterococcus faecalis*
280	E3M10000028C01	*Enterococcus faecalis*
281	E3M10000028C02	*Enterococcus faecalis*
282	E3M10000028C04	*Enterococcus faecalis*
283	E3M10000028C05	*Enterococcus faecalis*
284	E3M10000028C06	*Enterococcus faecalis*
285	E3M10000028C07	*Enterococcus faecalis*
286	E3M10000028C08	*Enterococcus faecalis*
287	E3M10000028D01	*Enterococcus faecalis*

SeqID	Clone name	Organism
288	E3M10000028D02	*Enterococcus faecalis*
289	E3M10000028D05	*Enterococcus faecalis*
290	E3M10000028D06	*Enterococcus faecalis*
291	E3M10000028D08	*Enterococcus faecalis*
292	E3M10000028E01	*Enterococcus faecalis*
293	E3M10000028E04	*Enterococcus faecalis*
294	E3M10000028E07	*Enterococcus faecalis*
295	E3M10000028F02	*Enterococcus faecalis*
296	E3M10000028F03	*Enterococcus faecalis*
297	E3M10000028F04	*Enterococcus faecalis*
298	E3M10000028F05	*Enterococcus faecalis*
299	E3M10000028F06	*Enterococcus faecalis*
300	E3M10000028F07	*Enterococcus faecalis*
301	E3M10000028G05	*Enterococcus faecalis*
302	E3M10000028G06	*Enterococcus faecalis*
303	E3M10000028G07	*Enterococcus faecalis*
304	E3M10000028H04	*Enterococcus faecalis*
305	E3M10000028H07	*Enterococcus faecalis*
306	E3M10000029A02	*Enterococcus faecalis*
307	E3M10000029A04	*Enterococcus faecalis*
308	E3M10000029A05	*Enterococcus faecalis*
309	E3M10000029A10	*Enterococcus faecalis*
310	E3M10000029A11	*Enterococcus faecalis*
311	E3M10000029B01	*Enterococcus faecalis*
312	E3M10000029B02	*Enterococcus faecalis*
313	E3M10000029B05	*Enterococcus faecalis*
314	E3M10000029B06	*Enterococcus faecalis*
315	E3M10000029B08	*Enterococcus faecalis*
316	E3M10000029B11	*Enterococcus faecalis*
317	E3M10000029B12	*Enterococcus faecalis*
318	E3M10000029C01	*Enterococcus faecalis*
319	E3M10000029C02	*Enterococcus faecalis*
320	E3M10000029C03	*Enterococcus faecalis*
321	E3M10000029C04	*Enterococcus faecalis*
322	E3M10000029C05	*Enterococcus faecalis*
323	E3M10000029C06	*Enterococcus faecalis*
324	E3M10000029C07	*Enterococcus faecalis*
325	E3M10000029C08	*Enterococcus faecalis*
326	E3M10000029C09	*Enterococcus faecalis*
327	E3M10000029C10	*Enterococcus faecalis*
328	E3M10000029C12	*Enterococcus faecalis*
329	E3M10000029D01	*Enterococcus faecalis*
330	E3M10000029D03	*Enterococcus faecalis*
331	E3M10000029D04	*Enterococcus faecalis*
332	E3M10000029D05	*Enterococcus faecalis*
333	E3M10000029D06	*Enterococcus faecalis*
334	E3M10000029D08	*Enterococcus faecalis*

SeqID	Clone name	Organism
335	E3M10000029D12	*Enterococcus faecalis*
336	E3M10000029E01	*Enterococcus faecalis*
337	E3M10000029E02	*Enterococcus faecalis*
338	E3M10000029E03	*Enterococcus faecalis*
339	E3M10000029E05	*Enterococcus faecalis*
340	E3M10000029E07	*Enterococcus faecalis*
341	E3M10000029E08	*Enterococcus faecalis*
342	E3M10000029E09	*Enterococcus faecalis*
343	E3M10000029E12	*Enterococcus faecalis*
344	E3M10000029F01	*Enterococcus faecalis*
345	E3M10000029F05	*Enterococcus faecalis*
346	E3M10000029F06	*Enterococcus faecalis*
347	E3M10000029F09	*Enterococcus faecalis*
348	E3M10000029F10	*Enterococcus faecalis*
349	E3M10000029F11	*Enterococcus faecalis*
350	E3M10000029F12	*Enterococcus faecalis*
351	E3M10000029G01	*Enterococcus faecalis*
352	E3M10000029G04	*Enterococcus faecalis*
353	E3M10000029G05	*Enterococcus faecalis*
354	E3M10000029G07	*Enterococcus faecalis*
355	E3M10000029G08	*Enterococcus faecalis*
356	E3M10000029G09	*Enterococcus faecalis*
357	E3M10000029G10	*Enterococcus faecalis*
358	E3M10000029G11	*Enterococcus faecalis*
359	E3M10000029G12	*Enterococcus faecalis*
360	E3M10000029H02	*Enterococcus faecalis*
361	E3M10000029H04	*Enterococcus faecalis*
362	E3M10000029H05	*Enterococcus faecalis*
363	E3M10000029H07	*Enterococcus faecalis*
364	E3M10000029H08	*Enterococcus faecalis*
365	E3M10000029H11	*Enterococcus faecalis*
366	E3M10000030A05	*Enterococcus faecalis*
367	E3M10000030A08	*Enterococcus faecalis*
368	E3M10000030A09	*Enterococcus faecalis*
369	E3M10000030A11	*Enterococcus faecalis*
370	E3M10000030B03	*Enterococcus faecalis*
371	E3M10000030B04	*Enterococcus faecalis*
372	E3M10000030B05	*Enterococcus faecalis*
373	E3M10000030B06	*Enterococcus faecalis*
374	E3M10000030B07	*Enterococcus faecalis*
375	E3M10000030B08	*Enterococcus faecalis*
376	E3M10000030B10	*Enterococcus faecalis*
377	E3M10000030B11	*Enterococcus faecalis*
378	E3M10000030B12	*Enterococcus faecalis*
379	E3M10000030C03	*Enterococcus faecalis*
380	E3M10000030C04	*Enterococcus faecalis*
381	E3M10000030C12	*Enterococcus faecalis*

SeqID	Clone name	Organism
382	E3M10000030D02	*Enterococcus faecalis*
383	E3M10000030D05	*Enterococcus faecalis*
384	E3M10000030D08	*Enterococcus faecalis*
385	E3M10000030D09	*Enterococcus faecalis*
386	E3M10000030D10	*Enterococcus faecalis*
387	E3M10000030D12	*Enterococcus faecalis*
388	E3M10000030E01	*Enterococcus faecalis*
389	E3M10000030E02	*Enterococcus faecalis*
390	E3M10000030E04	*Enterococcus faecalis*
391	E3M10000030E08	*Enterococcus faecalis*
392	E3M10000030E09	*Enterococcus faecalis*
393	E3M10000030E10	*Enterococcus faecalis*
394	E3M10000030F01	*Enterococcus faecalis*
395	E3M10000030F04	*Enterococcus faecalis*
396	E3M10000030F06	*Enterococcus faecalis*
397	E3M10000030F07	*Enterococcus faecalis*
398	E3M10000030F10	*Enterococcus faecalis*
399	E3M10000030F12	*Enterococcus faecalis*
400	E3M10000030G01	*Enterococcus faecalis*
401	E3M10000030G03	*Enterococcus faecalis*
402	E3M10000030G06	*Enterococcus faecalis*
403	E3M10000030G08	*Enterococcus faecalis*
404	E3M10000030G09	*Enterococcus faecalis*
405	E3M10000030G12	*Enterococcus faecalis*
406	E3M10000030H03	*Enterococcus faecalis*
407	E3M10000030H04	*Enterococcus faecalis*
408	E3M10000030H06	*Enterococcus faecalis*
409	E3M10000030H07	*Enterococcus faecalis*
410	E3M10000030H08	*Enterococcus faecalis*
411	E3M10000030H10	*Enterococcus faecalis*
412	E3M10000030H11	*Enterococcus faecalis*
413	E3M10000031A02	*Enterococcus faecalis*
414	E3M10000031A06	*Enterococcus faecalis*
415	E3M10000031A07	*Enterococcus faecalis*
416	E3M10000031A08	*Enterococcus faecalis*
417	E3M10000031B02	*Enterococcus faecalis*
418	E3M10000031B03	*Enterococcus faecalis*
419	E3M10000031B04	*Enterococcus faecalis*
420	E3M10000031B09	*Enterococcus faecalis*
421	E3M10000031B10	*Enterococcus faecalis*
422	E3M10000031B11	*Enterococcus faecalis*
423	E3M10000031B12	*Enterococcus faecalis*
424	E3M10000031C01	*Enterococcus faecalis*
425	E3M10000031C04	*Enterococcus faecalis*
426	E3M10000031C06	*Enterococcus faecalis*
427	E3M10000031C10	*Enterococcus faecalis*
428	E3M10000031C11	*Enterococcus faecalis*

SeqID	Clone name	Organism
429	E3M10000031C12	*Enterococcus faecalis*
430	E3M10000031D03	*Enterococcus faecalis*
431	E3M10000031D04	*Enterococcus faecalis*
432	E3M10000031D08	*Enterococcus faecalis*
433	E3M10000031E03	*Enterococcus faecalis*
434	E3M10000031E09	*Enterococcus faecalis*
435	E3M10000031F02	*Enterococcus faecalis*
436	E3M10000031F04	*Enterococcus faecalis*
437	E3M10000031F07	*Enterococcus faecalis*
438	E3M10000031F09	*Enterococcus faecalis*
439	E3M10000031F11	*Enterococcus faecalis*
440	E3M10000031G03	*Enterococcus faecalis*
441	E3M10000031G04	*Enterococcus faecalis*
442	E3M10000031G05	*Enterococcus faecalis*
443	E3M10000031G06	*Enterococcus faecalis*
444	E3M10000031G07	*Enterococcus faecalis*
445	E3M10000031G08	*Enterococcus faecalis*
446	E3M10000031G11	*Enterococcus faecalis*
447	E3M10000031H05	*Enterococcus faecalis*
448	E3M10000031H06	*Enterococcus faecalis*
449	E3M10000031H07	*Enterococcus faecalis*
450	E3M10000031H08	*Enterococcus faecalis*
451	E3M10000031H10	*Enterococcus faecalis*
452	E3M10000031H11	*Enterococcus faecalis*
453	E3M10000032A02	*Enterococcus faecalis*
454	E3M10000032A04	*Enterococcus faecalis*
455	E3M10000032A06	*Enterococcus faecalis*
456	E3M10000032A07	*Enterococcus faecalis*
457	E3M10000032A08	*Enterococcus faecalis*
458	E3M10000032A09	*Enterococcus faecalis*
459	E3M10000032A10	*Enterococcus faecalis*
460	E3M10000032A11	*Enterococcus faecalis*
461	E3M10000032B03	*Enterococcus faecalis*
462	E3M10000032B04	*Enterococcus faecalis*
463	E3M10000032B07	*Enterococcus faecalis*
464	E3M10000032B08	*Enterococcus faecalis*
465	E3M10000032B09	*Enterococcus faecalis*
466	E3M10000032B11	*Enterococcus faecalis*
467	E3M10000032B12	*Enterococcus faecalis*
468	E3M10000032C01	*Enterococcus faecalis*
469	E3M10000032C02	*Enterococcus faecalis*
470	E3M10000032C03	*Enterococcus faecalis*
471	E3M10000032C04	*Enterococcus faecalis*
472	E3M10000032C06	*Enterococcus faecalis*
473	E3M10000032C09	*Enterococcus faecalis*
474	E3M10000032C11	*Enterococcus faecalis*
475	E3M10000032C12	*Enterococcus faecalis*

SeqID	Clone name	Organism
476	E3M10000032D01	*Enterococcus faecalis*
477	E3M10000032D02	*Enterococcus faecalis*
478	E3M10000032D03	*Enterococcus faecalis*
479	E3M10000032D06	*Enterococcus faecalis*
480	E3M10000032D09	*Enterococcus faecalis*
481	E3M10000032D12	*Enterococcus faecalis*
482	E3M10000032E04	*Enterococcus faecalis*
483	E3M10000032E05	*Enterococcus faecalis*
484	E3M10000032E08	*Enterococcus faecalis*
485	E3M10000032E10	*Enterococcus faecalis*
486	E3M10000032E11	*Enterococcus faecalis*
487	E3M10000032E12	*Enterococcus faecalis*
488	E3M10000032F02	*Enterococcus faecalis*
489	E3M10000032F03	*Enterococcus faecalis*
490	E3M10000032F05	*Enterococcus faecalis*
491	E3M10000032F07	*Enterococcus faecalis*
492	E3M10000032F08	*Enterococcus faecalis*
493	E3M10000032F11	*Enterococcus faecalis*
494	E3M10000032F12	*Enterococcus faecalis*
495	E3M10000032G01	*Enterococcus faecalis*
496	E3M10000032G02	*Enterococcus faecalis*
497	E3M10000032G04	*Enterococcus faecalis*
498	E3M10000032G05	*Enterococcus faecalis*
499	E3M10000032G06	*Enterococcus faecalis*
500	E3M10000032G07	*Enterococcus faecalis*
501	E3M10000032H05	*Enterococcus faecalis*
502	E3M10000032H06	*Enterococcus faecalis*
503	E3M10000032H08	*Enterococcus faecalis*
504	E3M10000032H09	*Enterococcus faecalis*
505	E3M10000032H10	*Enterococcus faecalis*
506	E3M10000033A03	*Enterococcus faecalis*
507	E3M10000033A04	*Enterococcus faecalis*
508	E3M10000033A05	*Enterococcus faecalis*
509	E3M10000033A06	*Enterococcus faecalis*
510	E3M10000033A07	*Enterococcus faecalis*
511	E3M10000033A08	*Enterococcus faecalis*
512	E3M10000033A11	*Enterococcus faecalis*
513	E3M10000033B01	*Enterococcus faecalis*
514	E3M10000033B02	*Enterococcus faecalis*
515	E3M10000033B04	*Enterococcus faecalis*
516	E3M10000033B05	*Enterococcus faecalis*
517	E3M10000033B06	*Enterococcus faecalis*
518	E3M10000033B08	*Enterococcus faecalis*
519	E3M10000033B09	*Enterococcus faecalis*
520	E3M10000033C01	*Enterococcus faecalis*
521	E3M10000033C02	*Enterococcus faecalis*
522	E3M10000033C05	*Enterococcus faecalis*

SeqID	Clone name	Organism
523	E3M10000033C09	*Enterococcus faecalis*
524	E3M10000033C10	*Enterococcus faecalis*
525	E3M10000033C11	*Enterococcus faecalis*
526	E3M10000033C12	*Enterococcus faecalis*
527	E3M10000033D01	*Enterococcus faecalis*
528	E3M10000033D04	*Enterococcus faecalis*
529	E3M10000033D05	*Enterococcus faecalis*
530	E3M10000033D06	*Enterococcus faecalis*
531	E3M10000033D09	*Enterococcus faecalis*
532	E3M10000033D10	*Enterococcus faecalis*
533	E3M10000033D11	*Enterococcus faecalis*
534	E3M10000033E02	*Enterococcus faecalis*
535	E3M10000033E03	*Enterococcus faecalis*
536	E3M10000033E04	*Enterococcus faecalis*
537	E3M10000033E05	*Enterococcus faecalis*
538	E3M10000033E07	*Enterococcus faecalis*
539	E3M10000033E08	*Enterococcus faecalis*
540	E3M10000033E09	*Enterococcus faecalis*
541	E3M10000033E11	*Enterococcus faecalis*
542	E3M10000033F01	*Enterococcus faecalis*
543	E3M10000033F03	*Enterococcus faecalis*
544	E3M10000033F04	*Enterococcus faecalis*
545	E3M10000033F05	*Enterococcus faecalis*
546	E3M10000033F07	*Enterococcus faecalis*
547	E3M10000033F08	*Enterococcus faecalis*
548	E3M10000033F10	*Enterococcus faecalis*
549	E3M10000033F12	*Enterococcus faecalis*
550	E3M10000033G01	*Enterococcus faecalis*
551	E3M10000033G02	*Enterococcus faecalis*
552	E3M10000033G03	*Enterococcus faecalis*
553	E3M10000033G04	*Enterococcus faecalis*
554	E3M10000033G06	*Enterococcus faecalis*
555	E3M10000033G07	*Enterococcus faecalis*
556	E3M10000033G08	*Enterococcus faecalis*
557	E3M10000033G09	*Enterococcus faecalis*
558	E3M10000033G12	*Enterococcus faecalis*
559	E3M10000033H02	*Enterococcus faecalis*
560	E3M10000033H04	*Enterococcus faecalis*
561	E3M10000033H05	*Enterococcus faecalis*
562	E3M10000033H07	*Enterococcus faecalis*
563	E3M10000033H08	*Enterococcus faecalis*
564	E3M10000033H09	*Enterococcus faecalis*
565	E3M10000033H10	*Enterococcus faecalis*
566	E3M10000033H11	*Enterococcus faecalis*
567	E3M10000034A02	*Enterococcus faecalis*
568	E3M10000034A03	*Enterococcus faecalis*
569	E3M10000034A04	*Enterococcus faecalis*

SeqID	Clone name	Organism
570	E3M10000034B02	*Enterococcus faecalis*
571	E3M10000034B04	*Enterococcus faecalis*
572	E3M10000034C04	*Enterococcus faecalis*
573	E3M10000034D01	*Enterococcus faecalis*
574	E3M10000034D02	*Enterococcus faecalis*
575	E3M10000034E01	*Enterococcus faecalis*
576	E3M10000034E04	*Enterococcus faecalis*
577	E3M10000034F02	*Enterococcus faecalis*
578	E3M10000034F03	*Enterococcus faecalis*
579	E3M10000034F04	*Enterococcus faecalis*
580	E3M10000034G02	*Enterococcus faecalis*
581	E3M10000034G03	*Enterococcus faecalis*
582	E3M10000034H02	*Enterococcus faecalis*
583	E3M10000034H03	*Enterococcus faecalis*
584	E3M10000035A02	*Enterococcus faecalis*
585	E3M10000035A04	*Enterococcus faecalis*
586	E3M10000035A05	*Enterococcus faecalis*
587	E3M10000035A06	*Enterococcus faecalis*
588	E3M10000035A08	*Enterococcus faecalis*
589	E3M10000035A09	*Enterococcus faecalis*
590	E3M10000035A11	*Enterococcus faecalis*
591	E3M10000035B01	*Enterococcus faecalis*
592	E3M10000035B03	*Enterococcus faecalis*
593	E3M10000035B06	*Enterococcus faecalis*
594	E3M10000035B07	*Enterococcus faecalis*
595	E3M10000035B08	*Enterococcus faecalis*
596	E3M10000035B10	*Enterococcus faecalis*
597	E3M10000035B11	*Enterococcus faecalis*
598	E3M10000035B12	*Enterococcus faecalis*
599	E3M10000035C01	*Enterococcus faecalis*
600	E3M10000035C03	*Enterococcus faecalis*
601	E3M10000035C04	*Enterococcus faecalis*
602	E3M10000035C05	*Enterococcus faecalis*
603	E3M10000035C06	*Enterococcus faecalis*
604	E3M10000035C07	*Enterococcus faecalis*
605	E3M10000035C08	*Enterococcus faecalis*
606	E3M10000035C09	*Enterococcus faecalis*
607	E3M10000035C11	*Enterococcus faecalis*
608	E3M10000035C12	*Enterococcus faecalis*
609	E3M10000035D02	*Enterococcus faecalis*
610	E3M10000035D03	*Enterococcus faecalis*
611	E3M10000035D04	*Enterococcus faecalis*
612	E3M10000035D05	*Enterococcus faecalis*
613	E3M10000035D10	*Enterococcus faecalis*
614	E3M10000035D11	*Enterococcus faecalis*
615	E3M10000035E03	*Enterococcus faecalis*
616	E3M10000035E04	*Enterococcus faecalis*

SeqID	Clone name	Organism
617	E3M10000035E05	*Enterococcus faecalis*
618	E3M10000035E07	*Enterococcus faecalis*
619	E3M10000035E08	*Enterococcus faecalis*
620	E3M10000035E09	*Enterococcus faecalis*
621	E3M10000035E10	*Enterococcus faecalis*
622	E3M10000035E11	*Enterococcus faecalis*
623	E3M10000035E12	*Enterococcus faecalis*
624	E3M10000035F01	*Enterococcus faecalis*
625	E3M10000035F02	*Enterococcus faecalis*
626	E3M10000035F03	*Enterococcus faecalis*
627	E3M10000035F06	*Enterococcus faecalis*
628	E3M10000035F07	*Enterococcus faecalis*
629	E3M10000035F08	*Enterococcus faecalis*
630	E3M10000035F09	*Enterococcus faecalis*
631	E3M10000035F11	*Enterococcus faecalis*
632	E3M10000035F12	*Enterococcus faecalis*
633	E3M10000035G02	*Enterococcus faecalis*
634	E3M10000035G04	*Enterococcus faecalis*
635	E3M10000035G05	*Enterococcus faecalis*
636	E3M10000035G08	*Enterococcus faecalis*
637	E3M10000035G09	*Enterococcus faecalis*
638	E3M10000035G10	*Enterococcus faecalis*
639	E3M10000035G11	*Enterococcus faecalis*
640	E3M10000035H03	*Enterococcus faecalis*
641	E3M10000035H06	*Enterococcus faecalis*
642	E3M10000035H09	*Enterococcus faecalis*
643	E3M10000035H11	*Enterococcus faecalis*
644	E3M10000036A03	*Enterococcus faecalis*
645	E3M10000036A04	*Enterococcus faecalis*
646	E3M10000036A05	*Enterococcus faecalis*
647	E3M10000036A06	*Enterococcus faecalis*
648	E3M10000036A07	*Enterococcus faecalis*
649	E3M10000036A08	*Enterococcus faecalis*
650	E3M10000036A09	*Enterococcus faecalis*
651	E3M10000036A10	*Enterococcus faecalis*
652	E3M10000036B01	*Enterococcus faecalis*
653	E3M10000036B03	*Enterococcus faecalis*
654	E3M10000036B06	*Enterococcus faecalis*
655	E3M10000036B07	*Enterococcus faecalis*
656	E3M10000036B08	*Enterococcus faecalis*
657	E3M10000036B09	*Enterococcus faecalis*
658	E3M10000036B11	*Enterococcus faecalis*
659	E3M10000036B12	*Enterococcus faecalis*
660	E3M10000036C01	*Enterococcus faecalis*
661	E3M10000036C03	*Enterococcus faecalis*
662	E3M10000036C06	*Enterococcus faecalis*
663	E3M10000036C07	*Enterococcus faecalis*

SeqID	Clone name	Organism
664	E3M10000036C08	*Enterococcus faecalis*
665	E3M10000036C09	*Enterococcus faecalis*
666	E3M10000036C10	*Enterococcus faecalis*
667	E3M10000036C11	*Enterococcus faecalis*
668	E3M10000036D03	*Enterococcus faecalis*
669	E3M10000036D04	*Enterococcus faecalis*
670	E3M10000036D06	*Enterococcus faecalis*
671	E3M10000036D08	*Enterococcus faecalis*
672	E3M10000036D09	*Enterococcus faecalis*
673	E3M10000036D10	*Enterococcus faecalis*
674	E3M10000036D11	*Enterococcus faecalis*
675	E3M10000036D12	*Enterococcus faecalis*
676	E3M10000036E01	*Enterococcus faecalis*
677	E3M10000036E04	*Enterococcus faecalis*
678	E3M10000036E05	*Enterococcus faecalis*
679	E3M10000036E07	*Enterococcus faecalis*
680	E3M10000036E08	*Enterococcus faecalis*
681	E3M10000036F03	*Enterococcus faecalis*
682	E3M10000036F04	*Enterococcus faecalis*
683	E3M10000036F05	*Enterococcus faecalis*
684	E3M10000036F08	*Enterococcus faecalis*
685	E3M10000036F09	*Enterococcus faecalis*
686	E3M10000036F10	*Enterococcus faecalis*
687	E3M10000036F12	*Enterococcus faecalis*
688	E3M10000036G01	*Enterococcus faecalis*
689	E3M10000036G02	*Enterococcus faecalis*
690	E3M10000036G03	*Enterococcus faecalis*
691	E3M10000036G04	*Enterococcus faecalis*
692	E3M10000036G06	*Enterococcus faecalis*
693	E3M10000036G10	*Enterococcus faecalis*
694	E3M10000036H02	*Enterococcus faecalis*
695	E3M10000036H03	*Enterococcus faecalis*
696	E3M10000036H04	*Enterococcus faecalis*
697	E3M10000036H05	*Enterococcus faecalis*
698	E3M10000036H06	*Enterococcus faecalis*
699	E3M10000036H07	*Enterococcus faecalis*
700	E3M10000036H08	*Enterococcus faecalis*
701	E3M10000036H09	*Enterococcus faecalis*
702	E3M10000036H10	*Enterococcus faecalis*
703	E3M10000037A03	*Enterococcus faecalis*
704	E3M10000037A06	*Enterococcus faecalis*
705	E3M10000037A08	*Enterococcus faecalis*
706	E3M10000037A09	*Enterococcus faecalis*
707	E3M10000037A10	*Enterococcus faecalis*
708	E3M10000037B02	*Enterococcus faecalis*
709	E3M10000037B07	*Enterococcus faecalis*
710	E3M10000037B08	*Enterococcus faecalis*

SeqID	Clone name	Organism
711	E3M10000037B11	*Enterococcus faecalis*
712	E3M10000037C01	*Enterococcus faecalis*
713	E3M10000037C02	*Enterococcus faecalis*
714	E3M10000037C04	*Enterococcus faecalis*
715	E3M10000037C05	*Enterococcus faecalis*
716	E3M10000037C07	*Enterococcus faecalis*
717	E3M10000037C11	*Enterococcus faecalis*
718	E3M10000037C12	*Enterococcus faecalis*
719	E3M10000037D02	*Enterococcus faecalis*
720	E3M10000037D03	*Enterococcus faecalis*
721	E3M10000037D04	*Enterococcus faecalis*
722	E3M10000037D05	*Enterococcus faecalis*
723	E3M10000037D06	*Enterococcus faecalis*
724	E3M10000037D09	*Enterococcus faecalis*
725	E3M10000037D11	*Enterococcus faecalis*
726	E3M10000037E01	*Enterococcus faecalis*
727	E3M10000037E02	*Enterococcus faecalis*
728	E3M10000037E03	*Enterococcus faecalis*
729	E3M10000037E05	*Enterococcus faecalis*
730	E3M10000037E07	*Enterococcus faecalis*
731	E3M10000037E08	*Enterococcus faecalis*
732	E3M10000037E10	*Enterococcus faecalis*
733	E3M10000037E12	*Enterococcus faecalis*
734	E3M10000037F01	*Enterococcus faecalis*
735	E3M10000037F02	*Enterococcus faecalis*
736	E3M10000037F06	*Enterococcus faecalis*
737	E3M10000037F07	*Enterococcus faecalis*
738	E3M10000037F12	*Enterococcus faecalis*
739	E3M10000037G01	*Enterococcus faecalis*
740	E3M10000037G02	*Enterococcus faecalis*
741	E3M10000037G03	*Enterococcus faecalis*
742	E3M10000037G05	*Enterococcus faecalis*
743	E3M10000037G06	*Enterococcus faecalis*
744	E3M10000037G07	*Enterococcus faecalis*
745	E3M10000037G08	*Enterococcus faecalis*
746	E3M10000037G10	*Enterococcus faecalis*
747	E3M10000037G11	*Enterococcus faecalis*
748	E3M10000037H02	*Enterococcus faecalis*
749	E3M10000037H05	*Enterococcus faecalis*
750	E3M10000037H07	*Enterococcus faecalis*
751	E3M10000037H10	*Enterococcus faecalis*
752	E3M10000037H11	*Enterococcus faecalis*
753	E3M10000038A02	*Enterococcus faecalis*
754	E3M10000038A03	*Enterococcus faecalis*
755	E3M10000038A05	*Enterococcus faecalis*
756	E3M10000038A06	*Enterococcus faecalis*
757	E3M10000038A07	*Enterococcus faecalis*

SeqID	Clone name	Organism
758	E3M10000038A09	*Enterococcus faecalis*
759	E3M10000038A10	*Enterococcus faecalis*
760	E3M10000038A11	*Enterococcus faecalis*
761	E3M10000038B02	*Enterococcus faecalis*
762	E3M10000038B03	*Enterococcus faecalis*
763	E3M10000038B04	*Enterococcus faecalis*
764	E3M10000038B05	*Enterococcus faecalis*
765	E3M10000038B07	*Enterococcus faecalis*
766	E3M10000038B08	*Enterococcus faecalis*
767	E3M10000038B09	*Enterococcus faecalis*
768	E3M10000038B11	*Enterococcus faecalis*
769	E3M10000038C02	*Enterococcus faecalis*
770	E3M10000038C03	*Enterococcus faecalis*
771	E3M10000038C05	*Enterococcus faecalis*
772	E3M10000038C07	*Enterococcus faecalis*
773	E3M10000038C10	*Enterococcus faecalis*
774	E3M10000038C12	*Enterococcus faecalis*
775	E3M10000038D01	*Enterococcus faecalis*
776	E3M10000038D02	*Enterococcus faecalis*
777	E3M10000038D04	*Enterococcus faecalis*
778	E3M10000038D08	*Enterococcus faecalis*
779	E3M10000038D10	*Enterococcus faecalis*
780	E3M10000038D11	*Enterococcus faecalis*
781	E3M10000038D12	*Enterococcus faecalis*
782	E3M10000038E02	*Enterococcus faecalis*
783	E3M10000038E03	*Enterococcus faecalis*
784	E3M10000038E04	*Enterococcus faecalis*
785	E3M10000038E05	*Enterococcus faecalis*
786	E3M10000038E07	*Enterococcus faecalis*
787	E3M10000038E08	*Enterococcus faecalis*
788	E3M10000038E11	*Enterococcus faecalis*
789	E3M10000038F02	*Enterococcus faecalis*
790	E3M10000038F04	*Enterococcus faecalis*
791	E3M10000038F05	*Enterococcus faecalis*
792	E3M10000038F06	*Enterococcus faecalis*
793	E3M10000038F07	*Enterococcus faecalis*
794	E3M10000038F09	*Enterococcus faecalis*
795	E3M10000038F10	*Enterococcus faecalis*
796	E3M10000038F11	*Enterococcus faecalis*
797	E3M10000038G02	*Enterococcus faecalis*
798	E3M10000038G03	*Enterococcus faecalis*
799	E3M10000038G06	*Enterococcus faecalis*
800	E3M10000038G07	*Enterococcus faecalis*
801	E3M10000038G11	*Enterococcus faecalis*
802	E3M10000038H02	*Enterococcus faecalis*
803	E3M10000038H05	*Enterococcus faecalis*
804	E3M10000038H06	*Enterococcus faecalis*

SeqID	Clone name	Organism
805	E3M10000038H07	*Enterococcus faecalis*
806	E3M10000038H08	*Enterococcus faecalis*
807	E3M10000038H09	*Enterococcus faecalis*
808	E3M10000038H10	*Enterococcus faecalis*
809	E3M10000039A02	*Enterococcus faecalis*
810	E3M10000039A06	*Enterococcus faecalis*
811	E3M10000039A07	*Enterococcus faecalis*
812	E3M10000039A08	*Enterococcus faecalis*
813	E3M10000039A10	*Enterococcus faecalis*
814	E3M10000039A11	*Enterococcus faecalis*
815	E3M10000039B01	*Enterococcus faecalis*
816	E3M10000039B03	*Enterococcus faecalis*
817	E3M10000039B04	*Enterococcus faecalis*
818	E3M10000039B06	*Enterococcus faecalis*
819	E3M10000039B07	*Enterococcus faecalis*
820	E3M10000039B08	*Enterococcus faecalis*
821	E3M10000039B09	*Enterococcus faecalis*
822	E3M10000039B11	*Enterococcus faecalis*
823	E3M10000039C02	*Enterococcus faecalis*
824	E3M10000039C04	*Enterococcus faecalis*
825	E3M10000039C05	*Enterococcus faecalis*
826	E3M10000039C06	*Enterococcus faecalis*
827	E3M10000039C07	*Enterococcus faecalis*
828	E3M10000039C08	*Enterococcus faecalis*
829	E3M10000039C09	*Enterococcus faecalis*
830	E3M10000039C10	*Enterococcus faecalis*
831	E3M10000039D02	*Enterococcus faecalis*
832	E3M10000039D03	*Enterococcus faecalis*
833	E3M10000039D04	*Enterococcus faecalis*
834	E3M10000039D06	*Enterococcus faecalis*
835	E3M10000039E01	*Enterococcus faecalis*
836	E3M10000039E02	*Enterococcus faecalis*
837	E3M10000039E03	*Enterococcus faecalis*
838	E3M10000039E05	*Enterococcus faecalis*
839	E3M10000039E07	*Enterococcus faecalis*
840	E3M10000039E08	*Enterococcus faecalis*
841	E3M10000039F01	*Enterococcus faecalis*
842	E3M10000039F02	*Enterococcus faecalis*
843	E3M10000039F03	*Enterococcus faecalis*
844	E3M10000039F06	*Enterococcus faecalis*
845	E3M10000039F07	*Enterococcus faecalis*
846	E3M10000039F08	*Enterococcus faecalis*
847	E3M10000039G01	*Enterococcus faecalis*
848	E3M10000039G02	*Enterococcus faecalis*
849	E3M10000039G05	*Enterococcus faecalis*
850	E3M10000039G07	*Enterococcus faecalis*
851	E3M10000039G09	*Enterococcus faecalis*

SeqID	Clone name	Organism
852	E3M10000039G10	*Enterococcus faecalis*
853	E3M10000039H02	*Enterococcus faecalis*
854	E3M10000039H07	*Enterococcus faecalis*
855	E3M10000039H08	*Enterococcus faecalis*
856	E3M10000039H10	*Enterococcus faecalis*
857	E3M10000039H11	*Enterococcus faecalis*
858	E3M10000040A03	*Enterococcus faecalis*
859	E3M10000040A05	*Enterococcus faecalis*
860	E3M10000040A07	*Enterococcus faecalis*
861	E3M10000040A09	*Enterococcus faecalis*
862	E3M10000040A10	*Enterococcus faecalis*
863	E3M10000040A11	*Enterococcus faecalis*
864	E3M10000040B01	*Enterococcus faecalis*
865	E3M10000040B02	*Enterococcus faecalis*
866	E3M10000040B05	*Enterococcus faecalis*
867	E3M10000040B06	*Enterococcus faecalis*
868	E3M10000040B08	*Enterococcus faecalis*
869	E3M10000040B09	*Enterococcus faecalis*
870	E3M10000040B10	*Enterococcus faecalis*
871	E3M10000040B11	*Enterococcus faecalis*
872	E3M10000040B12	*Enterococcus faecalis*
873	E3M10000040C02	*Enterococcus faecalis*
874	E3M10000040C05	*Enterococcus faecalis*
875	E3M10000040C06	*Enterococcus faecalis*
876	E3M10000040C07	*Enterococcus faecalis*
877	E3M10000040C08	*Enterococcus faecalis*
878	E3M10000040C09	*Enterococcus faecalis*
879	E3M10000040C10	*Enterococcus faecalis*
880	E3M10000040C11	*Enterococcus faecalis*
881	E3M10000040C12	*Enterococcus faecalis*
882	E3M10000040D03	*Enterococcus faecalis*
883	E3M10000040D04	*Enterococcus faecalis*
884	E3M10000040D08	*Enterococcus faecalis*
885	E3M10000040D12	*Enterococcus faecalis*
886	E3M10000040E02	*Enterococcus faecalis*
887	E3M10000040E10	*Enterococcus faecalis*
888	E3M10000040E11	*Enterococcus faecalis*
889	E3M10000040E12	*Enterococcus faecalis*
890	E3M10000040F01	*Enterococcus faecalis*
891	E3M10000040F03	*Enterococcus faecalis*
892	E3M10000040F08	*Enterococcus faecalis*
893	E3M10000040F09	*Enterococcus faecalis*
894	E3M10000040F10	*Enterococcus faecalis*
895	E3M10000040G01	*Enterococcus faecalis*
896	E3M10000040G02	*Enterococcus faecalis*
897	E3M10000040G04	*Enterococcus faecalis*
898	E3M10000040G05	*Enterococcus faecalis*

SeqID	Clone name	Organism
899	E3M10000040G07	*Enterococcus faecalis*
900	E3M10000040G08	*Enterococcus faecalis*
901	E3M10000040G09	*Enterococcus faecalis*
902	E3M10000040G11	*Enterococcus faecalis*
903	E3M10000040H02	*Enterococcus faecalis*
904	E3M10000040H03	*Enterococcus faecalis*
905	E3M10000040H04	*Enterococcus faecalis*
906	E3M10000040H05	*Enterococcus faecalis*
907	E3M10000040H09	*Enterococcus faecalis*
908	E3M10000041A03	*Enterococcus faecalis*
909	E3M10000041A05	*Enterococcus faecalis*
910	E3M10000041A08	*Enterococcus faecalis*
911	E3M10000041A09	*Enterococcus faecalis*
912	E3M10000041A10	*Enterococcus faecalis*
913	E3M10000041A11	*Enterococcus faecalis*
914	E3M10000041B02	*Enterococcus faecalis*
915	E3M10000041B03	*Enterococcus faecalis*
916	E3M10000041B05	*Enterococcus faecalis*
917	E3M10000041B06	*Enterococcus faecalis*
918	E3M10000041B08	*Enterococcus faecalis*
919	E3M10000041B09	*Enterococcus faecalis*
920	E3M10000041B10	*Enterococcus faecalis*
921	E3M10000041B11	*Enterococcus faecalis*
922	E3M10000041B12	*Enterococcus faecalis*
923	E3M10000041C01	*Enterococcus faecalis*
924	E3M10000041C07	*Enterococcus faecalis*
925	E3M10000041C08	*Enterococcus faecalis*
926	E3M10000041C09	*Enterococcus faecalis*
927	E3M10000041C10	*Enterococcus faecalis*
928	E3M10000041C11	*Enterococcus faecalis*
929	E3M10000041C12	*Enterococcus faecalis*
930	E3M10000041D02	*Enterococcus faecalis*
931	E3M10000041D03	*Enterococcus faecalis*
932	E3M10000041D04	*Enterococcus faecalis*
933	E3M10000041D05	*Enterococcus faecalis*
934	E3M10000041D06	*Enterococcus faecalis*
935	E3M10000041D08	*Enterococcus faecalis*
936	E3M10000041D09	*Enterococcus faecalis*
937	E3M10000041D10	*Enterococcus faecalis*
938	E3M10000041D11	*Enterococcus faecalis*
939	E3M10000041D12	*Enterococcus faecalis*
940	E3M10000041E02	*Enterococcus faecalis*
941	E3M10000041E03	*Enterococcus faecalis*
942	E3M10000041E05	*Enterococcus faecalis*
943	E3M10000041E07	*Enterococcus faecalis*
944	E3M10000041E10	*Enterococcus faecalis*
945	E3M10000041E11	*Enterococcus faecalis*

SeqID	Clone name	Organism
946	E3M10000041F03	*Enterococcus faecalis*
947	E3M10000041F05	*Enterococcus faecalis*
948	E3M10000041F06	*Enterococcus faecalis*
949	E3M10000041F07	*Enterococcus faecalis*
950	E3M10000041F08	*Enterococcus faecalis*
951	E3M10000041F09	*Enterococcus faecalis*
952	E3M10000041F10	*Enterococcus faecalis*
953	E3M10000041F11	*Enterococcus faecalis*
954	E3M10000041G02	*Enterococcus faecalis*
955	E3M10000041G03	*Enterococcus faecalis*
956	E3M10000041G04	*Enterococcus faecalis*
957	E3M10000041G06	*Enterococcus faecalis*
958	E3M10000041G07	*Enterococcus faecalis*
959	E3M10000041G08	*Enterococcus faecalis*
960	E3M10000041G09	*Enterococcus faecalis*
961	E3M10000041G10	*Enterococcus faecalis*
962	E3M10000041G12	*Enterococcus faecalis*
963	E3M10000041H04	*Enterococcus faecalis*
964	E3M10000041H05	*Enterococcus faecalis*
965	E3M10000041H06	*Enterococcus faecalis*
966	E3M10000041H07	*Enterococcus faecalis*
967	E3M10000041H08	*Enterococcus faecalis*
968	E3M10000041H09	*Enterococcus faecalis*
969	E3M10000041H10	*Enterococcus faecalis*
970	E3M10000041H11	*Enterococcus faecalis*
971	E3M10000042A03	*Enterococcus faecalis*
972	E3M10000042A08	*Enterococcus faecalis*
973	E3M10000042A10	*Enterococcus faecalis*
974	E3M10000042B01	*Enterococcus faecalis*
975	E3M10000042B02	*Enterococcus faecalis*
976	E3M10000042B04	*Enterococcus faecalis*
977	E3M10000042B08	*Enterococcus faecalis*
978	E3M10000042B09	*Enterococcus faecalis*
979	E3M10000042B10	*Enterococcus faecalis*
980	E3M10000042B11	*Enterococcus faecalis*
981	E3M10000042C02	*Enterococcus faecalis*
982	E3M10000042C03	*Enterococcus faecalis*
983	E3M10000042C04	*Enterococcus faecalis*
984	E3M10000042C10	*Enterococcus faecalis*
985	E3M10000042D01	*Enterococcus faecalis*
986	E3M10000042D02	*Enterococcus faecalis*
987	E3M10000042D03	*Enterococcus faecalis*
988	E3M10000042D06	*Enterococcus faecalis*
989	E3M10000042D09	*Enterococcus faecalis*
990	E3M10000042D11	*Enterococcus faecalis*
991	E3M10000042D12	*Enterococcus faecalis*
992	E3M10000042E05	*Enterococcus faecalis*

SeqID	Clone name	Organism
993	E3M10000042E12	*Enterococcus faecalis*
994	E3M10000042F11	*Enterococcus faecalis*
995	E3M10000042G01	*Enterococcus faecalis*
996	E3M10000042G05	*Enterococcus faecalis*
997	E3M10000042G07	*Enterococcus faecalis*
998	E3M10000042G08	*Enterococcus faecalis*
999	E3M10000042G11	*Enterococcus faecalis*
1000	E3M10000042G12	*Enterococcus faecalis*
1001	E3M10000042H06	*Enterococcus faecalis*
1002	E3M10000042H08	*Enterococcus faecalis*
1003	E3M10000042H11	*Enterococcus faecalis*
1004	E3M10000043A02	*Enterococcus faecalis*
1005	E3M10000043A03	*Enterococcus faecalis*
1006	E3M10000043A05	*Enterococcus faecalis*
1007	E3M10000043A08	*Enterococcus faecalis*
1008	E3M10000043A09	*Enterococcus faecalis*
1009	E3M10000043A10	*Enterococcus faecalis*
1010	E3M10000043A11	*Enterococcus faecalis*
1011	E3M10000043B01	*Enterococcus faecalis*
1012	E3M10000043B02	*Enterococcus faecalis*
1013	E3M10000043B03	*Enterococcus faecalis*
1014	E3M10000043B06	*Enterococcus faecalis*
1015	E3M10000043B08	*Enterococcus faecalis*
1016	E3M10000043B09	*Enterococcus faecalis*
1017	E3M10000043B10	*Enterococcus faecalis*
1018	E3M10000043B11	*Enterococcus faecalis*
1019	E3M10000043B12	*Enterococcus faecalis*
1020	E3M10000043C01	*Enterococcus faecalis*
1021	E3M10000043C08	*Enterococcus faecalis*
1022	E3M10000043C09	*Enterococcus faecalis*
1023	E3M10000043D01	*Enterococcus faecalis*
1024	E3M10000043D02	*Enterococcus faecalis*
1025	E3M10000043D09	*Enterococcus faecalis*
1026	E3M10000043D10	*Enterococcus faecalis*
1027	E3M10000043D12	*Enterococcus faecalis*
1028	E3M10000043E03	*Enterococcus faecalis*
1029	E3M10000043E07	*Enterococcus faecalis*
1030	E3M10000043E08	*Enterococcus faecalis*
1031	E3M10000043E10	*Enterococcus faecalis*
1032	E3M10000043E11	*Enterococcus faecalis*
1033	E3M10000043F03	*Enterococcus faecalis*
1034	E3M10000043F04	*Enterococcus faecalis*
1035	E3M10000043F06	*Enterococcus faecalis*
1036	E3M10000043F08	*Enterococcus faecalis*
1037	E3M10000043F10	*Enterococcus faecalis*
1038	E3M10000043F12	*Enterococcus faecalis*
1039	E3M10000043G03	*Enterococcus faecalis*

SeqID	Clone name	Organism
1040	E3M10000043G04	*Enterococcus faecalis*
1041	E3M10000043G05	*Enterococcus faecalis*
1042	E3M10000043G07	*Enterococcus faecalis*
1043	E3M10000043G08	*Enterococcus faecalis*
1044	E3M10000043G10	*Enterococcus faecalis*
1045	E3M10000043G11	*Enterococcus faecalis*
1046	E3M10000043G12	*Enterococcus faecalis*
1047	E3M10000043H02	*Enterococcus faecalis*
1048	E3M10000043H05	*Enterococcus faecalis*
1049	E3M10000043H08	*Enterococcus faecalis*
1050	E3M10000043H09	*Enterococcus faecalis*
1051	E3M10000043H11	*Enterococcus faecalis*
1052	E3M10000044C02	*Enterococcus faecalis*
1053	E3M10000044E01	*Enterococcus faecalis*
1054	K1M10000002F02	*Klebsiella pneumoniae*
1055	K1M10000003C01	*Klebsiella pneumoniae*
1056	K1M10000004F06	*Klebsiella pneumoniae*
1057	K1M10000007F01	*Klebsiella pneumoniae*
1058	K1M10000008C02	*Klebsiella pneumoniae*
1059	K1M10000008C10	*Klebsiella pneumoniae*
1060	K1M10000008G10	*Klebsiella pneumoniae*
1061	K1M10000009D04	*Klebsiella pneumoniae*
1062	K1M10000013E04	*Klebsiella pneumoniae*
1063	K1M10000013E06	*Klebsiella pneumoniae*
1064	K1M10000019D06	*Klebsiella pneumoniae*
1065	K1M10000020B02	*Klebsiella pneumoniae*
1066	K1M10000021H06	*Klebsiella pneumoniae*
1067	K1M10000022C10	*Klebsiella pneumoniae*
1068	K1M10000023E09	*Klebsiella pneumoniae*
1069	K1M10000023E10	*Klebsiella pneumoniae*
1070	K1M10000030C07	*Klebsiella pneumoniae*
1071	K1M10000030E07	*Klebsiella pneumoniae*
1072	K1M10000031B11	*Klebsiella pneumoniae*
1073	K1M10000032E11	*Klebsiella pneumoniae*
1074	K1M10000033B02	*Klebsiella pneumoniae*
1075	K1M10000033E01	*Klebsiella pneumoniae*
1076	K1M10000036G08	*Klebsiella pneumoniae*
1077	K1M10000037D10	*Klebsiella pneumoniae*
1078	K1M10000038H09	*Klebsiella pneumoniae*
1079	K1M10000039H03	*Klebsiella pneumoniae*
1080	K1M10000043C01	*Klebsiella pneumoniae*
1081	K1M10000043D05	*Klebsiella pneumoniae*
1082	K1M10000043H10	*Klebsiella pneumoniae*
1083	K1M10000044D05	*Klebsiella pneumoniae*
1084	K1M10000044D08	*Klebsiella pneumoniae*
1085	K1M10000044E05	*Klebsiella pneumoniae*
1086	K1M10000044G05	*Klebsiella pneumoniae*

SeqID	Clone name	Organism
1087	K1M10000045A07	*Klebsiella pneumoniae*
1088	K1M10000045D10	*Klebsiella pneumoniae*
1089	K1M10000003D03	*Klebsiella pneumoniae*
1090	K1M10000010C02	*Klebsiella pneumoniae*
1091	K1M10000021H10	*Klebsiella pneumoniae*
1092	P1M10000008C06	*Pseudomonas aeruginosa*
1093	P1M10000008G04	*Pseudomonas aeruginosa*
1094	P1M10000010C03	*Pseudomonas aeruginosa*
1095	P1M10000014H10	*Pseudomonas aeruginosa*
1096	P1M10000015C06	*Pseudomonas aeruginosa*
1097	P1M10000015C09	*Pseudomonas aeruginosa*
1098	P1M10000016C04	*Pseudomonas aeruginosa*
1099	P1M10000018B01	*Pseudomonas aeruginosa*
1100	P1M10000018C01	*Pseudomonas aeruginosa*
1101	P1M10000018E01	*Pseudomonas aeruginosa*
1102	P1M10000018G01	*Pseudomonas aeruginosa*
1103	P1M10000019F01	*Pseudomonas aeruginosa*
1104	P1M10000021G03	*Pseudomonas aeruginosa*
1105	P1M10000021G05	*Pseudomonas aeruginosa*
1106	P1M10000022D09	*Pseudomonas aeruginosa*
1107	P1M10000024D06	*Pseudomonas aeruginosa*
1108	P1M10000024E06	*Pseudomonas aeruginosa*
1109	P1M10000024H03	*Pseudomonas aeruginosa*
1110	P1M10000025A06	*Pseudomonas aeruginosa*
1111	P1M10000025G07	*Pseudomonas aeruginosa*
1112	P1M10000025H07	*Pseudomonas aeruginosa*
1113	P1M10000026E06	*Pseudomonas aeruginosa*
1114	P1M10000026F04	*Pseudomonas aeruginosa*
1115	P1M10000026G09	*Pseudomonas aeruginosa*
1116	P1M10000026H02	*Pseudomonas aeruginosa*
1117	P1M10000026H05	*Pseudomonas aeruginosa*
1118	P1M10000027A06	*Pseudomonas aeruginosa*
1119	P1M10000027B02	*Pseudomonas aeruginosa*
1120	P1M10000027G05	*Pseudomonas aeruginosa*
1121	P1M10000028A08	*Pseudomonas aeruginosa*
1122	P1M10000028B01	*Pseudomonas aeruginosa*
1123	P1M10000028E02	*Pseudomonas aeruginosa*
1124	P1M10000029A09	*Pseudomonas aeruginosa*
1125	P1M10000029G03	*Pseudomonas aeruginosa*
1126	P1M10000029H05	*Pseudomonas aeruginosa*
1127	P1M10000032F04	*Pseudomonas aeruginosa*
1128	P1M10000033A02	*Pseudomonas aeruginosa*
1129	P1M10000033B08	*Pseudomonas aeruginosa*
1130	P1M10000033E03	*Pseudomonas aeruginosa*
1131	P1M10000033F01	*Pseudomonas aeruginosa*
1132	P1M10000033G08	*Pseudomonas aeruginosa*
1133	P1M10000035A06	*Pseudomonas aeruginosa*

SeqID	Clone name	Organism
1134	P1M10000037B12	*Pseudomonas aeruginosa*
1135	P1M10000037G12	*Pseudomonas aeruginosa*
1136	P1M10000038B08	*Pseudomonas aeruginosa*
1137	P1M10000038C03	*Pseudomonas aeruginosa*
1138	P1M10000038C06	*Pseudomonas aeruginosa*
1139	P1M10000038F04	*Pseudomonas aeruginosa*
1140	P1M10000038G02	*Pseudomonas aeruginosa*
1141	P1M10000039G05	*Pseudomonas aeruginosa*
1142	P1M10000039G12	*Pseudomonas aeruginosa*
1143	P1M10000040C01	*Pseudomonas aeruginosa*
1144	P1M10000040C04	*Pseudomonas aeruginosa*
1145	P1M10000040D04	*Pseudomonas aeruginosa*
1146	P1M10000040D05	*Pseudomonas aeruginosa*
1147	P1M10000040E10	*Pseudomonas aeruginosa*
1148	P1M10000040H03	*Pseudomonas aeruginosa*
1149	P1M10000041A12	*Pseudomonas aeruginosa*
1150	P1M10000041B02	*Pseudomonas aeruginosa*
1151	P1M10000041E01	*Pseudomonas aeruginosa*
1152	P1M10000041F01	*Pseudomonas aeruginosa*
1153	P1M10000042B12	*Pseudomonas aeruginosa*
1154	P1M10000042E08	*Pseudomonas aeruginosa*
1155	P1M10000043A03	*Pseudomonas aeruginosa*
1156	P1M10000043D06	*Pseudomonas aeruginosa*
1157	P1M10000044F07	*Pseudomonas aeruginosa*
1158	P1M10000046B03	*Pseudomonas aeruginosa*
1159	P1M10000046C07	*Pseudomonas aeruginosa*
1160	P1M10000046C08	*Pseudomonas aeruginosa*
1161	P1M10000046C09	*Pseudomonas aeruginosa*
1162	P1M10000046G11	*Pseudomonas aeruginosa*
1163	P1M10000047B04	*Pseudomonas aeruginosa*
1164	P1M10000047E11	*Pseudomonas aeruginosa*
1165	P1M10000047F07	*Pseudomonas aeruginosa*
1166	P1M10000047G10	*Pseudomonas aeruginosa*
1167	P1M10000048A03	*Pseudomonas aeruginosa*
1168	P1M10000049E08	*Pseudomonas aeruginosa*
1169	P1M10000049G10	*Pseudomonas aeruginosa*
1170	P1M10000050G11	*Pseudomonas aeruginosa*
1171	P1M10000051D11	*Pseudomonas aeruginosa*
1172	P1M10000051F01	*Pseudomonas aeruginosa*
1173	P1M10000052C03	*Pseudomonas aeruginosa*
1174	P1M10000052C12	*Pseudomonas aeruginosa*
1175	P1M10000052E04	*Pseudomonas aeruginosa*
1176	P1M10000053B12	*Pseudomonas aeruginosa*
1177	P1M10000053C02	*Pseudomonas aeruginosa*
1178	P1M10000053E07	*Pseudomonas aeruginosa*
1179	P1M10000053F08	*Pseudomonas aeruginosa*
1180	P1M10000055A11	*Pseudomonas aeruginosa*

SeqID	Clone name	Organism
1181	P1M10000055C08	*Pseudomonas aeruginosa*
1182	P1M10000055E05	*Pseudomonas aeruginosa*
1183	P1M10000056C07	*Pseudomonas aeruginosa*
1184	P1M10000056F05	*Pseudomonas aeruginosa*
1185	P1M10000056F06	*Pseudomonas aeruginosa*
1186	P1M10000056G01	*Pseudomonas aeruginosa*
1187	P1M10000058B07	*Pseudomonas aeruginosa*
1188	P1M10000059B04	*Pseudomonas aeruginosa*
1189	P1M10000059B10	*Pseudomonas aeruginosa*
1190	P1M10000059B11	*Pseudomonas aeruginosa*
1191	P1M10000059D11	*Pseudomonas aeruginosa*
1192	P1M10000059H08	*Pseudomonas aeruginosa*
1193	P1M10000059H09	*Pseudomonas aeruginosa*
1194	P1M10000060E03	*Pseudomonas aeruginosa*
1195	P1M10000060H02	*Pseudomonas aeruginosa*
1196	P1M10000060H04	*Pseudomonas aeruginosa*
1197	P1M10000061B04	*Pseudomonas aeruginosa*
1198	P1M10000061E04	*Pseudomonas aeruginosa*
1199	P1M10000061F04	*Pseudomonas aeruginosa*
1200	P1M10000062A12	*Pseudomonas aeruginosa*
1201	P1M10000062C03	*Pseudomonas aeruginosa*
1202	P1M10000062C04	*Pseudomonas aeruginosa*
1203	P1M10000062C07	*Pseudomonas aeruginosa*
1204	P1M10000062C12	*Pseudomonas aeruginosa*
1205	P1M10000062D07	*Pseudomonas aeruginosa*
1206	P1M10000062D08	*Pseudomonas aeruginosa*
1207	P1M10000062E08	*Pseudomonas aeruginosa*
1208	P1M10000062F06	*Pseudomonas aeruginosa*
1209	P1M10000062G11	*Pseudomonas aeruginosa*
1210	P1M10000062H01	*Pseudomonas aeruginosa*
1211	P1M10000062H04	*Pseudomonas aeruginosa*
1212	P1M10000063F02	*Pseudomonas aeruginosa*
1213	P1M10000063G02	*Pseudomonas aeruginosa*
1214	P1M10000063H02	*Pseudomonas aeruginosa*
1215	P1M10000064A10	*Pseudomonas aeruginosa*
1216	P1M10000064C02	*Pseudomonas aeruginosa*
1217	P1M10000064C03	*Pseudomonas aeruginosa*
1218	P1M10000064D03	*Pseudomonas aeruginosa*
1219	P1M10000064E05	*Pseudomonas aeruginosa*
1220	P1M10000064G12	*Pseudomonas aeruginosa*
1221	P1M10000064H07	*Pseudomonas aeruginosa*
1222	P1M10000065A04	*Pseudomonas aeruginosa*
1223	P1M10000065B07	*Pseudomonas aeruginosa*
1224	P1M10000065C03	*Pseudomonas aeruginosa*
1225	P1M10000065C05	*Pseudomonas aeruginosa*
1226	P1M10000065D06	*Pseudomonas aeruginosa*
1227	P1M10000065F01	*Pseudomonas aeruginosa*

SeqID	Clone name	Organism
1228	P1M10000065G06	*Pseudomonas aeruginosa*
1229	P1M10000065H07	*Pseudomonas aeruginosa*
1230	P1M10000066A10	*Pseudomonas aeruginosa*
1231	P1M10000066A11	*Pseudomonas aeruginosa*
1232	P1M10000066F04	*Pseudomonas aeruginosa*
1233	P1M10000067A05	*Pseudomonas aeruginosa*
1234	P1M10000067A06	*Pseudomonas aeruginosa*
1235	P1M10000067A08	*Pseudomonas aeruginosa*
1236	P1M10000067C04	*Pseudomonas aeruginosa*
1237	P1M10000067C06	*Pseudomonas aeruginosa*
1238	P1M10000067D05	*Pseudomonas aeruginosa*
1239	P1M10000067F05	*Pseudomonas aeruginosa*
1240	P1M10000067G05	*Pseudomonas aeruginosa*
1241	P1M10000068A09	*Pseudomonas aeruginosa*
1242	P1M10000068D04	*Pseudomonas aeruginosa*
1243	P1M10000068F04	*Pseudomonas aeruginosa*
1244	P1M10000068F08	*Pseudomonas aeruginosa*
1245	P1M10000068G01	*Pseudomonas aeruginosa*
1246	P1M10000068H05	*Pseudomonas aeruginosa*
1247	P1M10000069D09	*Pseudomonas aeruginosa*
1248	P1M10000069G06	*Pseudomonas aeruginosa*
1249	P1M10000069H02	*Pseudomonas aeruginosa*
1250	P1M10000070A05	*Pseudomonas aeruginosa*
1251	P1M10000070B10	*Pseudomonas aeruginosa*
1252	P1M10000070C06	*Pseudomonas aeruginosa*
1253	P1M10000070D08	*Pseudomonas aeruginosa*
1254	P1M10000070E03	*Pseudomonas aeruginosa*
1255	P1M10000070G06	*Pseudomonas aeruginosa*
1256	P1M10000070G12	*Pseudomonas aeruginosa*
1257	P1M10000070H06	*Pseudomonas aeruginosa*
1258	P1M10000071A03	*Pseudomonas aeruginosa*
1259	P1M10000071C01	*Pseudomonas aeruginosa*
1260	P1M10000071E04	*Pseudomonas aeruginosa*
1261	P1M10000071F01	*Pseudomonas aeruginosa*
1262	P1M10000073A06	*Pseudomonas aeruginosa*
1263	P1M10000073B10	*Pseudomonas aeruginosa*
1264	P1M10000073D04	*Pseudomonas aeruginosa*
1265	P1M10000073D09	*Pseudomonas aeruginosa*
1266	P1M10000073G03	*Pseudomonas aeruginosa*
1267	P1M10000074B01	*Pseudomonas aeruginosa*
1268	P1M10000074B04	*Pseudomonas aeruginosa*
1269	P1M10000074E04	*Pseudomonas aeruginosa*
1270	P1M10000074E09	*Pseudomonas aeruginosa*
1271	P1M10000074F10	*Pseudomonas aeruginosa*
1272	P1M10000074G12	*Pseudomonas aeruginosa*
1273	P1M10000075A04	*Pseudomonas aeruginosa*
1274	P1M10000075B03	*Pseudomonas aeruginosa*

SeqID	Clone name	Organism
1275	P1M10000075F02	*Pseudomonas aeruginosa*
1276	P1M10000075G05	*Pseudomonas aeruginosa*
1277	P1M10000076D05	*Pseudomonas aeruginosa*
1278	P1M10000076D10	*Pseudomonas aeruginosa*
1279	P1M10000077A08	*Pseudomonas aeruginosa*
1280	P1M10000077C08	*Pseudomonas aeruginosa*
1281	P1M10000077E04	*Pseudomonas aeruginosa*
1282	P1M10000077H05	*Pseudomonas aeruginosa*
1283	P1M10000079A10	*Pseudomonas aeruginosa*
1284	P1M10000079B10	*Pseudomonas aeruginosa*
1285	P1M10000079C10	*Pseudomonas aeruginosa*
1286	P1M10000079D01	*Pseudomonas aeruginosa*
1287	P1M10000079D10	*Pseudomonas aeruginosa*
1288	P1M10000079F06	*Pseudomonas aeruginosa*
1289	P1M10000080B01	*Pseudomonas aeruginosa*
1290	P1M10000080B06	*Pseudomonas aeruginosa*
1291	P1M10000080C01	*Pseudomonas aeruginosa*
1292	P1M10000080C06	*Pseudomonas aeruginosa*
1293	P1M10000080E04	*Pseudomonas aeruginosa*
1294	P1M10000081D12	*Pseudomonas aeruginosa*
1295	P1M10000081G05	*Pseudomonas aeruginosa*
1296	P1M10000081H05	*Pseudomonas aeruginosa*
1297	P1M10000082A05	*Pseudomonas aeruginosa*
1298	P1M10000082B04	*Pseudomonas aeruginosa*
1299	P1M10000082C05	*Pseudomonas aeruginosa*
1300	P1M10000082D05	*Pseudomonas aeruginosa*
1301	P1M10000082E05	*Pseudomonas aeruginosa*
1302	P1M10000083A11	*Pseudomonas aeruginosa*
1303	P1M10000083B01	*Pseudomonas aeruginosa*
1304	P1M10000083B12	*Pseudomonas aeruginosa*
1305	P1M10000083C11	*Pseudomonas aeruginosa*
1306	P1M10000083C12	*Pseudomonas aeruginosa*
1307	P1M10000084A04	*Pseudomonas aeruginosa*
1308	P1M10000084D03	*Pseudomonas aeruginosa*
1309	P1M10000084E04	*Pseudomonas aeruginosa*
1310	P1M10000084E11	*Pseudomonas aeruginosa*
1311	P1M10000084F08	*Pseudomonas aeruginosa*
1312	P1M10000085D06	*Pseudomonas aeruginosa*
1313	P1M10000086A02	*Pseudomonas aeruginosa*
1314	P1M10000086B01	*Pseudomonas aeruginosa*
1315	P1M10000086D02	*Pseudomonas aeruginosa*
1316	P1M10000086E05	*Pseudomonas aeruginosa*
1317	P1M10000087A11	*Pseudomonas aeruginosa*
1318	P1M10000087C09	*Pseudomonas aeruginosa*
1319	P1M10000087E04	*Pseudomonas aeruginosa*
1320	P1M10000087F04	*Pseudomonas aeruginosa*
1321	P1M10000087F09	*Pseudomonas aeruginosa*

SeqID	Clone name	Organism
1322	P1M10000088A07	*Pseudomonas aeruginosa*
1323	P1M10000088D06	*Pseudomonas aeruginosa*
1324	P1M10000089C08	*Pseudomonas aeruginosa*
1325	P1M10000089D11	*Pseudomonas aeruginosa*
1326	P1M10000089G08	*Pseudomonas aeruginosa*
1327	P1M10000090B11	*Pseudomonas aeruginosa*
1328	P1M10000090F06	*Pseudomonas aeruginosa*
1329	P1M10000090F08	*Pseudomonas aeruginosa*
1330	P1M10000091D02	*Pseudomonas aeruginosa*
1331	P1M10000091E09	*Pseudomonas aeruginosa*
1332	P1M10000091G10	*Pseudomonas aeruginosa*
1333	P1M10000092B02	*Pseudomonas aeruginosa*
1334	P1M10000092B10	*Pseudomonas aeruginosa*
1335	P1M10000092D09	*Pseudomonas aeruginosa*
1336	P1M10000092E02	*Pseudomonas aeruginosa*
1337	P1M10000092F05	*Pseudomonas aeruginosa*
1338	P1M10000093A03	*Pseudomonas aeruginosa*
1339	P1M10000093B09	*Pseudomonas aeruginosa*
1340	P1M10000093C08	*Pseudomonas aeruginosa*
1341	P1M10000093E09	*Pseudomonas aeruginosa*
1342	P1M10000093F03	*Pseudomonas aeruginosa*
1343	P1M10000093H07	*Pseudomonas aeruginosa*
1344	P1M10000094F04	*Pseudomonas aeruginosa*
1345	P1M10000094H03	*Pseudomonas aeruginosa*
1346	P1M10000095C01	*Pseudomonas aeruginosa*
1347	P1M10000095C09	*Pseudomonas aeruginosa*
1348	P1M10000095E04	*Pseudomonas aeruginosa*
1349	P1M10000095G04	*Pseudomonas aeruginosa*
1350	P1M10000096E04	*Pseudomonas aeruginosa*
1351	P1M10000096E12	*Pseudomonas aeruginosa*
1352	ID2	*Pseudomonas aeruginosa*
1353	4.1	*Pseudomonas aeruginosa*
1354	S1M10000001A05	*Staphylococcus aureus*
1355	S1M10000001A08	*Staphylococcus aureus*
1356	S1M10000001A09	*Staphylococcus aureus*
1357	S1M10000001A10	*Staphylococcus aureus*
1358	S1M10000001C06	*Staphylococcus aureus*
1359	S1M10000001D01	*Staphylococcus aureus*
1360	S1M10000001D02	*Staphylococcus aureus*
1361	S1M10000001D06	*Staphylococcus aureus*
1362	S1M10000001D07	*Staphylococcus aureus*
1363	S1M10000001E02	*Staphylococcus aureus*
1364	S1M10000001E04	*Staphylococcus aureus*
1365	S1M10000001E05	*Staphylococcus aureus*
1366	S1M10000001E09	*Staphylococcus aureus*
1367	S1M10000001E10	*Staphylococcus aureus*
1368	S1M10000001E11	*Staphylococcus aureus*

SeqID	Clone name	Organism
1369	S1M10000001F02	*Staphylococcus aureus*
1370	S1M10000001F04	*Staphylococcus aureus*
1371	S1M10000001F08	*Staphylococcus aureus*
1372	S1M10000001F09	*Staphylococcus aureus*
1373	S1M10000001F10	*Staphylococcus aureus*
1374	S1M10000001F11	*Staphylococcus aureus*
1375	S1M10000001G01	*Staphylococcus aureus*
1376	S1M10000001G07	*Staphylococcus aureus*
1377	S1M10000001G08	*Staphylococcus aureus*
1378	S1M10000001G10	*Staphylococcus aureus*
1379	S1M10000002A02	*Staphylococcus aureus*
1380	S1M10000002A09	*Staphylococcus aureus*
1381	S1M10000002A10	*Staphylococcus aureus*
1382	S1M10000002A12	*Staphylococcus aureus*
1383	S1M10000002B01	*Staphylococcus aureus*
1384	S1M10000002B03	*Staphylococcus aureus*
1385	S1M10000002B04	*Staphylococcus aureus*
1386	S1M10000002B05	*Staphylococcus aureus*
1387	S1M10000002B06	*Staphylococcus aureus*
1388	S1M10000002B07	*Staphylococcus aureus*
1389	S1M10000002B09	*Staphylococcus aureus*
1390	S1M10000002B11	*Staphylococcus aureus*
1391	S1M10000002C02	*Staphylococcus aureus*
1392	S1M10000002C09	*Staphylococcus aureus*
1393	S1M10000002C10	*Staphylococcus aureus*
1394	S1M10000002C11	*Staphylococcus aureus*
1395	S1M10000002C12	*Staphylococcus aureus*
1396	S1M10000002D01	*Staphylococcus aureus*
1397	S1M10000002D02	*Staphylococcus aureus*
1398	S1M10000002D03	*Staphylococcus aureus*
1399	S1M10000002D05	*Staphylococcus aureus*
1400	S1M10000002D07	*Staphylococcus aureus*
1401	S1M10000002D08	*Staphylococcus aureus*
1402	S1M10000002D10	*Staphylococcus aureus*
1403	S1M10000002D12	*Staphylococcus aureus*
1404	S1M10000002E01	*Staphylococcus aureus*
1405	S1M10000002E02	*Staphylococcus aureus*
1406	S1M10000002E07	*Staphylococcus aureus*
1407	S1M10000002E09	*Staphylococcus aureus*
1408	S1M10000002E11	*Staphylococcus aureus*
1409	S1M10000002E12	*Staphylococcus aureus*
1410	S1M10000002F01	*Staphylococcus aureus*
1411	S1M10000002F02	*Staphylococcus aureus*
1412	S1M10000002F04	*Staphylococcus aureus*
1413	S1M10000002F09	*Staphylococcus aureus*
1414	S1M10000002F12	*Staphylococcus aureus*
1415	S1M10000002G01	*Staphylococcus aureus*

SeqID	Clone name	Organism
1416	S1M10000002G03	*Staphylococcus aureus*
1417	S1M10000002G05	*Staphylococcus aureus*
1418	S1M10000002G06	*Staphylococcus aureus*
1419	S1M10000002G07	*Staphylococcus aureus*
1420	S1M10000002G08	*Staphylococcus aureus*
1421	S1M10000002G09	*Staphylococcus aureus*
1422	S1M10000002G10	*Staphylococcus aureus*
1423	S1M10000002G11	*Staphylococcus aureus*
1424	S1M10000002G12	*Staphylococcus aureus*
1425	S1M10000003A01	*Staphylococcus aureus*
1426	S1M10000003A02	*Staphylococcus aureus*
1427	S1M10000003A03	*Staphylococcus aureus*
1428	S1M10000003A04	*Staphylococcus aureus*
1429	S1M10000003A06	*Staphylococcus aureus*
1430	S1M10000003A07	*Staphylococcus aureus*
1431	S1M10000003A08	*Staphylococcus aureus*
1432	S1M10000003A10	*Staphylococcus aureus*
1433	S1M10000003A11	*Staphylococcus aureus*
1434	S1M10000003B06	*Staphylococcus aureus*
1435	S1M10000003B08	*Staphylococcus aureus*
1436	S1M10000003B09	*Staphylococcus aureus*
1437	S1M10000003B12	*Staphylococcus aureus*
1438	S1M10000003C06	*Staphylococcus aureus*
1439	S1M10000003C07	*Staphylococcus aureus*
1440	S1M10000003C10	*Staphylococcus aureus*
1441	S1M10000003C12	*Staphylococcus aureus*
1442	S1M10000003D05	*Staphylococcus aureus*
1443	S1M10000003D06	*Staphylococcus aureus*
1444	S1M10000003D08	*Staphylococcus aureus*
1445	S1M10000003D10	*Staphylococcus aureus*
1446	S1M10000003E07	*Staphylococcus aureus*
1447	S1M10000003E09	*Staphylococcus aureus*
1448	S1M10000003E10	*Staphylococcus aureus*
1449	S1M10000003E11	*Staphylococcus aureus*
1450	S1M10000003F02	*Staphylococcus aureus*
1451	S1M10000003F05	*Staphylococcus aureus*
1452	S1M10000003F06	*Staphylococcus aureus*
1453	S1M10000003F07	*Staphylococcus aureus*
1454	S1M10000003F08	*Staphylococcus aureus*
1455	S1M10000003F12	*Staphylococcus aureus*
1456	S1M10000003G03	*Staphylococcus aureus*
1457	S1M10000003G04	*Staphylococcus aureus*
1458	S1M10000003G08	*Staphylococcus aureus*
1459	S1M10000003G10	*Staphylococcus aureus*
1460	S1M10000004A04	*Staphylococcus aureus*
1461	S1M10000004A06	*Staphylococcus aureus*
1462	S1M10000004A07	*Staphylococcus aureus*

SeqID	Clone name	Organism
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1464	S1M10000004A12	*Staphylococcus aureus*
1465	S1M10000004B03	*Staphylococcus aureus*
1466	S1M10000004B04	*Staphylococcus aureus*
1467	S1M10000004B06	*Staphylococcus aureus*
1468	S1M10000004B08	*Staphylococcus aureus*
1469	S1M10000004B09	*Staphylococcus aureus*
1470	S1M10000004B11	*Staphylococcus aureus*
1471	S1M10000004C01	*Staphylococcus aureus*
1472	S1M10000004C02	*Staphylococcus aureus*
1473	S1M10000004C03	*Staphylococcus aureus*
1474	S1M10000004C06	*Staphylococcus aureus*
1475	S1M10000004C07	*Staphylococcus aureus*
1476	S1M10000004C08	*Staphylococcus aureus*
1477	S1M10000004C09	*Staphylococcus aureus*
1478	S1M10000004C10	*Staphylococcus aureus*
1479	S1M10000004C12	*Staphylococcus aureus*
1480	S1M10000004D01	*Staphylococcus aureus*
1481	S1M10000004D03	*Staphylococcus aureus*
1482	S1M10000004D04	*Staphylococcus aureus*
1483	S1M10000004D06	*Staphylococcus aureus*
1484	S1M10000004D07	*Staphylococcus aureus*
1485	S1M10000004D08	*Staphylococcus aureus*
1486	S1M10000004D10	*Staphylococcus aureus*
1487	S1M10000004D12	*Staphylococcus aureus*
1488	S1M10000004E03	*Staphylococcus aureus*
1489	S1M10000004E04	*Staphylococcus aureus*
1490	S1M10000004E06	*Staphylococcus aureus*
1491	S1M10000004E07	*Staphylococcus aureus*
1492	S1M10000004E11	*Staphylococcus aureus*
1493	S1M10000004E12	*Staphylococcus aureus*
1494	S1M10000004F01	*Staphylococcus aureus*
1495	S1M10000004F02	*Staphylococcus aureus*
1496	S1M10000004F06	*Staphylococcus aureus*
1497	S1M10000004F07	*Staphylococcus aureus*
1498	S1M10000004F08	*Staphylococcus aureus*
1499	S1M10000004F09	*Staphylococcus aureus*
1500	S1M10000004F12	*Staphylococcus aureus*
1501	S1M10000004G01	*Staphylococcus aureus*
1502	S1M10000004G02	*Staphylococcus aureus*
1503	S1M10000004G03	*Staphylococcus aureus*
1504	S1M10000004G05	*Staphylococcus aureus*
1505	S1M10000004G06	*Staphylococcus aureus*
1506	S1M10000004G07	*Staphylococcus aureus*
1507	S1M10000004G09	*Staphylococcus aureus*
1508	S1M10000004G12	*Staphylococcus aureus*
1509	S1M10000005A01	*Staphylococcus aureus*

SeqID	Clone name	Organism
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1511	S1M10000005A05	*Staphylococcus aureus*
1512	S1M10000005A06	*Staphylococcus aureus*
1513	S1M10000005A07	*Staphylococcus aureus*
1514	S1M10000005A08	*Staphylococcus aureus*
1515	S1M10000005A09	*Staphylococcus aureus*
1516	S1M10000005A10	*Staphylococcus aureus*
1517	S1M10000005A11	*Staphylococcus aureus*
1518	S1M10000005B02	*Staphylococcus aureus*
1519	S1M10000005B04	*Staphylococcus aureus*
1520	S1M10000005B07	*Staphylococcus aureus*
1521	S1M10000005B08	*Staphylococcus aureus*
1522	S1M10000005B09	*Staphylococcus aureus*
1523	S1M10000005B12	*Staphylococcus aureus*
1524	S1M10000005C01	*Staphylococcus aureus*
1525	S1M10000005C05	*Staphylococcus aureus*
1526	S1M10000005C06	*Staphylococcus aureus*
1527	S1M10000005C09	*Staphylococcus aureus*
1528	S1M10000005C11	*Staphylococcus aureus*
1529	S1M10000005D01	*Staphylococcus aureus*
1530	S1M10000005D02	*Staphylococcus aureus*
1531	S1M10000005D03	*Staphylococcus aureus*
1532	S1M10000005D04	*Staphylococcus aureus*
1533	S1M10000005D05	*Staphylococcus aureus*
1534	S1M10000005D06	*Staphylococcus aureus*
1535	S1M10000005D07	*Staphylococcus aureus*
1536	S1M10000005D08	*Staphylococcus aureus*
1537	S1M10000005D09	*Staphylococcus aureus*
1538	S1M10000005D11	*Staphylococcus aureus*
1539	S1M10000005D12	*Staphylococcus aureus*
1540	S1M10000005E01	*Staphylococcus aureus*
1541	S1M10000005E02	*Staphylococcus aureus*
1542	S1M10000005E05	*Staphylococcus aureus*
1543	S1M10000005E06	*Staphylococcus aureus*
1544	S1M10000005E07	*Staphylococcus aureus*
1545	S1M10000005E08	*Staphylococcus aureus*
1546	S1M10000005E10	*Staphylococcus aureus*
1547	S1M10000005E11	*Staphylococcus aureus*
1548	S1M10000005E12	*Staphylococcus aureus*
1549	S1M10000005F02	*Staphylococcus aureus*
1550	S1M10000005F03	*Staphylococcus aureus*
1551	S1M10000005F04	*Staphylococcus aureus*
1552	S1M10000006A03	*Staphylococcus aureus*
1553	S1M10000006A04	*Staphylococcus aureus*
1554	S1M10000006A05	*Staphylococcus aureus*
1555	S1M10000006A07	*Staphylococcus aureus*
1556	S1M10000006A08	*Staphylococcus aureus*

SeqID	Clone name	Organism
1557	S1M10000006A10	*Staphylococcus aureus*
1558	S1M10000006A12	*Staphylococcus aureus*
1559	S1M10000006B02	*Staphylococcus aureus*
1560	S1M10000006B03	*Staphylococcus aureus*
1561	S1M10000006B04	*Staphylococcus aureus*
1562	S1M10000006B07	*Staphylococcus aureus*
1563	S1M10000006B10	*Staphylococcus aureus*
1564	S1M10000006B11	*Staphylococcus aureus*
1565	S1M10000006C02	*Staphylococcus aureus*
1566	S1M10000006C04	*Staphylococcus aureus*
1567	S1M10000006C06	*Staphylococcus aureus*
1568	S1M10000006C07	*Staphylococcus aureus*
1569	S1M10000006C08	*Staphylococcus aureus*
1570	S1M10000006C10	*Staphylococcus aureus*
1571	S1M10000006D03	*Staphylococcus aureus*
1572	S1M10000006D05	*Staphylococcus aureus*
1573	S1M10000006D06	*Staphylococcus aureus*
1574	S1M10000006D07	*Staphylococcus aureus*
1575	S1M10000006D08	*Staphylococcus aureus*
1576	S1M10000006E02	*Staphylococcus aureus*
1577	S1M10000006E03	*Staphylococcus aureus*
1578	S1M10000006E04	*Staphylococcus aureus*
1579	S1M10000006E07	*Staphylococcus aureus*
1580	S1M10000006E08	*Staphylococcus aureus*
1581	S1M10000006F01	*Staphylococcus aureus*
1582	S1M10000006F02	*Staphylococcus aureus*
1583	S1M10000006F03	*Staphylococcus aureus*
1584	S1M10000006F04	*Staphylococcus aureus*
1585	S1M10000006F06	*Staphylococcus aureus*
1586	S1M10000006G02	*Staphylococcus aureus*
1587	S1M10000006G03	*Staphylococcus aureus*
1588	S1M10000006G05	*Staphylococcus aureus*
1589	S1M10000006G06	*Staphylococcus aureus*
1590	S1M10000006G07	*Staphylococcus aureus*
1591	S1M10000006G09	*Staphylococcus aureus*
1592	S1M10000006G10	*Staphylococcus aureus*
1593	S1M10000006G11	*Staphylococcus aureus*
1594	S1M10000007A02	*Staphylococcus aureus*
1595	S1M10000007A03	*Staphylococcus aureus*
1596	S1M10000007B02	*Staphylococcus aureus*
1597	S1M10000007B11	*Staphylococcus aureus*
1598	S1M10000007C02	*Staphylococcus aureus*
1599	S1M10000007C04	*Staphylococcus aureus*
1600	S1M10000007C05	*Staphylococcus aureus*
1601	S1M10000007C06	*Staphylococcus aureus*
1602	S1M10000007C07	*Staphylococcus aureus*
1603	S1M10000007C08	*Staphylococcus aureus*

SeqID	Clone name	Organism
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1605	S1M10000007D03	*Staphylococcus aureus*
1606	S1M10000007D06	*Staphylococcus aureus*
1607	S1M10000007D08	*Staphylococcus aureus*
1608	S1M10000007D10	*Staphylococcus aureus*
1609	S1M10000007D11	*Staphylococcus aureus*
1610	S1M10000007E04	*Staphylococcus aureus*
1611	S1M10000007E06	*Staphylococcus aureus*
1612	S1M10000007E07	*Staphylococcus aureus*
1613	S1M10000007F01	*Staphylococcus aureus*
1614	S1M10000007F02	*Staphylococcus aureus*
1615	S1M10000007F04	*Staphylococcus aureus*
1616	S1M10000007F08	*Staphylococcus aureus*
1617	S1M10000007F09	*Staphylococcus aureus*
1618	S1M10000007F10	*Staphylococcus aureus*
1619	S1M10000007F11	*Staphylococcus aureus*
1620	S1M10000007F12	*Staphylococcus aureus*
1621	S1M10000007G02	*Staphylococcus aureus*
1622	S1M10000007G03	*Staphylococcus aureus*
1623	S1M10000007G05	*Staphylococcus aureus*
1624	S1M10000007G07	*Staphylococcus aureus*
1625	S1M10000007G08	*Staphylococcus aureus*
1626	S1M10000008A03	*Staphylococcus aureus*
1627	S1M10000008A04	*Staphylococcus aureus*
1628	S1M10000008A05	*Staphylococcus aureus*
1629	S1M10000008A08	*Staphylococcus aureus*
1630	S1M10000008A09	*Staphylococcus aureus*
1631	S1M10000008A12	*Staphylococcus aureus*
1632	S1M10000008B03	*Staphylococcus aureus*
1633	S1M10000008B04	*Staphylococcus aureus*
1634	S1M10000008B06	*Staphylococcus aureus*
1635	S1M10000008B08	*Staphylococcus aureus*
1636	S1M10000008B09	*Staphylococcus aureus*
1637	S1M10000008B10	*Staphylococcus aureus*
1638	S1M10000008C05	*Staphylococcus aureus*
1639	S1M10000008C06	*Staphylococcus aureus*
1640	S1M10000008C07	*Staphylococcus aureus*
1641	S1M10000008C08	*Staphylococcus aureus*
1642	S1M10000008C09	*Staphylococcus aureus*
1643	S1M10000008D05	*Staphylococcus aureus*
1644	S1M10000008D09	*Staphylococcus aureus*
1645	S1M10000008E05	*Staphylococcus aureus*
1646	S1M10000008E08	*Staphylococcus aureus*
1647	S1M10000008E09	*Staphylococcus aureus*
1648	S1M10000008E10	*Staphylococcus aureus*
1649	S1M10000008F01	*Staphylococcus aureus*
1650	S1M10000008F02	*Staphylococcus aureus*

SeqID	Clone name	Organism
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1652	S1M10000008F06	*Staphylococcus aureus*
1653	S1M10000008F08	*Staphylococcus aureus*
1654	S1M10000008F09	*Staphylococcus aureus*
1655	S1M10000008F10	*Staphylococcus aureus*
1656	S1M10000008F11	*Staphylococcus aureus*
1657	S1M10000008G02	*Staphylococcus aureus*
1658	S1M10000008G03	*Staphylococcus aureus*
1659	S1M10000008G05	*Staphylococcus aureus*
1660	S1M10000009A02	*Staphylococcus aureus*
1661	S1M10000009A04	*Staphylococcus aureus*
1662	S1M10000009A07	*Staphylococcus aureus*
1663	S1M10000009A08	*Staphylococcus aureus*
1664	S1M10000009A09	*Staphylococcus aureus*
1665	S1M10000009A10	*Staphylococcus aureus*
1666	S1M10000009A11	*Staphylococcus aureus*
1667	S1M10000009B01	*Staphylococcus aureus*
1668	S1M10000009B02	*Staphylococcus aureus*
1669	S1M10000009B03	*Staphylococcus aureus*
1670	S1M10000009B04	*Staphylococcus aureus*
1671	S1M10000009B05	*Staphylococcus aureus*
1672	S1M10000009B06	*Staphylococcus aureus*
1673	S1M10000009B07	*Staphylococcus aureus*
1674	S1M10000009B10	*Staphylococcus aureus*
1675	S1M10000009B11	*Staphylococcus aureus*
1676	S1M10000009B12	*Staphylococcus aureus*
1677	S1M10000009C01	*Staphylococcus aureus*
1678	S1M10000009C02	*Staphylococcus aureus*
1679	S1M10000009C05	*Staphylococcus aureus*
1680	S1M10000009C06	*Staphylococcus aureus*
1681	S1M10000009C07	*Staphylococcus aureus*
1682	S1M10000009C08	*Staphylococcus aureus*
1683	S1M10000009C09	*Staphylococcus aureus*
1684	S1M10000009C10	*Staphylococcus aureus*
1685	S1M10000009C11	*Staphylococcus aureus*
1686	S1M10000009D01	*Staphylococcus aureus*
1687	S1M10000009D02	*Staphylococcus aureus*
1688	S1M10000009D03	*Staphylococcus aureus*
1689	S1M10000009D04	*Staphylococcus aureus*
1690	S1M10000009D05	*Staphylococcus aureus*
1691	S1M10000009D07	*Staphylococcus aureus*
1692	S1M10000009D09	*Staphylococcus aureus*
1693	S1M10000009D11	*Staphylococcus aureus*
1694	S1M10000009E02	*Staphylococcus aureus*
1695	S1M10000009E06	*Staphylococcus aureus*
1696	S1M10000009E08	*Staphylococcus aureus*
1697	S1M10000009E09	*Staphylococcus aureus*

SeqID	Clone name	Organism
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1699	S1M10000009E12	*Staphylococcus aureus*
1700	S1M10000009F01	*Staphylococcus aureus*
1701	S1M10000009F02	*Staphylococcus aureus*
1702	S1M10000009F03	*Staphylococcus aureus*
1703	S1M10000009F05	*Staphylococcus aureus*
1704	S1M10000009F06	*Staphylococcus aureus*
1705	S1M10000009F07	*Staphylococcus aureus*
1706	S1M10000009F09	*Staphylococcus aureus*
1707	S1M10000009F10	*Staphylococcus aureus*
1708	S1M10000009G02	*Staphylococcus aureus*
1709	S1M10000009G03	*Staphylococcus aureus*
1710	S1M10000009G05	*Staphylococcus aureus*
1711	S1M10000009G06	*Staphylococcus aureus*
1712	S1M10000009G07	*Staphylococcus aureus*
1713	S1M10000009G09	*Staphylococcus aureus*
1714	S1M10000009G10	*Staphylococcus aureus*
1715	S1M10000009G11	*Staphylococcus aureus*
1716	S1M10000009H01	*Staphylococcus aureus*
1717	S1M10000009H02	*Staphylococcus aureus*
1718	S1M10000009H03	*Staphylococcus aureus*
1719	S1M10000009H05	*Staphylococcus aureus*
1720	S1M10000009H07	*Staphylococcus aureus*
1721	S1M10000009H09	*Staphylococcus aureus*
1722	S1M10000009H11	*Staphylococcus aureus*
1723	S1M10000011A02	*Staphylococcus aureus*
1724	S1M10000011A03	*Staphylococcus aureus*
1725	S1M10000011A04	*Staphylococcus aureus*
1726	S1M10000011A06	*Staphylococcus aureus*
1727	S1M10000011B01	*Staphylococcus aureus*
1728	S1M10000011B02	*Staphylococcus aureus*
1729	S1M10000011B03	*Staphylococcus aureus*
1730	S1M10000011B04	*Staphylococcus aureus*
1731	S1M10000011B05	*Staphylococcus aureus*
1732	S1M10000011C01	*Staphylococcus aureus*
1733	S1M10000011C05	*Staphylococcus aureus*
1734	S1M10000011C06	*Staphylococcus aureus*
1735	S1M10000011D01	*Staphylococcus aureus*
1736	S1M10000011D02	*Staphylococcus aureus*
1737	S1M10000011D04	*Staphylococcus aureus*
1738	S1M10000011D06	*Staphylococcus aureus*
1739	S1M10000011E02	*Staphylococcus aureus*
1740	S1M10000011E03	*Staphylococcus aureus*
1741	S1M10000011E04	*Staphylococcus aureus*
1742	S1M10000011F01	*Staphylococcus aureus*
1743	S1M10000011F03	*Staphylococcus aureus*
1744	S1M10000011F04	*Staphylococcus aureus*

SeqID	Clone name	Organism
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1746	S1M10000011G01	*Staphylococcus aureus*
1747	S1M10000011G03	*Staphylococcus aureus*
1748	S1M10000011G04	*Staphylococcus aureus*
1749	S1M10000011G05	*Staphylococcus aureus*
1750	S1M10000011G06	*Staphylococcus aureus*
1751	S1M10000011H01	*Staphylococcus aureus*
1752	S1M10000011H03	*Staphylococcus aureus*
1753	S1M10000011H04	*Staphylococcus aureus*
1754	S1M10000012A02	*Staphylococcus aureus*
1755	S1M10000012A06	*Staphylococcus aureus*
1756	S1M10000012A08	*Staphylococcus aureus*
1757	S1M10000012A09	*Staphylococcus aureus*
1758	S1M10000012A10	*Staphylococcus aureus*
1759	S1M10000012A11	*Staphylococcus aureus*
1760	S1M10000012B01	*Staphylococcus aureus*
1761	S1M10000012B05	*Staphylococcus aureus*
1762	S1M10000012B06	*Staphylococcus aureus*
1763	S1M10000012B07	*Staphylococcus aureus*
1764	S1M10000012B11	*Staphylococcus aureus*
1765	S1M10000012C01	*Staphylococcus aureus*
1766	S1M10000012C03	*Staphylococcus aureus*
1767	S1M10000012C04	*Staphylococcus aureus*
1768	S1M10000012C05	*Staphylococcus aureus*
1769	S1M10000012C06	*Staphylococcus aureus*
1770	S1M10000012C11	*Staphylococcus aureus*
1771	S1M10000012C12	*Staphylococcus aureus*
1772	S1M10000012D04	*Staphylococcus aureus*
1773	S1M10000012D06	*Staphylococcus aureus*
1774	S1M10000012D07	*Staphylococcus aureus*
1775	S1M10000012D08	*Staphylococcus aureus*
1776	S1M10000012D09	*Staphylococcus aureus*
1777	S1M10000012D12	*Staphylococcus aureus*
1778	S1M10000012E01	*Staphylococcus aureus*
1779	S1M10000012E02	*Staphylococcus aureus*
1780	S1M10000012E04	*Staphylococcus aureus*
1781	S1M10000012E07	*Staphylococcus aureus*
1782	S1M10000012E08	*Staphylococcus aureus*
1783	S1M10000012E12	*Staphylococcus aureus*
1784	S1M10000012F04	*Staphylococcus aureus*
1785	S1M10000012F07	*Staphylococcus aureus*
1786	S1M10000012F08	*Staphylococcus aureus*
1787	S1M10000012F09	*Staphylococcus aureus*
1788	S1M10000012F10	*Staphylococcus aureus*
1789	S1M10000012F11	*Staphylococcus aureus*
1790	S1M10000012F12	*Staphylococcus aureus*
1791	S1M10000012G01	*Staphylococcus aureus*

SeqID	Clone name	Organism
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1793	S1M10000012G03	*Staphylococcus aureus*
1794	S1M10000012G06	*Staphylococcus aureus*
1795	S1M10000012G07	*Staphylococcus aureus*
1796	S1M10000012G08	*Staphylococcus aureus*
1797	S1M10000012G10	*Staphylococcus aureus*
1798	S1M10000012H05	*Staphylococcus aureus*
1799	S1M10000012H08	*Staphylococcus aureus*
1800	S1M10000012H09	*Staphylococcus aureus*
1801	S1M10000012H10	*Staphylococcus aureus*
1802	S1M10000012H11	*Staphylococcus aureus*
1803	S1M10000013A02	*Staphylococcus aureus*
1804	S1M10000013A03	*Staphylococcus aureus*
1805	S1M10000013A05	*Staphylococcus aureus*
1806	S1M10000013A07	*Staphylococcus aureus*
1807	S1M10000013A08	*Staphylococcus aureus*
1808	S1M10000013A09	*Staphylococcus aureus*
1809	S1M10000013A10	*Staphylococcus aureus*
1810	S1M10000013A11	*Staphylococcus aureus*
1811	S1M10000013A12	*Staphylococcus aureus*
1812	S1M10000013B02	*Staphylococcus aureus*
1813	S1M10000013B03	*Staphylococcus aureus*
1814	S1M10000013B04	*Staphylococcus aureus*
1815	S1M10000013B05	*Staphylococcus aureus*
1816	S1M10000013B06	*Staphylococcus aureus*
1817	S1M10000013B07	*Staphylococcus aureus*
1818	S1M10000013B09	*Staphylococcus aureus*
1819	S1M10000013B11	*Staphylococcus aureus*
1820	S1M10000013C03	*Staphylococcus aureus*
1821	S1M10000013C05	*Staphylococcus aureus*
1822	S1M10000013C07	*Staphylococcus aureus*
1823	S1M10000013C08	*Staphylococcus aureus*
1824	S1M10000013C09	*Staphylococcus aureus*
1825	S1M10000013C10	*Staphylococcus aureus*
1826	S1M10000013C11	*Staphylococcus aureus*
1827	S1M10000013C12	*Staphylococcus aureus*
1828	S1M10000013D08	*Staphylococcus aureus*
1829	S1M10000013D09	*Staphylococcus aureus*
1830	S1M10000013D11	*Staphylococcus aureus*
1831	S1M10000013E01	*Staphylococcus aureus*
1832	S1M10000013E02	*Staphylococcus aureus*
1833	S1M10000013E04	*Staphylococcus aureus*
1834	S1M10000013E06	*Staphylococcus aureus*
1835	S1M10000013E08	*Staphylococcus aureus*
1836	S1M10000013E09	*Staphylococcus aureus*
1837	S1M10000013E10	*Staphylococcus aureus*
1838	S1M10000013F02	*Staphylococcus aureus*

SeqID	Clone name	Organism
1839	S1M10000013F03	*Staphylococcus aureus*
1840	S1M10000013F06	*Staphylococcus aureus*
1841	S1M10000013F07	*Staphylococcus aureus*
1842	S1M10000013F08	*Staphylococcus aureus*
1843	S1M10000013F09	*Staphylococcus aureus*
1844	S1M10000013F12	*Staphylococcus aureus*
1845	S1M10000013G01	*Staphylococcus aureus*
1846	S1M10000013G04	*Staphylococcus aureus*
1847	S1M10000013G05	*Staphylococcus aureus*
1848	S1M10000013G06	*Staphylococcus aureus*
1849	S1M10000013G07	*Staphylococcus aureus*
1850	S1M10000013G10	*Staphylococcus aureus*
1851	S1M10000013G11	*Staphylococcus aureus*
1852	S1M10000013G12	*Staphylococcus aureus*
1853	S1M10000013H03	*Staphylococcus aureus*
1854	S1M10000013H04	*Staphylococcus aureus*
1855	S1M10000013H05	*Staphylococcus aureus*
1856	S1M10000013H07	*Staphylococcus aureus*
1857	S1M10000013H09	*Staphylococcus aureus*
1858	S1M10000013H10	*Staphylococcus aureus*
1859	S1M10000013H11	*Staphylococcus aureus*
1860	S1M10000014A02	*Staphylococcus aureus*
1861	S1M10000014A03	*Staphylococcus aureus*
1862	S1M10000014A05	*Staphylococcus aureus*
1863	S1M10000014A07	*Staphylococcus aureus*
1864	S1M10000014A08	*Staphylococcus aureus*
1865	S1M10000014A11	*Staphylococcus aureus*
1866	S1M10000014A12	*Staphylococcus aureus*
1867	S1M10000014B01	*Staphylococcus aureus*
1868	S1M10000014B02	*Staphylococcus aureus*
1869	S1M10000014B03	*Staphylococcus aureus*
1870	S1M10000014B04	*Staphylococcus aureus*
1871	S1M10000014B05	*Staphylococcus aureus*
1872	S1M10000014B06	*Staphylococcus aureus*
1873	S1M10000014B07	*Staphylococcus aureus*
1874	S1M10000014B08	*Staphylococcus aureus*
1875	S1M10000014B10	*Staphylococcus aureus*
1876	S1M10000014B11	*Staphylococcus aureus*
1877	S1M10000014B12	*Staphylococcus aureus*
1878	S1M10000014C01	*Staphylococcus aureus*
1879	S1M10000014C05	*Staphylococcus aureus*
1880	S1M10000014C06	*Staphylococcus aureus*
1881	S1M10000014C07	*Staphylococcus aureus*
1882	S1M10000014C09	*Staphylococcus aureus*
1883	S1M10000014C10	*Staphylococcus aureus*
1884	S1M10000014C11	*Staphylococcus aureus*
1885	S1M10000014C12	*Staphylococcus aureus*

SeqID	Clone name	Organism
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1887	S1M10000014D06	*Staphylococcus aureus*
1888	S1M10000014D08	*Staphylococcus aureus*
1889	S1M10000014D09	*Staphylococcus aureus*
1890	S1M10000014D10	*Staphylococcus aureus*
1891	S1M10000014E01	*Staphylococcus aureus*
1892	S1M10000014E04	*Staphylococcus aureus*
1893	S1M10000014E05	*Staphylococcus aureus*
1894	S1M10000014E07	*Staphylococcus aureus*
1895	S1M10000014E08	*Staphylococcus aureus*
1896	S1M10000014E09	*Staphylococcus aureus*
1897	S1M10000014E10	*Staphylococcus aureus*
1898	S1M10000014E12	*Staphylococcus aureus*
1899	S1M10000014F02	*Staphylococcus aureus*
1900	S1M10000014F03	*Staphylococcus aureus*
1901	S1M10000014F04	*Staphylococcus aureus*
1902	S1M10000014F05	*Staphylococcus aureus*
1903	S1M10000014F08	*Staphylococcus aureus*
1904	S1M10000014F09	*Staphylococcus aureus*
1905	S1M10000014F10	*Staphylococcus aureus*
1906	S1M10000014G02	*Staphylococcus aureus*
1907	S1M10000014G04	*Staphylococcus aureus*
1908	S1M10000014G06	*Staphylococcus aureus*
1909	S1M10000014G07	*Staphylococcus aureus*
1910	S1M10000014G08	*Staphylococcus aureus*
1911	S1M10000014G12	*Staphylococcus aureus*
1912	S1M10000014H02	*Staphylococcus aureus*
1913	S1M10000014H03	*Staphylococcus aureus*
1914	S1M10000014H04	*Staphylococcus aureus*
1915	S1M10000014H05	*Staphylococcus aureus*
1916	S1M10000014H06	*Staphylococcus aureus*
1917	S1M10000014H07	*Staphylococcus aureus*
1918	S1M10000014H08	*Staphylococcus aureus*
1919	S1M10000014H11	*Staphylococcus aureus*
1920	S1M10000015A02	*Staphylococcus aureus*
1921	S1M10000015A03	*Staphylococcus aureus*
1922	S1M10000015A05	*Staphylococcus aureus*
1923	S1M10000015A06	*Staphylococcus aureus*
1924	S1M10000015A09	*Staphylococcus aureus*
1925	S1M10000015A10	*Staphylococcus aureus*
1926	S1M10000015A11	*Staphylococcus aureus*
1927	S1M10000015A12	*Staphylococcus aureus*
1928	S1M10000015B02	*Staphylococcus aureus*
1929	S1M10000015B05	*Staphylococcus aureus*
1930	S1M10000015B08	*Staphylococcus aureus*
1931	S1M10000015B09	*Staphylococcus aureus*
1932	S1M10000015B10	*Staphylococcus aureus*

SeqID	Clone name	Organism
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1934	S1M10000015C02	*Staphylococcus aureus*
1935	S1M10000015C03	*Staphylococcus aureus*
1936	S1M10000015C05	*Staphylococcus aureus*
1937	S1M10000015C06	*Staphylococcus aureus*
1938	S1M10000015C08	*Staphylococcus aureus*
1939	S1M10000015C10	*Staphylococcus aureus*
1940	S1M10000015C12	*Staphylococcus aureus*
1941	S1M10000015D02	*Staphylococcus aureus*
1942	S1M10000015D03	*Staphylococcus aureus*
1943	S1M10000015D04	*Staphylococcus aureus*
1944	S1M10000015D05	*Staphylococcus aureus*
1945	S1M10000015D06	*Staphylococcus aureus*
1946	S1M10000015D12	*Staphylococcus aureus*
1947	S1M10000015E02	*Staphylococcus aureus*
1948	S1M10000015E03	*Staphylococcus aureus*
1949	S1M10000015E06	*Staphylococcus aureus*
1950	S1M10000015E07	*Staphylococcus aureus*
1951	S1M10000015E09	*Staphylococcus aureus*
1952	S1M10000015E10	*Staphylococcus aureus*
1953	S1M10000015E11	*Staphylococcus aureus*
1954	S1M10000015E12	*Staphylococcus aureus*
1955	S1M10000015F01	*Staphylococcus aureus*
1956	S1M10000015F02	*Staphylococcus aureus*
1957	S1M10000015F03	*Staphylococcus aureus*
1958	S1M10000015F04	*Staphylococcus aureus*
1959	S1M10000015F06	*Staphylococcus aureus*
1960	S1M10000015F07	*Staphylococcus aureus*
1961	S1M10000015F08	*Staphylococcus aureus*
1962	S1M10000015F09	*Staphylococcus aureus*
1963	S1M10000015F10	*Staphylococcus aureus*
1964	S1M10000015G01	*Staphylococcus aureus*
1965	S1M10000015G02	*Staphylococcus aureus*
1966	S1M10000015G03	*Staphylococcus aureus*
1967	S1M10000015G04	*Staphylococcus aureus*
1968	S1M10000015G05	*Staphylococcus aureus*
1969	S1M10000015G06	*Staphylococcus aureus*
1970	S1M10000015G07	*Staphylococcus aureus*
1971	S1M10000015G08	*Staphylococcus aureus*
1972	S1M10000015G09	*Staphylococcus aureus*
1973	S1M10000015G10	*Staphylococcus aureus*
1974	S1M10000015G11	*Staphylococcus aureus*
1975	S1M10000015H04	*Staphylococcus aureus*
1976	S1M10000015H06	*Staphylococcus aureus*
1977	S1M10000016A03	*Staphylococcus aureus*
1978	S1M10000016A04	*Staphylococcus aureus*
1979	S1M10000016A06	*Staphylococcus aureus*

SeqID	Clone name	Organism
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1981	S1M10000016A09	*Staphylococcus aureus*
1982	S1M10000016A10	*Staphylococcus aureus*
1983	S1M10000016A12	*Staphylococcus aureus*
1984	S1M10000016B02	*Staphylococcus aureus*
1985	S1M10000016B05	*Staphylococcus aureus*
1986	S1M10000016B06	*Staphylococcus aureus*
1987	S1M10000016B07	*Staphylococcus aureus*
1988	S1M10000016B08	*Staphylococcus aureus*
1989	S1M10000016B09	*Staphylococcus aureus*
1990	S1M10000016B10	*Staphylococcus aureus*
1991	S1M10000016B11	*Staphylococcus aureus*
1992	S1M10000016B12	*Staphylococcus aureus*
1993	S1M10000016C01	*Staphylococcus aureus*
1994	S1M10000016C02	*Staphylococcus aureus*
1995	S1M10000016C04	*Staphylococcus aureus*
1996	S1M10000016C05	*Staphylococcus aureus*
1997	S1M10000016C06	*Staphylococcus aureus*
1998	S1M10000016C08	*Staphylococcus aureus*
1999	S1M10000016C09	*Staphylococcus aureus*
2000	S1M10000016C10	*Staphylococcus aureus*
2001	S1M10000016C11	*Staphylococcus aureus*
2002	S1M10000016C12	*Staphylococcus aureus*
2003	S1M10000016D01	*Staphylococcus aureus*
2004	S1M10000016D02	*Staphylococcus aureus*
2005	S1M10000016D04	*Staphylococcus aureus*
2006	S1M10000016D05	*Staphylococcus aureus*
2007	S1M10000016D06	*Staphylococcus aureus*
2008	S1M10000016D08	*Staphylococcus aureus*
2009	S1M10000016D09	*Staphylococcus aureus*
2010	S1M10000016D10	*Staphylococcus aureus*
2011	S1M10000016D11	*Staphylococcus aureus*
2012	S1M10000016E04	*Staphylococcus aureus*
2013	S1M10000016E05	*Staphylococcus aureus*
2014	S1M10000016E06	*Staphylococcus aureus*
2015	S1M10000016E07	*Staphylococcus aureus*
2016	S1M10000016E08	*Staphylococcus aureus*
2017	S1M10000016E09	*Staphylococcus aureus*
2018	S1M10000016E10	*Staphylococcus aureus*
2019	S1M10000016E11	*Staphylococcus aureus*
2020	S1M10000016E12	*Staphylococcus aureus*
2021	S1M10000016F02	*Staphylococcus aureus*
2022	S1M10000016F03	*Staphylococcus aureus*
2023	S1M10000016F05	*Staphylococcus aureus*
2024	S1M10000016F06	*Staphylococcus aureus*
2025	S1M10000016F08	*Staphylococcus aureus*
2026	S1M10000016F09	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2028	S1M10000016G01	*Staphylococcus aureus*
2029	S1M10000016G03	*Staphylococcus aureus*
2030	S1M10000016G04	*Staphylococcus aureus*
2031	S1M10000016G05	*Staphylococcus aureus*
2032	S1M10000016H03	*Staphylococcus aureus*
2033	S1M10000016H04	*Staphylococcus aureus*
2034	S1M10000016H08	*Staphylococcus aureus*
2035	S1M10000016H10	*Staphylococcus aureus*
2036	S1M10000017A02	*Staphylococcus aureus*
2037	S1M10000017A03	*Staphylococcus aureus*
2038	S1M10000017A04	*Staphylococcus aureus*
2039	S1M10000017A08	*Staphylococcus aureus*
2040	S1M10000017A11	*Staphylococcus aureus*
2041	S1M10000017A12	*Staphylococcus aureus*
2042	S1M10000017B02	*Staphylococcus aureus*
2043	S1M10000017B05	*Staphylococcus aureus*
2044	S1M10000017B07	*Staphylococcus aureus*
2045	S1M10000017B08	*Staphylococcus aureus*
2046	S1M10000017B09	*Staphylococcus aureus*
2047	S1M10000017B10	*Staphylococcus aureus*
2048	S1M10000017B11	*Staphylococcus aureus*
2049	S1M10000017B12	*Staphylococcus aureus*
2050	S1M10000017C01	*Staphylococcus aureus*
2051	S1M10000017C03	*Staphylococcus aureus*
2052	S1M10000017C05	*Staphylococcus aureus*
2053	S1M10000017C08	*Staphylococcus aureus*
2054	S1M10000017C09	*Staphylococcus aureus*
2055	S1M10000017C10	*Staphylococcus aureus*
2056	S1M10000017C11	*Staphylococcus aureus*
2057	S1M10000017C12	*Staphylococcus aureus*
2058	S1M10000017D03	*Staphylococcus aureus*
2059	S1M10000017D09	*Staphylococcus aureus*
2060	S1M10000017D10	*Staphylococcus aureus*
2061	S1M10000017E04	*Staphylococcus aureus*
2062	S1M10000017E05	*Staphylococcus aureus*
2063	S1M10000017E08	*Staphylococcus aureus*
2064	S1M10000017E11	*Staphylococcus aureus*
2065	S1M10000017F01	*Staphylococcus aureus*
2066	S1M10000017F04	*Staphylococcus aureus*
2067	S1M10000017F05	*Staphylococcus aureus*
2068	S1M10000017F06	*Staphylococcus aureus*
2069	S1M10000017F11	*Staphylococcus aureus*
2070	S1M10000017G02	*Staphylococcus aureus*
2071	S1M10000017G05	*Staphylococcus aureus*
2072	S1M10000017G06	*Staphylococcus aureus*
2073	S1M10000018A03	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2075	S1M10000018A05	*Staphylococcus aureus*
2076	S1M10000018A06	*Staphylococcus aureus*
2077	S1M10000018A08	*Staphylococcus aureus*
2078	S1M10000018A09	*Staphylococcus aureus*
2079	S1M10000018A10	*Staphylococcus aureus*
2080	S1M10000018A11	*Staphylococcus aureus*
2081	S1M10000018B02	*Staphylococcus aureus*
2082	S1M10000018B03	*Staphylococcus aureus*
2083	S1M10000018B05	*Staphylococcus aureus*
2084	S1M10000018B09	*Staphylococcus aureus*
2085	S1M10000018B10	*Staphylococcus aureus*
2086	S1M10000018B11	*Staphylococcus aureus*
2087	S1M10000018C01	*Staphylococcus aureus*
2088	S1M10000018C02	*Staphylococcus aureus*
2089	S1M10000018C03	*Staphylococcus aureus*
2090	S1M10000018C04	*Staphylococcus aureus*
2091	S1M10000018C05	*Staphylococcus aureus*
2092	S1M10000018C06	*Staphylococcus aureus*
2093	S1M10000018C08	*Staphylococcus aureus*
2094	S1M10000018C09	*Staphylococcus aureus*
2095	S1M10000018C10	*Staphylococcus aureus*
2096	S1M10000018C11	*Staphylococcus aureus*
2097	S1M10000018C12	*Staphylococcus aureus*
2098	S1M10000018D01	*Staphylococcus aureus*
2099	S1M10000018D02	*Staphylococcus aureus*
2100	S1M10000018D03	*Staphylococcus aureus*
2101	S1M10000018D04	*Staphylococcus aureus*
2102	S1M10000018D09	*Staphylococcus aureus*
2103	S1M10000018D10	*Staphylococcus aureus*
2104	S1M10000018D11	*Staphylococcus aureus*
2105	S1M10000018D12	*Staphylococcus aureus*
2106	S1M10000018E01	*Staphylococcus aureus*
2107	S1M10000018E02	*Staphylococcus aureus*
2108	S1M10000018E03	*Staphylococcus aureus*
2109	S1M10000018E04	*Staphylococcus aureus*
2110	S1M10000018E05	*Staphylococcus aureus*
2111	S1M10000018E08	*Staphylococcus aureus*
2112	S1M10000018E09	*Staphylococcus aureus*
2113	S1M10000018E11	*Staphylococcus aureus*
2114	S1M10000018E12	*Staphylococcus aureus*
2115	S1M10000018F03	*Staphylococcus aureus*
2116	S1M10000018F04	*Staphylococcus aureus*
2117	S1M10000018F07	*Staphylococcus aureus*
2118	S1M10000018F09	*Staphylococcus aureus*
2119	S1M10000018F10	*Staphylococcus aureus*
2120	S1M10000018F12	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2122	S1M10000018G05	*Staphylococcus aureus*
2123	S1M10000018G07	*Staphylococcus aureus*
2124	S1M10000018G08	*Staphylococcus aureus*
2125	S1M10000018G09	*Staphylococcus aureus*
2126	S1M10000018G10	*Staphylococcus aureus*
2127	S1M10000018G12	*Staphylococcus aureus*
2128	S1M10000018H01	*Staphylococcus aureus*
2129	S1M10000018H02	*Staphylococcus aureus*
2130	S1M10000018H07	*Staphylococcus aureus*
2131	S1M10000018H09	*Staphylococcus aureus*
2132	S1M10000018H10	*Staphylococcus aureus*
2133	S1M10000019A02	*Staphylococcus aureus*
2134	S1M10000019A03	*Staphylococcus aureus*
2135	S1M10000019A05	*Staphylococcus aureus*
2136	S1M10000019A06	*Staphylococcus aureus*
2137	S1M10000019A07	*Staphylococcus aureus*
2138	S1M10000019A09	*Staphylococcus aureus*
2139	S1M10000019A11	*Staphylococcus aureus*
2140	S1M10000019A12	*Staphylococcus aureus*
2141	S1M10000019B03	*Staphylococcus aureus*
2142	S1M10000019B04	*Staphylococcus aureus*
2143	S1M10000019B07	*Staphylococcus aureus*
2144	S1M10000019B08	*Staphylococcus aureus*
2145	S1M10000019B09	*Staphylococcus aureus*
2146	S1M10000019B10	*Staphylococcus aureus*
2147	S1M10000019B11	*Staphylococcus aureus*
2148	S1M10000019B12	*Staphylococcus aureus*
2149	S1M10000019C01	*Staphylococcus aureus*
2150	S1M10000019C04	*Staphylococcus aureus*
2151	S1M10000019C05	*Staphylococcus aureus*
2152	S1M10000019C06	*Staphylococcus aureus*
2153	S1M10000019C07	*Staphylococcus aureus*
2154	S1M10000019C08	*Staphylococcus aureus*
2155	S1M10000019C11	*Staphylococcus aureus*
2156	S1M10000019C12	*Staphylococcus aureus*
2157	S1M10000019D01	*Staphylococcus aureus*
2158	S1M10000019D02	*Staphylococcus aureus*
2159	S1M10000019D04	*Staphylococcus aureus*
2160	S1M10000019D05	*Staphylococcus aureus*
2161	S1M10000019D06	*Staphylococcus aureus*
2162	S1M10000019D07	*Staphylococcus aureus*
2163	S1M10000019D09	*Staphylococcus aureus*
2164	S1M10000019D12	*Staphylococcus aureus*
2165	S1M10000019E01	*Staphylococcus aureus*
2166	S1M10000019E02	*Staphylococcus aureus*
2167	S1M10000019E07	*Staphylococcus aureus*

SeqID	Clone name	Organism
2168	S1M10000019F01	*Staphylococcus aureus*
2169	S1M10000019F05	*Staphylococcus aureus*
2170	S1M10000019F06	*Staphylococcus aureus*
2171	S1M10000019F08	*Staphylococcus aureus*
2172	S1M10000019F09	*Staphylococcus aureus*
2173	S1M10000019F11	*Staphylococcus aureus*
2174	S1M10000019G04	*Staphylococcus aureus*
2175	S1M10000019G07	*Staphylococcus aureus*
2176	S1M10000019G09	*Staphylococcus aureus*
2177	S1M10000019G10	*Staphylococcus aureus*
2178	S1M10000019G11	*Staphylococcus aureus*
2179	S1M10000019H05	*Staphylococcus aureus*
2180	S1M10000019H08	*Staphylococcus aureus*
2181	S1M10000020A05	*Staphylococcus aureus*
2182	S1M10000020A06	*Staphylococcus aureus*
2183	S1M10000020A07	*Staphylococcus aureus*
2184	S1M10000020A11	*Staphylococcus aureus*
2185	S1M10000020A12	*Staphylococcus aureus*
2186	S1M10000020B02	*Staphylococcus aureus*
2187	S1M10000020B03	*Staphylococcus aureus*
2188	S1M10000020B05	*Staphylococcus aureus*
2189	S1M10000020B06	*Staphylococcus aureus*
2190	S1M10000020B07	*Staphylococcus aureus*
2191	S1M10000020B09	*Staphylococcus aureus*
2192	S1M10000020B12	*Staphylococcus aureus*
2193	S1M10000020C09	*Staphylococcus aureus*
2194	S1M10000020C10	*Staphylococcus aureus*
2195	S1M10000020C11	*Staphylococcus aureus*
2196	S1M10000020D03	*Staphylococcus aureus*
2197	S1M10000020D04	*Staphylococcus aureus*
2198	S1M10000020D06	*Staphylococcus aureus*
2199	S1M10000020D07	*Staphylococcus aureus*
2200	S1M10000020D08	*Staphylococcus aureus*
2201	S1M10000020D09	*Staphylococcus aureus*
2202	S1M10000020D12	*Staphylococcus aureus*
2203	S1M10000020E01	*Staphylococcus aureus*
2204	S1M10000020E03	*Staphylococcus aureus*
2205	S1M10000020E04	*Staphylococcus aureus*
2206	S1M10000020E06	*Staphylococcus aureus*
2207	S1M10000020E08	*Staphylococcus aureus*
2208	S1M10000020E11	*Staphylococcus aureus*
2209	S1M10000020E12	*Staphylococcus aureus*
2210	S1M10000020F01	*Staphylococcus aureus*
2211	S1M10000020F05	*Staphylococcus aureus*
2212	S1M10000020F06	*Staphylococcus aureus*
2213	S1M10000020F07	*Staphylococcus aureus*
2214	S1M10000020F09	*Staphylococcus aureus*

SeqID	Clone name	Organism
2215	S1M10000020F11	*Staphylococcus aureus*
2216	S1M10000020F12	*Staphylococcus aureus*
2217	S1M10000020G01	*Staphylococcus aureus*
2218	S1M10000020G05	*Staphylococcus aureus*
2219	S1M10000020G07	*Staphylococcus aureus*
2220	S1M10000020G08	*Staphylococcus aureus*
2221	S1M10000020G09	*Staphylococcus aureus*
2222	S1M10000020G10	*Staphylococcus aureus*
2223	S1M10000020G11	*Staphylococcus aureus*
2224	S1M10000020G12	*Staphylococcus aureus*
2225	S1M10000020H01	*Staphylococcus aureus*
2226	S1M10000020H02	*Staphylococcus aureus*
2227	S1M10000020H04	*Staphylococcus aureus*
2228	S1M10000020H06	*Staphylococcus aureus*
2229	S1M10000020H08	*Staphylococcus aureus*
2230	S1M10000020H10	*Staphylococcus aureus*
2231	S1M10000020H11	*Staphylococcus aureus*
2232	S1M10000021A04	*Staphylococcus aureus*
2233	S1M10000021A05	*Staphylococcus aureus*
2234	S1M10000021A06	*Staphylococcus aureus*
2235	S1M10000021A07	*Staphylococcus aureus*
2236	S1M10000021A08	*Staphylococcus aureus*
2237	S1M10000021A09	*Staphylococcus aureus*
2238	S1M10000021A10	*Staphylococcus aureus*
2239	S1M10000021B05	*Staphylococcus aureus*
2240	S1M10000021B06	*Staphylococcus aureus*
2241	S1M10000021B07	*Staphylococcus aureus*
2242	S1M10000021B10	*Staphylococcus aureus*
2243	S1M10000021C04	*Staphylococcus aureus*
2244	S1M10000021C05	*Staphylococcus aureus*
2245	S1M10000021C07	*Staphylococcus aureus*
2246	S1M10000021C08	*Staphylococcus aureus*
2247	S1M10000021C10	*Staphylococcus aureus*
2248	S1M10000021C11	*Staphylococcus aureus*
2249	S1M10000021C12	*Staphylococcus aureus*
2250	S1M10000021D01	*Staphylococcus aureus*
2251	S1M10000021D03	*Staphylococcus aureus*
2252	S1M10000021D04	*Staphylococcus aureus*
2253	S1M10000021D06	*Staphylococcus aureus*
2254	S1M10000021D09	*Staphylococcus aureus*
2255	S1M10000021D10	*Staphylococcus aureus*
2256	S1M10000021E01	*Staphylococcus aureus*
2257	S1M10000021E02	*Staphylococcus aureus*
2258	S1M10000021E03	*Staphylococcus aureus*
2259	S1M10000021E05	*Staphylococcus aureus*
2260	S1M10000021E06	*Staphylococcus aureus*
2261	S1M10000021E09	*Staphylococcus aureus*

SeqID	Clone name	Organism
2262	S1M10000021E12	*Staphylococcus aureus*
2263	S1M10000021F02	*Staphylococcus aureus*
2264	S1M10000021F04	*Staphylococcus aureus*
2265	S1M10000021F05	*Staphylococcus aureus*
2266	S1M10000021F06	*Staphylococcus aureus*
2267	S1M10000021F07	*Staphylococcus aureus*
2268	S1M10000021F09	*Staphylococcus aureus*
2269	S1M10000021F11	*Staphylococcus aureus*
2270	S1M10000021G01	*Staphylococcus aureus*
2271	S1M10000021G03	*Staphylococcus aureus*
2272	S1M10000021G08	*Staphylococcus aureus*
2273	S1M10000021H04	*Staphylococcus aureus*
2274	S1M10000021H05	*Staphylococcus aureus*
2275	S1M10000021H07	*Staphylococcus aureus*
2276	S1M10000021H08	*Staphylococcus aureus*
2277	S1M10000021H11	*Staphylococcus aureus*
2278	S1M10000022A02	*Staphylococcus aureus*
2279	S1M10000022A03	*Staphylococcus aureus*
2280	S1M10000022A05	*Staphylococcus aureus*
2281	S1M10000022A08	*Staphylococcus aureus*
2282	S1M10000022A09	*Staphylococcus aureus*
2283	S1M10000022A12	*Staphylococcus aureus*
2284	S1M10000022B02	*Staphylococcus aureus*
2285	S1M10000022B03	*Staphylococcus aureus*
2286	S1M10000022B05	*Staphylococcus aureus*
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2288	S1M10000022B08	*Staphylococcus aureus*
2289	S1M10000022B09	*Staphylococcus aureus*
2290	S1M10000022B10	*Staphylococcus aureus*
2291	S1M10000022B11	*Staphylococcus aureus*
2292	S1M10000022B12	*Staphylococcus aureus*
2293	S1M10000022C02	*Staphylococcus aureus*
2294	S1M10000022C03	*Staphylococcus aureus*
2295	S1M10000022C04	*Staphylococcus aureus*
2296	S1M10000022C06	*Staphylococcus aureus*
2297	S1M10000022C07	*Staphylococcus aureus*
2298	S1M10000022C08	*Staphylococcus aureus*
2299	S1M10000022C11	*Staphylococcus aureus*
2300	S1M10000022D03	*Staphylococcus aureus*
2301	S1M10000022D05	*Staphylococcus aureus*
2302	S1M10000022D06	*Staphylococcus aureus*
2303	S1M10000022D07	*Staphylococcus aureus*
2304	S1M10000022D08	*Staphylococcus aureus*
2305	S1M10000022D09	*Staphylococcus aureus*
2306	S1M10000022D11	*Staphylococcus aureus*
2307	S1M10000022E01	*Staphylococcus aureus*
2308	S1M10000022E03	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2310	S1M10000022E09	*Staphylococcus aureus*
2311	S1M10000022F04	*Staphylococcus aureus*
2312	S1M10000022F06	*Staphylococcus aureus*
2313	S1M10000022F07	*Staphylococcus aureus*
2314	S1M10000022F08	*Staphylococcus aureus*
2315	S1M10000022F11	*Staphylococcus aureus*
2316	S1M10000022G03	*Staphylococcus aureus*
2317	S1M10000022G04	*Staphylococcus aureus*
2318	S1M10000022G07	*Staphylococcus aureus*
2319	S1M10000022G08	*Staphylococcus aureus*
2320	S1M10000022G12	*Staphylococcus aureus*
2321	S1M10000022H03	*Staphylococcus aureus*
2322	S1M10000022H05	*Staphylococcus aureus*
2323	S1M10000022H06	*Staphylococcus aureus*
2324	S1M10000022H07	*Staphylococcus aureus*
2325	S1M10000022H08	*Staphylococcus aureus*
2326	S1M10000022H11	*Staphylococcus aureus*
2327	S1M10000023A05	*Staphylococcus aureus*
2328	S1M10000023A09	*Staphylococcus aureus*
2329	S1M10000023A11	*Staphylococcus aureus*
2330	S1M10000023A12	*Staphylococcus aureus*
2331	S1M10000023B01	*Staphylococcus aureus*
2332	S1M10000023B03	*Staphylococcus aureus*
2333	S1M10000023B07	*Staphylococcus aureus*
2334	S1M10000023B08	*Staphylococcus aureus*
2335	S1M10000023B09	*Staphylococcus aureus*
2336	S1M10000023B10	*Staphylococcus aureus*
2337	S1M10000023B11	*Staphylococcus aureus*
2338	S1M10000023B12	*Staphylococcus aureus*
2339	S1M10000023C02	*Staphylococcus aureus*
2340	S1M10000023C10	*Staphylococcus aureus*
2341	S1M10000023C11	*Staphylococcus aureus*
2342	S1M10000023C12	*Staphylococcus aureus*
2343	S1M10000023D01	*Staphylococcus aureus*
2344	S1M10000023D03	*Staphylococcus aureus*
2345	S1M10000023D04	*Staphylococcus aureus*
2346	S1M10000023D07	*Staphylococcus aureus*
2347	S1M10000023D08	*Staphylococcus aureus*
2348	S1M10000023D09	*Staphylococcus aureus*
2349	S1M10000023D10	*Staphylococcus aureus*
2350	S1M10000023D12	*Staphylococcus aureus*
2351	S1M10000023E01	*Staphylococcus aureus*
2352	S1M10000023E04	*Staphylococcus aureus*
2353	S1M10000023E07	*Staphylococcus aureus*
2354	S1M10000023E10	*Staphylococcus aureus*
2355	S1M10000023E11	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2360	S1M10000023F11	*Staphylococcus aureus*
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2364	S1M10000023G06	*Staphylococcus aureus*
2365	S1M10000023G07	*Staphylococcus aureus*
2366	S1M10000023G08	*Staphylococcus aureus*
2367	S1M10000023G09	*Staphylococcus aureus*
2368	S1M10000023G11	*Staphylococcus aureus*
2369	S1M10000023H02	*Staphylococcus aureus*
2370	S1M10000023H06	*Staphylococcus aureus*
2371	S1M10000023H07	*Staphylococcus aureus*
2372	S1M10000023H09	*Staphylococcus aureus*
2373	S1M10000023H10	*Staphylococcus aureus*
2374	S1M10000024A02	*Staphylococcus aureus*
2375	S1M10000024A04	*Staphylococcus aureus*
2376	S1M10000024A07	*Staphylococcus aureus*
2377	S1M10000024A08	*Staphylococcus aureus*
2378	S1M10000024A11	*Staphylococcus aureus*
2379	S1M10000024B05	*Staphylococcus aureus*
2380	S1M10000024B06	*Staphylococcus aureus*
2381	S1M10000024B08	*Staphylococcus aureus*
2382	S1M10000024B09	*Staphylococcus aureus*
2383	S1M10000024B10	*Staphylococcus aureus*
2384	S1M10000024C02	*Staphylococcus aureus*
2385	S1M10000024C04	*Staphylococcus aureus*
2386	S1M10000024C07	*Staphylococcus aureus*
2387	S1M10000024D02	*Staphylococcus aureus*
2388	S1M10000024D03	*Staphylococcus aureus*
2389	S1M10000024D10	*Staphylococcus aureus*
2390	S1M10000024D11	*Staphylococcus aureus*
2391	S1M10000024E03	*Staphylococcus aureus*
2392	S1M10000024E05	*Staphylococcus aureus*
2393	S1M10000024E06	*Staphylococcus aureus*
2394	S1M10000024E07	*Staphylococcus aureus*
2395	S1M10000024E08	*Staphylococcus aureus*
2396	S1M10000024F02	*Staphylococcus aureus*
2397	S1M10000024F03	*Staphylococcus aureus*
2398	S1M10000024F05	*Staphylococcus aureus*
2399	S1M10000024F08	*Staphylococcus aureus*
2400	S1M10000024F10	*Staphylococcus aureus*
2401	S1M10000024G05	*Staphylococcus aureus*
2402	S1M10000024G06	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2405	S1M10000024G10	*Staphylococcus aureus*
2406	S1M10000024G12	*Staphylococcus aureus*
2407	S1M10000024H02	*Staphylococcus aureus*
2408	S1M10000024H04	*Staphylococcus aureus*
2409	S1M10000024H07	*Staphylococcus aureus*
2410	S1M10000024H08	*Staphylococcus aureus*
2411	S1M10000025A03	*Staphylococcus aureus*
2412	S1M10000025A08	*Staphylococcus aureus*
2413	S1M10000025A09	*Staphylococcus aureus*
2414	S1M10000025A10	*Staphylococcus aureus*
2415	S1M10000025B01	*Staphylococcus aureus*
2416	S1M10000025B02	*Staphylococcus aureus*
2417	S1M10000025B03	*Staphylococcus aureus*
2418	S1M10000025B05	*Staphylococcus aureus*
2419	S1M10000025B06	*Staphylococcus aureus*
2420	S1M10000025B09	*Staphylococcus aureus*
2421	S1M10000025B12	*Staphylococcus aureus*
2422	S1M10000025C01	*Staphylococcus aureus*
2423	S1M10000025C03	*Staphylococcus aureus*
2424	S1M10000025C05	*Staphylococcus aureus*
2425	S1M10000025C09	*Staphylococcus aureus*
2426	S1M10000025C10	*Staphylococcus aureus*
2427	S1M10000025C11	*Staphylococcus aureus*
2428	S1M10000025D01	*Staphylococcus aureus*
2429	S1M10000025D03	*Staphylococcus aureus*
2430	S1M10000025D04	*Staphylococcus aureus*
2431	S1M10000025D06	*Staphylococcus aureus*
2432	S1M10000025D08	*Staphylococcus aureus*
2433	S1M10000025D09	*Staphylococcus aureus*
2434	S1M10000025D10	*Staphylococcus aureus*
2435	S1M10000025E01	*Staphylococcus aureus*
2436	S1M10000025E04	*Staphylococcus aureus*
2437	S1M10000025E09	*Staphylococcus aureus*
2438	S1M10000025E11	*Staphylococcus aureus*
2439	S1M10000025F03	*Staphylococcus aureus*
2440	S1M10000025F05	*Staphylococcus aureus*
2441	S1M10000025F08	*Staphylococcus aureus*
2442	S1M10000025F09	*Staphylococcus aureus*
2443	S1M10000025F10	*Staphylococcus aureus*
2444	S1M10000025F12	*Staphylococcus aureus*
2445	S1M10000025G04	*Staphylococcus aureus*
2446	S1M10000025G06	*Staphylococcus aureus*
2447	S1M10000025G10	*Staphylococcus aureus*
2448	S1M10000025H05	*Staphylococcus aureus*
2449	S1M10000025H06	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2451	S1M10000025H10	*Staphylococcus aureus*
2452	S1M10000026A02	*Staphylococcus aureus*
2453	S1M10000026A04	*Staphylococcus aureus*
2454	S1M10000026A05	*Staphylococcus aureus*
2455	S1M10000026A06	*Staphylococcus aureus*
2456	S1M10000026A07	*Staphylococcus aureus*
2457	S1M10000026A08	*Staphylococcus aureus*
2458	S1M10000026A09	*Staphylococcus aureus*
2459	S1M10000026A10	*Staphylococcus aureus*
2460	S1M10000026A11	*Staphylococcus aureus*
2461	S1M10000026B02	*Staphylococcus aureus*
2462	S1M10000026B03	*Staphylococcus aureus*
2463	S1M10000026B05	*Staphylococcus aureus*
2464	S1M10000026B06	*Staphylococcus aureus*
2465	S1M10000026B07	*Staphylococcus aureus*
2466	S1M10000026B10	*Staphylococcus aureus*
2467	S1M10000026B11	*Staphylococcus aureus*
2468	S1M10000026B12	*Staphylococcus aureus*
2469	S1M10000026C01	*Staphylococcus aureus*
2470	S1M10000026C06	*Staphylococcus aureus*
2471	S1M10000026C07	*Staphylococcus aureus*
2472	S1M10000026C08	*Staphylococcus aureus*
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2474	S1M10000026C12	*Staphylococcus aureus*
2475	S1M10000026D04	*Staphylococcus aureus*
2476	S1M10000026D05	*Staphylococcus aureus*
2477	S1M10000026D06	*Staphylococcus aureus*
2478	S1M10000026D07	*Staphylococcus aureus*
2479	S1M10000026D08	*Staphylococcus aureus*
2480	S1M10000026D10	*Staphylococcus aureus*
2481	S1M10000026D12	*Staphylococcus aureus*
2482	S1M10000026E01	*Staphylococcus aureus*
2483	S1M10000026E07	*Staphylococcus aureus*
2484	S1M10000026E09	*Staphylococcus aureus*
2485	S1M10000026E10	*Staphylococcus aureus*
2486	S1M10000026E11	*Staphylococcus aureus*
2487	S1M10000026E12	*Staphylococcus aureus*
2488	S1M10000026F01	*Staphylococcus aureus*
2489	S1M10000026F03	*Staphylococcus aureus*
2490	S1M10000026F04	*Staphylococcus aureus*
2491	S1M10000026F05	*Staphylococcus aureus*
2492	S1M10000026F06	*Staphylococcus aureus*
2493	S1M10000026F07	*Staphylococcus aureus*
2494	S1M10000026F08	*Staphylococcus aureus*
2495	S1M10000026F09	*Staphylococcus aureus*
2496	S1M10000026F10	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2499	S1M10000026G01	*Staphylococcus aureus*
2500	S1M10000026G03	*Staphylococcus aureus*
2501	S1M10000026G04	*Staphylococcus aureus*
2502	S1M10000026G05	*Staphylococcus aureus*
2503	S1M10000026G06	*Staphylococcus aureus*
2504	S1M10000026G07	*Staphylococcus aureus*
2505	S1M10000026G09	*Staphylococcus aureus*
2506	S1M10000026G10	*Staphylococcus aureus*
2507	S1M10000026G12	*Staphylococcus aureus*
2508	S1M10000026H01	*Staphylococcus aureus*
2509	S1M10000026H02	*Staphylococcus aureus*
2510	S1M10000026H03	*Staphylococcus aureus*
2511	S1M10000026H04	*Staphylococcus aureus*
2512	S1M10000026H05	*Staphylococcus aureus*
2513	S1M10000026H07	*Staphylococcus aureus*
2514	S1M10000026H09	*Staphylococcus aureus*
2515	S1M10000026H10	*Staphylococcus aureus*
2516	S1M10000027A04	*Staphylococcus aureus*
2517	S1M10000027A05	*Staphylococcus aureus*
2518	S1M10000027A08	*Staphylococcus aureus*
2519	S1M10000027A11	*Staphylococcus aureus*
2520	S1M10000027B04	*Staphylococcus aureus*
2521	S1M10000027B06	*Staphylococcus aureus*
2522	S1M10000027B07	*Staphylococcus aureus*
2523	S1M10000027B08	*Staphylococcus aureus*
2524	S1M10000027B09	*Staphylococcus aureus*
2525	S1M10000027B11	*Staphylococcus aureus*
2526	S1M10000027C02	*Staphylococcus aureus*
2527	S1M10000027C04	*Staphylococcus aureus*
2528	S1M10000027C05	*Staphylococcus aureus*
2529	S1M10000027C06	*Staphylococcus aureus*
2530	S1M10000027C08	*Staphylococcus aureus*
2531	S1M10000027C09	*Staphylococcus aureus*
2532	S1M10000027D02	*Staphylococcus aureus*
2533	S1M10000027D03	*Staphylococcus aureus*
2534	S1M10000027D05	*Staphylococcus aureus*
2535	S1M10000027D06	*Staphylococcus aureus*
2536	S1M10000027D08	*Staphylococcus aureus*
2537	S1M10000027D09	*Staphylococcus aureus*
2538	S1M10000027D10	*Staphylococcus aureus*
2539	S1M10000027D11	*Staphylococcus aureus*
2540	S1M10000027E05	*Staphylococcus aureus*
2541	S1M10000027E06	*Staphylococcus aureus*
2542	S1M10000027E07	*Staphylococcus aureus*
2543	S1M10000027E08	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2545	S1M10000027E11	*Staphylococcus aureus*
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2547	S1M10000027F02	*Staphylococcus aureus*
2548	S1M10000027F05	*Staphylococcus aureus*
2549	S1M10000027F06	*Staphylococcus aureus*
2550	S1M10000027F08	*Staphylococcus aureus*
2551	S1M10000027F09	*Staphylococcus aureus*
2552	S1M10000027G03	*Staphylococcus aureus*
2553	S1M10000027G04	*Staphylococcus aureus*
2554	S1M10000027G05	*Staphylococcus aureus*
2555	S1M10000027G06	*Staphylococcus aureus*
2556	S1M10000027G07	*Staphylococcus aureus*
2557	S1M10000027G09	*Staphylococcus aureus*
2558	S1M10000027G11	*Staphylococcus aureus*
2559	S1M10000027H02	*Staphylococcus aureus*
2560	S1M10000027H04	*Staphylococcus aureus*
2561	S1M10000027H05	*Staphylococcus aureus*
2562	S1M10000027H06	*Staphylococcus aureus*
2563	S1M10000027H07	*Staphylococcus aureus*
2564	S1M10000027H08	*Staphylococcus aureus*
2565	S1M10000027H09	*Staphylococcus aureus*
2566	S1M10000027H10	*Staphylococcus aureus*
2567	S1M10000027H11	*Staphylococcus aureus*
2568	S1M10000028A02	*Staphylococcus aureus*
2569	S1M10000028A04	*Staphylococcus aureus*
2570	S1M10000028A06	*Staphylococcus aureus*
2571	S1M10000028A08	*Staphylococcus aureus*
2572	S1M10000028B01	*Staphylococcus aureus*
2573	S1M10000028B02	*Staphylococcus aureus*
2574	S1M10000028B03	*Staphylococcus aureus*
2575	S1M10000028B04	*Staphylococcus aureus*
2576	S1M10000028B05	*Staphylococcus aureus*
2577	S1M10000028B06	*Staphylococcus aureus*
2578	S1M10000028B08	*Staphylococcus aureus*
2579	S1M10000028B09	*Staphylococcus aureus*
2580	S1M10000028C02	*Staphylococcus aureus*
2581	S1M10000028C04	*Staphylococcus aureus*
2582	S1M10000028C05	*Staphylococcus aureus*
2583	S1M10000028C06	*Staphylococcus aureus*
2584	S1M10000028C08	*Staphylococcus aureus*
2585	S1M10000028D03	*Staphylococcus aureus*
2586	S1M10000028D04	*Staphylococcus aureus*
2587	S1M10000028D06	*Staphylococcus aureus*
2588	S1M10000028D07	*Staphylococcus aureus*
2589	S1M10000028D08	*Staphylococcus aureus*
2590	S1M10000028D09	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2592	S1M10000028E03	*Staphylococcus aureus*
2593	S1M10000028E08	*Staphylococcus aureus*
2594	S1M10000028F01	*Staphylococcus aureus*
2595	S1M10000028F03	*Staphylococcus aureus*
2596	S1M10000028F04	*Staphylococcus aureus*
2597	S1M10000028F05	*Staphylococcus aureus*
2598	S1M10000028F06	*Staphylococcus aureus*
2599	S1M10000028F07	*Staphylococcus aureus*
2600	S1M10000028G01	*Staphylococcus aureus*
2601	S1M10000028G02	*Staphylococcus aureus*
2602	S1M10000028G03	*Staphylococcus aureus*
2603	S1M10000028G04	*Staphylococcus aureus*
2604	S1M10000028G05	*Staphylococcus aureus*
2605	S1M10000028G06	*Staphylococcus aureus*
2606	S1M10000028G08	*Staphylococcus aureus*
2607	S1M10000028H03	*Staphylococcus aureus*
2608	S1M10000028H04	*Staphylococcus aureus*
2609	S1M10000028H05	*Staphylococcus aureus*
2610	S1M10000029A02	*Staphylococcus aureus*
2611	S1M10000029A04	*Staphylococcus aureus*
2612	S1M10000029A09	*Staphylococcus aureus*
2613	S1M10000029A10	*Staphylococcus aureus*
2614	S1M10000029A11	*Staphylococcus aureus*
2615	S1M10000029A12	*Staphylococcus aureus*
2616	S1M10000029B02	*Staphylococcus aureus*
2617	S1M10000029B03	*Staphylococcus aureus*
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2619	S1M10000029B05	*Staphylococcus aureus*
2620	S1M10000029B06	*Staphylococcus aureus*
2621	S1M10000029B08	*Staphylococcus aureus*
2622	S1M10000029B10	*Staphylococcus aureus*
2623	S1M10000029C02	*Staphylococcus aureus*
2624	S1M10000029C03	*Staphylococcus aureus*
2625	S1M10000029C05	*Staphylococcus aureus*
2626	S1M10000029C07	*Staphylococcus aureus*
2627	S1M10000029C09	*Staphylococcus aureus*
2628	S1M10000029C10	*Staphylococcus aureus*
2629	S1M10000029C12	*Staphylococcus aureus*
2630	S1M10000029D02	*Staphylococcus aureus*
2631	S1M10000029D05	*Staphylococcus aureus*
2632	S1M10000029D09	*Staphylococcus aureus*
2633	S1M10000029D10	*Staphylococcus aureus*
2634	S1M10000029D12	*Staphylococcus aureus*
2635	S1M10000029E02	*Staphylococcus aureus*
2636	S1M10000029E05	*Staphylococcus aureus*
2637	S1M10000029E10	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2639	S1M10000029F01	*Staphylococcus aureus*
2640	S1M10000029F02	*Staphylococcus aureus*
2641	S1M10000029F04	*Staphylococcus aureus*
2642	S1M10000029F09	*Staphylococcus aureus*
2643	S1M10000029F10	*Staphylococcus aureus*
2644	S1M10000029F11	*Staphylococcus aureus*
2645	S1M10000029F12	*Staphylococcus aureus*
2646	S1M10000029G01	*Staphylococcus aureus*
2647	S1M10000029G02	*Staphylococcus aureus*
2648	S1M10000029G03	*Staphylococcus aureus*
2649	S1M10000029G05	*Staphylococcus aureus*
2650	S1M10000029G07	*Staphylococcus aureus*
2651	S1M10000029G08	*Staphylococcus aureus*
2652	S1M10000029G12	*Staphylococcus aureus*
2653	S1M10000029H01	*Staphylococcus aureus*
2654	S1M10000029H05	*Staphylococcus aureus*
2655	S1M10000029H06	*Staphylococcus aureus*
2656	S1M10000029H08	*Staphylococcus aureus*
2657	S1M10000029H09	*Staphylococcus aureus*
2658	S1M10000029H10	*Staphylococcus aureus*
2659	S1M10000030A02	*Staphylococcus aureus*
2660	S1M10000030A05	*Staphylococcus aureus*
2661	S1M10000030A09	*Staphylococcus aureus*
2662	S1M10000030A10	*Staphylococcus aureus*
2663	S1M10000030A11	*Staphylococcus aureus*
2664	S1M10000030B02	*Staphylococcus aureus*
2665	S1M10000030B05	*Staphylococcus aureus*
2666	S1M10000030B07	*Staphylococcus aureus*
2667	S1M10000030B09	*Staphylococcus aureus*
2668	S1M10000030C02	*Staphylococcus aureus*
2669	S1M10000030C03	*Staphylococcus aureus*
2670	S1M10000030C04	*Staphylococcus aureus*
2671	S1M10000030C05	*Staphylococcus aureus*
2672	S1M10000030C08	*Staphylococcus aureus*
2673	S1M10000030C09	*Staphylococcus aureus*
2674	S1M10000030C10	*Staphylococcus aureus*
2675	S1M10000030C12	*Staphylococcus aureus*
2676	S1M10000030D01	*Staphylococcus aureus*
2677	S1M10000030D02	*Staphylococcus aureus*
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2679	S1M10000030D05	*Staphylococcus aureus*
2680	S1M10000030D06	*Staphylococcus aureus*
2681	S1M10000030D07	*Staphylococcus aureus*
2682	S1M10000030D09	*Staphylococcus aureus*
2683	S1M10000030D10	*Staphylococcus aureus*
2684	S1M10000030D11	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2686	S1M10000030E06	*Staphylococcus aureus*
2687	S1M10000030E07	*Staphylococcus aureus*
2688	S1M10000030E11	*Staphylococcus aureus*
2689	S1M10000030E12	*Staphylococcus aureus*
2690	S1M10000030F01	*Staphylococcus aureus*
2691	S1M10000030F07	*Staphylococcus aureus*
2692	S1M10000030F08	*Staphylococcus aureus*
2693	S1M10000030F09	*Staphylococcus aureus*
2694	S1M10000030F10	*Staphylococcus aureus*
2695	S1M10000030G03	*Staphylococcus aureus*
2696	S1M10000030G05	*Staphylococcus aureus*
2697	S1M10000030G07	*Staphylococcus aureus*
2698	S1M10000030G08	*Staphylococcus aureus*
2699	S1M10000030G09	*Staphylococcus aureus*
2700	S1M10000030G10	*Staphylococcus aureus*
2701	S1M10000030G11	*Staphylococcus aureus*
2702	S1M10000030G12	*Staphylococcus aureus*
2703	S1M10000030H01	*Staphylococcus aureus*
2704	S1M10000030H02	*Staphylococcus aureus*
2705	S1M10000030H03	*Staphylococcus aureus*
2706	S1M10000030H05	*Staphylococcus aureus*
2707	S1M10000030H07	*Staphylococcus aureus*
2708	S1M10000030H09	*Staphylococcus aureus*
2709	S1M10000031A03	*Staphylococcus aureus*
2710	S1M10000031A08	*Staphylococcus aureus*
2711	S1M10000031A10	*Staphylococcus aureus*
2712	S1M10000031B01	*Staphylococcus aureus*
2713	S1M10000031B02	*Staphylococcus aureus*
2714	S1M10000031B04	*Staphylococcus aureus*
2715	S1M10000031B11	*Staphylococcus aureus*
2716	S1M10000031B12	*Staphylococcus aureus*
2717	S1M10000031C04	*Staphylococcus aureus*
2718	S1M10000031C07	*Staphylococcus aureus*
2719	S1M10000031C09	*Staphylococcus aureus*
2720	S1M10000031C11	*Staphylococcus aureus*
2721	S1M10000031D06	*Staphylococcus aureus*
2722	S1M10000031D07	*Staphylococcus aureus*
2723	S1M10000031D08	*Staphylococcus aureus*
2724	S1M10000031D09	*Staphylococcus aureus*
2725	S1M10000031E02	*Staphylococcus aureus*
2726	S1M10000031E03	*Staphylococcus aureus*
2727	S1M10000031E04	*Staphylococcus aureus*
2728	S1M10000031E07	*Staphylococcus aureus*
2729	S1M10000031E08	*Staphylococcus aureus*
2730	S1M10000031E10	*Staphylococcus aureus*
2731	S1M10000031E12	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2733	S1M10000031F03	*Staphylococcus aureus*
2734	S1M10000031F04	*Staphylococcus aureus*
2735	S1M10000031F05	*Staphylococcus aureus*
2736	S1M10000031F08	*Staphylococcus aureus*
2737	S1M10000031F10	*Staphylococcus aureus*
2738	S1M10000031F11	*Staphylococcus aureus*
2739	S1M10000031F12	*Staphylococcus aureus*
2740	S1M10000031G02	*Staphylococcus aureus*
2741	S1M10000031G03	*Staphylococcus aureus*
2742	S1M10000031G04	*Staphylococcus aureus*
2743	S1M10000031G06	*Staphylococcus aureus*
2744	S1M10000031G09	*Staphylococcus aureus*
2745	S1M10000031G10	*Staphylococcus aureus*
2746	S1M10000031G11	*Staphylococcus aureus*
2747	S1M10000031H01	*Staphylococcus aureus*
2748	S1M10000031H02	*Staphylococcus aureus*
2749	S1M10000031H06	*Staphylococcus aureus*
2750	S1M10000031H09	*Staphylococcus aureus*
2751	S1M10000031H11	*Staphylococcus aureus*
2752	S1M10000032A03	*Staphylococcus aureus*
2753	S1M10000032A05	*Staphylococcus aureus*
2754	S1M10000032A06	*Staphylococcus aureus*
2755	S1M10000032A07	*Staphylococcus aureus*
2756	S1M10000032A08	*Staphylococcus aureus*
2757	S1M10000032A10	*Staphylococcus aureus*
2758	S1M10000032B01	*Staphylococcus aureus*
2759	S1M10000032B05	*Staphylococcus aureus*
2760	S1M10000032B07	*Staphylococcus aureus*
2761	S1M10000032B08	*Staphylococcus aureus*
2762	S1M10000032B11	*Staphylococcus aureus*
2763	S1M10000032B12	*Staphylococcus aureus*
2764	S1M10000032C01	*Staphylococcus aureus*
2765	S1M10000032C03	*Staphylococcus aureus*
2766	S1M10000032C04	*Staphylococcus aureus*
2767	S1M10000032C05	*Staphylococcus aureus*
2768	S1M10000032C09	*Staphylococcus aureus*
2769	S1M10000032C10	*Staphylococcus aureus*
2770	S1M10000032C11	*Staphylococcus aureus*
2771	S1M10000032C12	*Staphylococcus aureus*
2772	S1M10000032D03	*Staphylococcus aureus*
2773	S1M10000032D06	*Staphylococcus aureus*
2774	S1M10000032D07	*Staphylococcus aureus*
2775	S1M10000032D09	*Staphylococcus aureus*
2776	S1M10000032D11	*Staphylococcus aureus*
2777	S1M10000032E02	*Staphylococcus aureus*
2778	S1M10000032E03	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2780	S1M10000032E06	*Staphylococcus aureus*
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2782	S1M10000032E09	*Staphylococcus aureus*
2783	S1M10000032E10	*Staphylococcus aureus*
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2785	S1M10000032E12	*Staphylococcus aureus*
2786	S1M10000032F01	*Staphylococcus aureus*
2787	S1M10000032F04	*Staphylococcus aureus*
2788	S1M10000032F05	*Staphylococcus aureus*
2789	S1M10000032F10	*Staphylococcus aureus*
2790	S1M10000032F11	*Staphylococcus aureus*
2791	S1M10000032F12	*Staphylococcus aureus*
2792	S1M10000032G02	*Staphylococcus aureus*
2793	S1M10000032G03	*Staphylococcus aureus*
2794	S1M10000032G04	*Staphylococcus aureus*
2795	S1M10000032G06	*Staphylococcus aureus*
2796	S1M10000032G08	*Staphylococcus aureus*
2797	S1M10000032G10	*Staphylococcus aureus*
2798	S1M10000032G12	*Staphylococcus aureus*
2799	S1M10000032H01	*Staphylococcus aureus*
2800	S1M10000032H04	*Staphylococcus aureus*
2801	S1M10000032H07	*Staphylococcus aureus*
2802	S1M10000032H09	*Staphylococcus aureus*
2803	S1M10000032H11	*Staphylococcus aureus*
2804	S1M10000033A02	*Staphylococcus aureus*
2805	S1M10000033A07	*Staphylococcus aureus*
2806	S1M10000033A08	*Staphylococcus aureus*
2807	S1M10000033A10	*Staphylococcus aureus*
2808	S1M10000033B02	*Staphylococcus aureus*
2809	S1M10000033B07	*Staphylococcus aureus*
2810	S1M10000033B08	*Staphylococcus aureus*
2811	S1M10000033B11	*Staphylococcus aureus*
2812	S1M10000033B12	*Staphylococcus aureus*
2813	S1M10000033C04	*Staphylococcus aureus*
2814	S1M10000033D02	*Staphylococcus aureus*
2815	S1M10000033D03	*Staphylococcus aureus*
2816	S1M10000033D04	*Staphylococcus aureus*
2817	S1M10000033D05	*Staphylococcus aureus*
2818	S1M10000033D06	*Staphylococcus aureus*
2819	S1M10000033D10	*Staphylococcus aureus*
2820	S1M10000033D12	*Staphylococcus aureus*
2821	S1M10000033E04	*Staphylococcus aureus*
2822	S1M10000033E10	*Staphylococcus aureus*
2823	S1M10000033E12	*Staphylococcus aureus*
2824	S1M10000033F02	*Staphylococcus aureus*
2825	S1M10000033F03	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2827	S1M10000033F07	*Staphylococcus aureus*
2828	S1M10000033F09	*Staphylococcus aureus*
2829	S1M10000033F11	*Staphylococcus aureus*
2830	S1M10000033G05	*Staphylococcus aureus*
2831	S1M10000033G07	*Staphylococcus aureus*
2832	S1M10000033G09	*Staphylococcus aureus*
2833	S1M10000033G10	*Staphylococcus aureus*
2834	S1M10000033G11	*Staphylococcus aureus*
2835	S1M10000033G12	*Staphylococcus aureus*
2836	S1M10000033H01	*Staphylococcus aureus*
2837	S1M10000033H02	*Staphylococcus aureus*
2838	S1M10000033H03	*Staphylococcus aureus*
2839	S1M10000033H07	*Staphylococcus aureus*
2840	S1M10000033H08	*Staphylococcus aureus*
2841	S1M10000033H09	*Staphylococcus aureus*
2842	S1M10000033H10	*Staphylococcus aureus*
2843	S1M10000033H11	*Staphylococcus aureus*
2844	S1M10000034A02	*Staphylococcus aureus*
2845	S1M10000034A03	*Staphylococcus aureus*
2846	S1M10000034A04	*Staphylococcus aureus*
2847	S1M10000034A05	*Staphylococcus aureus*
2848	S1M10000034A08	*Staphylococcus aureus*
2849	S1M10000034A09	*Staphylococcus aureus*
2850	S1M10000034A11	*Staphylococcus aureus*
2851	S1M10000034A12	*Staphylococcus aureus*
2852	S1M10000034B03	*Staphylococcus aureus*
2853	S1M10000034B05	*Staphylococcus aureus*
2854	S1M10000034B06	*Staphylococcus aureus*
2855	S1M10000034B07	*Staphylococcus aureus*
2856	S1M10000034B08	*Staphylococcus aureus*
2857	S1M10000034B09	*Staphylococcus aureus*
2858	S1M10000034B10	*Staphylococcus aureus*
2859	S1M10000034B12	*Staphylococcus aureus*
2860	S1M10000034C02	*Staphylococcus aureus*
2861	S1M10000034C06	*Staphylococcus aureus*
2862	S1M10000034C07	*Staphylococcus aureus*
2863	S1M10000034C09	*Staphylococcus aureus*
2864	S1M10000034C12	*Staphylococcus aureus*
2865	S1M10000034D01	*Staphylococcus aureus*
2866	S1M10000034D05	*Staphylococcus aureus*
2867	S1M10000034D06	*Staphylococcus aureus*
2868	S1M10000034D07	*Staphylococcus aureus*
2869	S1M10000034D08	*Staphylococcus aureus*
2870	S1M10000034D10	*Staphylococcus aureus*
2871	S1M10000034D11	*Staphylococcus aureus*
2872	S1M10000034D12	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2874	S1M10000034E02	*Staphylococcus aureus*
2875	S1M10000034E04	*Staphylococcus aureus*
2876	S1M10000034E05	*Staphylococcus aureus*
2877	S1M10000034E06	*Staphylococcus aureus*
2878	S1M10000034E07	*Staphylococcus aureus*
2879	S1M10000034E10	*Staphylococcus aureus*
2880	S1M10000034E11	*Staphylococcus aureus*
2881	S1M10000034E12	*Staphylococcus aureus*
2882	S1M10000034F01	*Staphylococcus aureus*
2883	S1M10000034F02	*Staphylococcus aureus*
2884	S1M10000034F03	*Staphylococcus aureus*
2885	S1M10000034F04	*Staphylococcus aureus*
2886	S1M10000034F05	*Staphylococcus aureus*
2887	S1M10000034F07	*Staphylococcus aureus*
2888	S1M10000034F08	*Staphylococcus aureus*
2889	S1M10000034F09	*Staphylococcus aureus*
2890	S1M10000034F10	*Staphylococcus aureus*
2891	S1M10000034F12	*Staphylococcus aureus*
2892	S1M10000034G02	*Staphylococcus aureus*
2893	S1M10000034G03	*Staphylococcus aureus*
2894	S1M10000034G06	*Staphylococcus aureus*
2895	S1M10000034G07	*Staphylococcus aureus*
2896	S1M10000034G08	*Staphylococcus aureus*
2897	S1M10000034G09	*Staphylococcus aureus*
2898	S1M10000034G11	*Staphylococcus aureus*
2899	S1M10000034G12	*Staphylococcus aureus*
2900	S1M10000034H01	*Staphylococcus aureus*
2901	S1M10000034H02	*Staphylococcus aureus*
2902	S1M10000034H03	*Staphylococcus aureus*
2903	S1M10000034H06	*Staphylococcus aureus*
2904	S1M10000034H07	*Staphylococcus aureus*
2905	S1M10000034H08	*Staphylococcus aureus*
2906	S1M10000034H09	*Staphylococcus aureus*
2907	S1M10000034H10	*Staphylococcus aureus*
2908	S1M10000035A03	*Staphylococcus aureus*
2909	S1M10000035A08	*Staphylococcus aureus*
2910	S1M10000035A09	*Staphylococcus aureus*
2911	S1M10000035A10	*Staphylococcus aureus*
2912	S1M10000035A11	*Staphylococcus aureus*
2913	S1M10000035A12	*Staphylococcus aureus*
2914	S1M10000035B01	*Staphylococcus aureus*
2915	S1M10000035B03	*Staphylococcus aureus*
2916	S1M10000035B04	*Staphylococcus aureus*
2917	S1M10000035B08	*Staphylococcus aureus*
2918	S1M10000035B11	*Staphylococcus aureus*
2919	S1M10000035C01	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2921	S1M10000035C04	*Staphylococcus aureus*
2922	S1M10000035C06	*Staphylococcus aureus*
2923	S1M10000035C11	*Staphylococcus aureus*
2924	S1M10000035D01	*Staphylococcus aureus*
2925	S1M10000035D04	*Staphylococcus aureus*
2926	S1M10000035D06	*Staphylococcus aureus*
2927	S1M10000035D09	*Staphylococcus aureus*
2928	S1M10000035D12	*Staphylococcus aureus*
2929	S1M10000035E02	*Staphylococcus aureus*
2930	S1M10000035E03	*Staphylococcus aureus*
2931	S1M10000035E04	*Staphylococcus aureus*
2932	S1M10000035E08	*Staphylococcus aureus*
2933	S1M10000035E09	*Staphylococcus aureus*
2934	S1M10000035E12	*Staphylococcus aureus*
2935	S1M10000035F03	*Staphylococcus aureus*
2936	S1M10000035F04	*Staphylococcus aureus*
2937	S1M10000035F09	*Staphylococcus aureus*
2938	S1M10000035F12	*Staphylococcus aureus*
2939	S1M10000035G02	*Staphylococcus aureus*
2940	S1M10000035G09	*Staphylococcus aureus*
2941	S1M10000035G11	*Staphylococcus aureus*
2942	S1M10000035G12	*Staphylococcus aureus*
2943	S1M10000035H01	*Staphylococcus aureus*
2944	S1M10000035H07	*Staphylococcus aureus*
2945	S1M10000035H08	*Staphylococcus aureus*
2946	S1M10000035H09	*Staphylococcus aureus*
2947	S1M10000035H10	*Staphylococcus aureus*
2948	S1M10000035H11	*Staphylococcus aureus*
2949	S1M10000036A02	*Staphylococcus aureus*
2950	S1M10000036A03	*Staphylococcus aureus*
2951	S1M10000036A04	*Staphylococcus aureus*
2952	S1M10000036A05	*Staphylococcus aureus*
2953	S1M10000036A08	*Staphylococcus aureus*
2954	S1M10000036A11	*Staphylococcus aureus*
2955	S1M10000036A12	*Staphylococcus aureus*
2956	S1M10000036B04	*Staphylococcus aureus*
2957	S1M10000036B06	*Staphylococcus aureus*
2958	S1M10000036B07	*Staphylococcus aureus*
2959	S1M10000036B08	*Staphylococcus aureus*
2960	S1M10000036B11	*Staphylococcus aureus*
2961	S1M10000036B12	*Staphylococcus aureus*
2962	S1M10000036C01	*Staphylococcus aureus*
2963	S1M10000036C03	*Staphylococcus aureus*
2964	S1M10000036C04	*Staphylococcus aureus*
2965	S1M10000036C05	*Staphylococcus aureus*
2966	S1M10000036C06	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2968	S1M10000036C09	*Staphylococcus aureus*
2969	S1M10000036C10	*Staphylococcus aureus*
2970	S1M10000036D02	*Staphylococcus aureus*
2971	S1M10000036D03	*Staphylococcus aureus*
2972	S1M10000036D06	*Staphylococcus aureus*
2973	S1M10000036D08	*Staphylococcus aureus*
2974	S1M10000036D10	*Staphylococcus aureus*
2975	S1M10000036D11	*Staphylococcus aureus*
2976	S1M10000036D12	*Staphylococcus aureus*
2977	S1M10000036E06	*Staphylococcus aureus*
2978	S1M10000036E08	*Staphylococcus aureus*
2979	S1M10000036E11	*Staphylococcus aureus*
2980	S1M10000036F06	*Staphylococcus aureus*
2981	S1M10000036F07	*Staphylococcus aureus*
2982	S1M10000036F08	*Staphylococcus aureus*
2983	S1M10000036F09	*Staphylococcus aureus*
2984	S1M10000036F10	*Staphylococcus aureus*
2985	S1M10000036F11	*Staphylococcus aureus*
2986	S1M10000036G03	*Staphylococcus aureus*
2987	S1M10000036G07	*Staphylococcus aureus*
2988	S1M10000036G08	*Staphylococcus aureus*
2989	S1M10000036G11	*Staphylococcus aureus*
2990	S1M10000036H01	*Staphylococcus aureus*
2991	S1M10000036H02	*Staphylococcus aureus*
2992	S1M10000036H03	*Staphylococcus aureus*
2993	S1M10000036H04	*Staphylococcus aureus*
2994	S1M10000036H05	*Staphylococcus aureus*
2995	S1M10000036H06	*Staphylococcus aureus*
2996	S1M10000036H08	*Staphylococcus aureus*
2997	S1M10000036H11	*Staphylococcus aureus*
2998	S1M10000037A02	*Staphylococcus aureus*
2999	S1M10000037A03	*Staphylococcus aureus*
3000	S1M10000037A06	*Staphylococcus aureus*
3001	S1M10000037A08	*Staphylococcus aureus*
3002	S1M10000037A09	*Staphylococcus aureus*
3003	S1M10000037A11	*Staphylococcus aureus*
3004	S1M10000037A12	*Staphylococcus aureus*
3005	S1M10000037B03	*Staphylococcus aureus*
3006	S1M10000037B04	*Staphylococcus aureus*
3007	S1M10000037B05	*Staphylococcus aureus*
3008	S1M10000037B06	*Staphylococcus aureus*
3009	S1M10000037B07	*Staphylococcus aureus*
3010	S1M10000037B08	*Staphylococcus aureus*
3011	S1M10000037B10	*Staphylococcus aureus*
3012	S1M10000037B11	*Staphylococcus aureus*
3013	S1M10000037B12	*Staphylococcus aureus*

SeqID	Clone name	Organism
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3015	S1M10000037C06	*Staphylococcus aureus*
3016	S1M10000037C07	*Staphylococcus aureus*
3017	S1M10000037C08	*Staphylococcus aureus*
3018	S1M10000037C09	*Staphylococcus aureus*
3019	S1M10000037C10	*Staphylococcus aureus*
3020	S1M10000037D04	*Staphylococcus aureus*
3021	S1M10000037D05	*Staphylococcus aureus*
3022	S1M10000037D06	*Staphylococcus aureus*
3023	S1M10000037D09	*Staphylococcus aureus*
3024	S1M10000037D12	*Staphylococcus aureus*
3025	S1M10000037E02	*Staphylococcus aureus*
3026	S1M10000037E03	*Staphylococcus aureus*
3027	S1M10000037E06	*Staphylococcus aureus*
3028	S1M10000037E08	*Staphylococcus aureus*
3029	S1M10000037E09	*Staphylococcus aureus*
3030	S1M10000037E10	*Staphylococcus aureus*
3031	S1M10000037E11	*Staphylococcus aureus*
3032	S1M10000037E12	*Staphylococcus aureus*
3033	S1M10000037F02	*Staphylococcus aureus*
3034	S1M10000037F03	*Staphylococcus aureus*
3035	S1M10000037F04	*Staphylococcus aureus*
3036	S1M10000037F05	*Staphylococcus aureus*
3037	S1M10000037F06	*Staphylococcus aureus*
3038	S1M10000037F07	*Staphylococcus aureus*
3039	S1M10000037F08	*Staphylococcus aureus*
3040	S1M10000037F09	*Staphylococcus aureus*
3041	S1M10000037F10	*Staphylococcus aureus*
3042	S1M10000037G01	*Staphylococcus aureus*
3043	S1M10000037G02	*Staphylococcus aureus*
3044	S1M10000037G03	*Staphylococcus aureus*
3045	S1M10000037G06	*Staphylococcus aureus*
3046	S1M10000037G07	*Staphylococcus aureus*
3047	S1M10000037G08	*Staphylococcus aureus*
3048	S1M10000037G10	*Staphylococcus aureus*
3049	S1M10000037H02	*Staphylococcus aureus*
3050	S1M10000037H03	*Staphylococcus aureus*
3051	S1M10000037H05	*Staphylococcus aureus*
3052	S1M10000037H07	*Staphylococcus aureus*
3053	S1M10000037H08	*Staphylococcus aureus*
3054	S1M10000037H09	*Staphylococcus aureus*
3055	S1M10000037H11	*Staphylococcus aureus*
3056	S1M10000038A04	*Staphylococcus aureus*
3057	S1M10000038A07	*Staphylococcus aureus*
3058	S1M10000038A08	*Staphylococcus aureus*
3059	S1M10000038A09	*Staphylococcus aureus*
3060	S1M10000038A11	*Staphylococcus aureus*

SeqID	Clone name	Organism
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3062	S1M10000038B01	*Staphylococcus aureus*
3063	S1M10000038B03	*Staphylococcus aureus*
3064	S1M10000038B07	*Staphylococcus aureus*
3065	S1M10000038B08	*Staphylococcus aureus*
3066	S1M10000038B09	*Staphylococcus aureus*
3067	S1M10000038B12	*Staphylococcus aureus*
3068	S1M10000038C01	*Staphylococcus aureus*
3069	S1M10000038C02	*Staphylococcus aureus*
3070	S1M10000038C06	*Staphylococcus aureus*
3071	S1M10000038C08	*Staphylococcus aureus*
3072	S1M10000038C10	*Staphylococcus aureus*
3073	S1M10000038C11	*Staphylococcus aureus*
3074	S1M10000038C12	*Staphylococcus aureus*
3075	S1M10000038D02	*Staphylococcus aureus*
3076	S1M10000038D05	*Staphylococcus aureus*
3077	S1M10000038D07	*Staphylococcus aureus*
3078	S1M10000038D08	*Staphylococcus aureus*
3079	S1M10000038D09	*Staphylococcus aureus*
3080	S1M10000038D10	*Staphylococcus aureus*
3081	S1M10000038D11	*Staphylococcus aureus*
3082	S1M10000038D12	*Staphylococcus aureus*
3083	S1M10000038E01	*Staphylococcus aureus*
3084	S1M10000038E02	*Staphylococcus aureus*
3085	S1M10000038E03	*Staphylococcus aureus*
3086	S1M10000038E04	*Staphylococcus aureus*
3087	S1M10000038E05	*Staphylococcus aureus*
3088	S1M10000038E06	*Staphylococcus aureus*
3089	S1M10000038E07	*Staphylococcus aureus*
3090	S1M10000038E10	*Staphylococcus aureus*
3091	S1M10000038E12	*Staphylococcus aureus*
3092	S1M10000038F03	*Staphylococcus aureus*
3093	S1M10000038F04	*Staphylococcus aureus*
3094	S1M10000038F05	*Staphylococcus aureus*
3095	S1M10000038F06	*Staphylococcus aureus*
3096	S1M10000038F08	*Staphylococcus aureus*
3097	S1M10000038F09	*Staphylococcus aureus*
3098	S1M10000038F10	*Staphylococcus aureus*
3099	S1M10000038F11	*Staphylococcus aureus*
3100	S1M10000038F12	*Staphylococcus aureus*
3101	S1M10000038G01	*Staphylococcus aureus*
3102	S1M10000038G03	*Staphylococcus aureus*
3103	S1M10000038G04	*Staphylococcus aureus*
3104	S1M10000038G06	*Staphylococcus aureus*
3105	S1M10000038G08	*Staphylococcus aureus*
3106	S1M10000038G10	*Staphylococcus aureus*
3107	S1M10000038G11	*Staphylococcus aureus*

SeqID	Clone name	Organism
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3109	S1M10000038H03	*Staphylococcus aureus*
3110	S1M10000038H07	*Staphylococcus aureus*
3111	S1M10000038H09	*Staphylococcus aureus*
3112	S1M10000038H11	*Staphylococcus aureus*
3113	S1M10000039A02	*Staphylococcus aureus*
3114	S1M10000039A05	*Staphylococcus aureus*
3115	S1M10000039A07	*Staphylococcus aureus*
3116	S1M10000039A08	*Staphylococcus aureus*
3117	S1M10000039A11	*Staphylococcus aureus*
3118	S1M10000039A12	*Staphylococcus aureus*
3119	S1M10000039B02	*Staphylococcus aureus*
3120	S1M10000039B06	*Staphylococcus aureus*
3121	S1M10000039B07	*Staphylococcus aureus*
3122	S1M10000039B10	*Staphylococcus aureus*
3123	S1M10000039B12	*Staphylococcus aureus*
3124	S1M10000039C04	*Staphylococcus aureus*
3125	S1M10000039C06	*Staphylococcus aureus*
3126	S1M10000039C07	*Staphylococcus aureus*
3127	S1M10000039C08	*Staphylococcus aureus*
3128	S1M10000039C09	*Staphylococcus aureus*
3129	S1M10000039C10	*Staphylococcus aureus*
3130	S1M10000039C11	*Staphylococcus aureus*
3131	S1M10000039D02	*Staphylococcus aureus*
3132	S1M10000039D09	*Staphylococcus aureus*
3133	S1M10000039D10	*Staphylococcus aureus*
3134	S1M10000039E01	*Staphylococcus aureus*
3135	S1M10000039E08	*Staphylococcus aureus*
3136	S1M10000039E09	*Staphylococcus aureus*
3137	S1M10000039E10	*Staphylococcus aureus*
3138	S1M10000039E11	*Staphylococcus aureus*
3139	S1M10000039F02	*Staphylococcus aureus*
3140	S1M10000039F03	*Staphylococcus aureus*
3141	S1M10000039F05	*Staphylococcus aureus*
3142	S1M10000039F07	*Staphylococcus aureus*
3143	S1M10000039F08	*Staphylococcus aureus*
3144	S1M10000039F09	*Staphylococcus aureus*
3145	S1M10000039F10	*Staphylococcus aureus*
3146	S1M10000039F12	*Staphylococcus aureus*
3147	S1M10000039G03	*Staphylococcus aureus*
3148	S1M10000039G04	*Staphylococcus aureus*
3149	S1M10000039G07	*Staphylococcus aureus*
3150	S1M10000039G10	*Staphylococcus aureus*
3151	S1M10000039H02	*Staphylococcus aureus*
3152	S1M10000039H03	*Staphylococcus aureus*
3153	S1M10000039H04	*Staphylococcus aureus*
3154	S1M10000039H06	*Staphylococcus aureus*

SeqID	Clone name	Organism
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3156	S1M10000039H08	*Staphylococcus aureus*
3157	S1M10000040A04	*Staphylococcus aureus*
3158	S1M10000040A05	*Staphylococcus aureus*
3159	S1M10000040A07	*Staphylococcus aureus*
3160	S1M10000040A08	*Staphylococcus aureus*
3161	S1M10000040A10	*Staphylococcus aureus*
3162	S1M10000040A11	*Staphylococcus aureus*
3163	S1M10000040B01	*Staphylococcus aureus*
3164	S1M10000040B03	*Staphylococcus aureus*
3165	S1M10000040B07	*Staphylococcus aureus*
3166	S1M10000040B11	*Staphylococcus aureus*
3167	S1M10000040C03	*Staphylococcus aureus*
3168	S1M10000040C04	*Staphylococcus aureus*
3169	S1M10000040C05	*Staphylococcus aureus*
3170	S1M10000040C06	*Staphylococcus aureus*
3171	S1M10000040C07	*Staphylococcus aureus*
3172	S1M10000040C08	*Staphylococcus aureus*
3173	S1M10000040C10	*Staphylococcus aureus*
3174	S1M10000040C11	*Staphylococcus aureus*
3175	S1M10000040D01	*Staphylococcus aureus*
3176	S1M10000040D03	*Staphylococcus aureus*
3177	S1M10000040D08	*Staphylococcus aureus*
3178	S1M10000040D09	*Staphylococcus aureus*
3179	S1M10000040D11	*Staphylococcus aureus*
3180	S1M10000040E01	*Staphylococcus aureus*
3181	S1M10000040E02	*Staphylococcus aureus*
3182	S1M10000040E04	*Staphylococcus aureus*
3183	S1M10000040E05	*Staphylococcus aureus*
3184	S1M10000040E06	*Staphylococcus aureus*
3185	S1M10000040E07	*Staphylococcus aureus*
3186	S1M10000040E09	*Staphylococcus aureus*
3187	S1M10000040E10	*Staphylococcus aureus*
3188	S1M10000040E11	*Staphylococcus aureus*
3189	S1M10000040E12	*Staphylococcus aureus*
3190	S1M10000040F01	*Staphylococcus aureus*
3191	S1M10000040F02	*Staphylococcus aureus*
3192	S1M10000040F03	*Staphylococcus aureus*
3193	S1M10000040F04	*Staphylococcus aureus*
3194	S1M10000040F05	*Staphylococcus aureus*
3195	S1M10000040F06	*Staphylococcus aureus*
3196	S1M10000040F08	*Staphylococcus aureus*
3197	S1M10000040F09	*Staphylococcus aureus*
3198	S1M10000040F12	*Staphylococcus aureus*
3199	S1M10000040G01	*Staphylococcus aureus*
3200	S1M10000040G02	*Staphylococcus aureus*
3201	S1M10000040G04	*Staphylococcus aureus*

SeqID	Clone name	Organism
3202	S1M10000040G07	*Staphylococcus aureus*
3203	S1M10000040G08	*Staphylococcus aureus*
3204	S1M10000040G12	*Staphylococcus aureus*
3205	S1M10000040H02	*Staphylococcus aureus*
3206	S1M10000040H03	*Staphylococcus aureus*
3207	S1M10000040H04	*Staphylococcus aureus*
3208	S1M10000040H05	*Staphylococcus aureus*
3209	S1M10000040H07	*Staphylococcus aureus*
3210	S1M10000040H10	*Staphylococcus aureus*
3211	S1M10000041A03	*Staphylococcus aureus*
3212	S1M10000041B02	*Staphylococcus aureus*
3213	S1M10000041B03	*Staphylococcus aureus*
3214	S1M10000041B05	*Staphylococcus aureus*
3215	S1M10000041B06	*Staphylococcus aureus*
3216	S1M10000041B07	*Staphylococcus aureus*
3217	S1M10000041B12	*Staphylococcus aureus*
3218	S1M10000041C08	*Staphylococcus aureus*
3219	S1M10000041C10	*Staphylococcus aureus*
3220	S1M10000041C11	*Staphylococcus aureus*
3221	S1M10000041D06	*Staphylococcus aureus*
3222	S1M10000041D07	*Staphylococcus aureus*
3223	S1M10000041D08	*Staphylococcus aureus*
3224	S1M10000041D10	*Staphylococcus aureus*
3225	S1M10000041D12	*Staphylococcus aureus*
3226	S1M10000041E03	*Staphylococcus aureus*
3227	S1M10000041E06	*Staphylococcus aureus*
3228	S1M10000041E09	*Staphylococcus aureus*
3229	S1M10000041E12	*Staphylococcus aureus*
3230	S1M10000041F03	*Staphylococcus aureus*
3231	S1M10000041F11	*Staphylococcus aureus*
3232	S1M10000041F12	*Staphylococcus aureus*
3233	S1M10000041G01	*Staphylococcus aureus*
3234	S1M10000041G06	*Staphylococcus aureus*
3235	S1M10000041G08	*Staphylococcus aureus*
3236	S1M10000041G10	*Staphylococcus aureus*
3237	S1M10000041G11	*Staphylococcus aureus*
3238	S1M10000041H01	*Staphylococcus aureus*
3239	S1M10000041H04	*Staphylococcus aureus*
3240	S1M10000041H05	*Staphylococcus aureus*
3241	S1M10000041H07	*Staphylococcus aureus*
3242	S1M10000041H08	*Staphylococcus aureus*
3243	S1M10000041H09	*Staphylococcus aureus*
3244	S1M10000042A04	*Staphylococcus aureus*
3245	S1M10000042A05	*Staphylococcus aureus*
3246	S1M10000042A06	*Staphylococcus aureus*
3247	S1M10000042A07	*Staphylococcus aureus*
3248	S1M10000042A09	*Staphylococcus aureus*

SeqID	Clone name	Organism
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3250	S1M10000042A12	*Staphylococcus aureus*
3251	S1M10000042B02	*Staphylococcus aureus*
3252	S1M10000042B03	*Staphylococcus aureus*
3253	S1M10000042B06	*Staphylococcus aureus*
3254	S1M10000042B07	*Staphylococcus aureus*
3255	S1M10000042B08	*Staphylococcus aureus*
3256	S1M10000042B09	*Staphylococcus aureus*
3257	S1M10000042B10	*Staphylococcus aureus*
3258	S1M10000042B11	*Staphylococcus aureus*
3259	S1M10000042B12	*Staphylococcus aureus*
3260	S1M10000042C02	*Staphylococcus aureus*
3261	S1M10000042C06	*Staphylococcus aureus*
3262	S1M10000042C10	*Staphylococcus aureus*
3263	S1M10000042C11	*Staphylococcus aureus*
3264	S1M10000042D04	*Staphylococcus aureus*
3265	S1M10000042D07	*Staphylococcus aureus*
3266	S1M10000042D10	*Staphylococcus aureus*
3267	S1M10000042D11	*Staphylococcus aureus*
3268	S1M10000042E03	*Staphylococcus aureus*
3269	S1M10000042E06	*Staphylococcus aureus*
3270	S1M10000042E08	*Staphylococcus aureus*
3271	S1M10000042F01	*Staphylococcus aureus*
3272	S1M10000042F02	*Staphylococcus aureus*
3273	S1M10000042F05	*Staphylococcus aureus*
3274	S1M10000042F06	*Staphylococcus aureus*
3275	S1M10000042F08	*Staphylococcus aureus*
3276	S1M10000042F09	*Staphylococcus aureus*
3277	S1M10000042F10	*Staphylococcus aureus*
3278	S1M10000042F11	*Staphylococcus aureus*
3279	S1M10000042G01	*Staphylococcus aureus*
3280	S1M10000042G03	*Staphylococcus aureus*
3281	S1M10000042G08	*Staphylococcus aureus*
3282	S1M10000042G09	*Staphylococcus aureus*
3283	S1M10000042G12	*Staphylococcus aureus*
3284	S1M10000042H05	*Staphylococcus aureus*
3285	S1M10000042H07	*Staphylococcus aureus*
3286	S1M10000042H11	*Staphylococcus aureus*
3287	S1M10000043A02	*Staphylococcus aureus*
3288	S1M10000043A03	*Staphylococcus aureus*
3289	S1M10000043A04	*Staphylococcus aureus*
3290	S1M10000043A06	*Staphylococcus aureus*
3291	S1M10000043A07	*Staphylococcus aureus*
3292	S1M10000043A08	*Staphylococcus aureus*
3293	S1M10000043A10	*Staphylococcus aureus*
3294	S1M10000043A11	*Staphylococcus aureus*
3295	S1M10000043A12	*Staphylococcus aureus*

SeqID	Clone name	Organism
3296	S1M10000043B01	*Staphylococcus aureus*
3297	S1M10000043B02	*Staphylococcus aureus*
3298	S1M10000043B07	*Staphylococcus aureus*
3299	S1M10000043B08	*Staphylococcus aureus*
3300	S1M10000043B09	*Staphylococcus aureus*
3301	S1M10000043B10	*Staphylococcus aureus*
3302	S1M10000043B12	*Staphylococcus aureus*
3303	S1M10000043C02	*Staphylococcus aureus*
3304	S1M10000043C07	*Staphylococcus aureus*
3305	S1M10000043C11	*Staphylococcus aureus*
3306	S1M10000043C12	*Staphylococcus aureus*
3307	S1M10000043D01	*Staphylococcus aureus*
3308	S1M10000043D02	*Staphylococcus aureus*
3309	S1M10000043D04	*Staphylococcus aureus*
3310	S1M10000043D10	*Staphylococcus aureus*
3311	S1M10000043D12	*Staphylococcus aureus*
3312	S1M10000043E02	*Staphylococcus aureus*
3313	S1M10000043E03	*Staphylococcus aureus*
3314	S1M10000043E05	*Staphylococcus aureus*
3315	S1M10000043E07	*Staphylococcus aureus*
3316	S1M10000043E08	*Staphylococcus aureus*
3317	S1M10000043E10	*Staphylococcus aureus*
3318	S1M10000043E11	*Staphylococcus aureus*
3319	S1M10000043E12	*Staphylococcus aureus*
3320	S1M10000043F01	*Staphylococcus aureus*
3321	S1M10000043F05	*Staphylococcus aureus*
3322	S1M10000043F07	*Staphylococcus aureus*
3323	S1M10000043F08	*Staphylococcus aureus*
3324	S1M10000043F09	*Staphylococcus aureus*
3325	S1M10000043G01	*Staphylococcus aureus*
3326	S1M10000043G04	*Staphylococcus aureus*
3327	S1M10000043G05	*Staphylococcus aureus*
3328	S1M10000043G09	*Staphylococcus aureus*
3329	S1M10000043G10	*Staphylococcus aureus*
3330	S1M10000043H01	*Staphylococcus aureus*
3331	S1M10000043H03	*Staphylococcus aureus*
3332	S1M10000043H04	*Staphylococcus aureus*
3333	S1M10000043H05	*Staphylococcus aureus*
3334	S1M10000043H06	*Staphylococcus aureus*
3335	S1M10000043H09	*Staphylococcus aureus*
3336	S1M10000043H10	*Staphylococcus aureus*
3337	S1M10000043H11	*Staphylococcus aureus*
3338	S1M10000044A02	*Staphylococcus aureus*
3339	S1M10000044A06	*Staphylococcus aureus*
3340	S1M10000044A08	*Staphylococcus aureus*
3341	S1M10000044A09	*Staphylococcus aureus*
3342	S1M10000044A11	*Staphylococcus aureus*

SeqID	Clone name	Organism
3343	S1M10000044A12	*Staphylococcus aureus*
3344	S1M10000044B01	*Staphylococcus aureus*
3345	S1M10000044B02	*Staphylococcus aureus*
3346	S1M10000044B05	*Staphylococcus aureus*
3347	S1M10000044B06	*Staphylococcus aureus*
3348	S1M10000044B08	*Staphylococcus aureus*
3349	S1M10000044B11	*Staphylococcus aureus*
3350	S1M10000044B12	*Staphylococcus aureus*
3351	S1M10000044C04	*Staphylococcus aureus*
3352	S1M10000044C06	*Staphylococcus aureus*
3353	S1M10000044C07	*Staphylococcus aureus*
3354	S1M10000044C08	*Staphylococcus aureus*
3355	S1M10000044C11	*Staphylococcus aureus*
3356	S1M10000044C12	*Staphylococcus aureus*
3357	S1M10000044D01	*Staphylococcus aureus*
3358	S1M10000044D04	*Staphylococcus aureus*
3359	S1M10000044D06	*Staphylococcus aureus*
3360	S1M10000044D08	*Staphylococcus aureus*
3361	S1M10000044D09	*Staphylococcus aureus*
3362	S1M10000044D10	*Staphylococcus aureus*
3363	S1M10000044D11	*Staphylococcus aureus*
3364	S1M10000044D12	*Staphylococcus aureus*
3365	S1M10000044E01	*Staphylococcus aureus*
3366	S1M10000044E02	*Staphylococcus aureus*
3367	S1M10000044E06	*Staphylococcus aureus*
3368	S1M10000044E07	*Staphylococcus aureus*
3369	S1M10000044E09	*Staphylococcus aureus*
3370	S1M10000044E10	*Staphylococcus aureus*
3371	S1M10000044E11	*Staphylococcus aureus*
3372	S1M10000044F02	*Staphylococcus aureus*
3373	S1M10000044F06	*Staphylococcus aureus*
3374	S1M10000044F08	*Staphylococcus aureus*
3375	S1M10000044F10	*Staphylococcus aureus*
3376	S1M10000044G02	*Staphylococcus aureus*
3377	S1M10000044G05	*Staphylococcus aureus*
3378	S1M10000044G08	*Staphylococcus aureus*
3379	S1M10000044G10	*Staphylococcus aureus*
3380	S1M10000044G11	*Staphylococcus aureus*
3381	S1M10000044H06	*Staphylococcus aureus*
3382	S1M10000044H07	*Staphylococcus aureus*
3383	S1M10000044H08	*Staphylococcus aureus*
3384	S1M10000044H09	*Staphylococcus aureus*
3385	S1M10000044H10	*Staphylococcus aureus*
3386	S1M10000044H11	*Staphylococcus aureus*
3387	S1M10000045A02	*Staphylococcus aureus*
3388	S1M10000045A06	*Staphylococcus aureus*
3389	S1M10000045A07	*Staphylococcus aureus*

SeqID	Clone name	Organism
3390	S1M10000045A08	*Staphylococcus aureus*
3391	S1M10000045A12	*Staphylococcus aureus*
3392	S1M10000045B01	*Staphylococcus aureus*
3393	S1M10000045B02	*Staphylococcus aureus*
3394	S1M10000045B03	*Staphylococcus aureus*
3395	S1M10000045B07	*Staphylococcus aureus*
3396	S1M10000045B10	*Staphylococcus aureus*
3397	S1M10000045B11	*Staphylococcus aureus*
3398	S1M10000045B12	*Staphylococcus aureus*
3399	S1M10000045C02	*Staphylococcus aureus*
3400	S1M10000045C03	*Staphylococcus aureus*
3401	S1M10000045C04	*Staphylococcus aureus*
3402	S1M10000045C05	*Staphylococcus aureus*
3403	S1M10000045C07	*Staphylococcus aureus*
3404	S1M10000045C09	*Staphylococcus aureus*
3405	S1M10000045D01	*Staphylococcus aureus*
3406	S1M10000045D03	*Staphylococcus aureus*
3407	S1M10000045D07	*Staphylococcus aureus*
3408	S1M10000045D08	*Staphylococcus aureus*
3409	S1M10000045D09	*Staphylococcus aureus*
3410	S1M10000045D10	*Staphylococcus aureus*
3411	S1M10000045D11	*Staphylococcus aureus*
3412	S1M10000045D12	*Staphylococcus aureus*
3413	S1M10000045E04	*Staphylococcus aureus*
3414	S1M10000045E05	*Staphylococcus aureus*
3415	S1M10000045E08	*Staphylococcus aureus*
3416	S1M10000045E09	*Staphylococcus aureus*
3417	S1M10000045E10	*Staphylococcus aureus*
3418	S1M10000045E11	*Staphylococcus aureus*
3419	S1M10000045E12	*Staphylococcus aureus*
3420	S1M10000045F04	*Staphylococcus aureus*
3421	S1M10000045F05	*Staphylococcus aureus*
3422	S1M10000045F08	*Staphylococcus aureus*
3423	S1M10000045F11	*Staphylococcus aureus*
3424	S1M10000045F12	*Staphylococcus aureus*
3425	S1M10000045G03	*Staphylococcus aureus*
3426	S1M10000045G06	*Staphylococcus aureus*
3427	S1M10000045G07	*Staphylococcus aureus*
3428	S1M10000045G08	*Staphylococcus aureus*
3429	S1M10000045G10	*Staphylococcus aureus*
3430	S1M10000045G12	*Staphylococcus aureus*
3431	S1M10000045H06	*Staphylococcus aureus*
3432	S1M10000045H10	*Staphylococcus aureus*
3433	S1M10000045H11	*Staphylococcus aureus*
3434	S1M10000046A03	*Staphylococcus aureus*
3435	S1M10000046A04	*Staphylococcus aureus*
3436	S1M10000046A06	*Staphylococcus aureus*

SeqID	Clone name	Organism
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3438	S1M10000046A09	*Staphylococcus aureus*
3439	S1M10000046A11	*Staphylococcus aureus*
3440	S1M10000046A12	*Staphylococcus aureus*
3441	S1M10000046B01	*Staphylococcus aureus*
3442	S1M10000046B03	*Staphylococcus aureus*
3443	S1M10000046B04	*Staphylococcus aureus*
3444	S1M10000046B05	*Staphylococcus aureus*
3445	S1M10000046B07	*Staphylococcus aureus*
3446	S1M10000046B08	*Staphylococcus aureus*
3447	S1M10000046B09	*Staphylococcus aureus*
3448	S1M10000046B11	*Staphylococcus aureus*
3449	S1M10000046B12	*Staphylococcus aureus*
3450	S1M10000046C02	*Staphylococcus aureus*
3451	S1M10000046C04	*Staphylococcus aureus*
3452	S1M10000046C05	*Staphylococcus aureus*
3453	S1M10000046C06	*Staphylococcus aureus*
3454	S1M10000046C07	*Staphylococcus aureus*
3455	S1M10000046C08	*Staphylococcus aureus*
3456	S1M10000046C11	*Staphylococcus aureus*
3457	S1M10000046C12	*Staphylococcus aureus*
3458	S1M10000046D01	*Staphylococcus aureus*
3459	S1M10000046D02	*Staphylococcus aureus*
3460	S1M10000046D03	*Staphylococcus aureus*
3461	S1M10000046D04	*Staphylococcus aureus*
3462	S1M10000046D05	*Staphylococcus aureus*
3463	S1M10000046D08	*Staphylococcus aureus*
3464	S1M10000046D09	*Staphylococcus aureus*
3465	S1M10000046D10	*Staphylococcus aureus*
3466	S1M10000046D11	*Staphylococcus aureus*
3467	S1M10000046D12	*Staphylococcus aureus*
3468	S1M10000046E01	*Staphylococcus aureus*
3469	S1M10000046E02	*Staphylococcus aureus*
3470	S1M10000046E04	*Staphylococcus aureus*
3471	S1M10000046E07	*Staphylococcus aureus*
3472	S1M10000046E08	*Staphylococcus aureus*
3473	S1M10000046E10	*Staphylococcus aureus*
3474	S1M10000046F01	*Staphylococcus aureus*
3475	S1M10000046F02	*Staphylococcus aureus*
3476	S1M10000046F05	*Staphylococcus aureus*
3477	S1M10000046F06	*Staphylococcus aureus*
3478	S1M10000046F08	*Staphylococcus aureus*
3479	S1M10000046F09	*Staphylococcus aureus*
3480	S1M10000046F10	*Staphylococcus aureus*
3481	S1M10000046F12	*Staphylococcus aureus*
3482	S1M10000046G01	*Staphylococcus aureus*
3483	S1M10000046G02	*Staphylococcus aureus*

SeqID	Clone name	Organism
3484	S1M10000046G03	*Staphylococcus aureus*
3485	S1M10000046G04	*Staphylococcus aureus*
3486	S1M10000046G07	*Staphylococcus aureus*
3487	S1M10000046G09	*Staphylococcus aureus*
3488	S1M10000046G10	*Staphylococcus aureus*
3489	S1M10000046H01	*Staphylococcus aureus*
3490	S1M10000046H10	*Staphylococcus aureus*
3491	S1M10000047A03	*Staphylococcus aureus*
3492	S1M10000047A04	*Staphylococcus aureus*
3493	S1M10000047A05	*Staphylococcus aureus*
3494	S1M10000047A06	*Staphylococcus aureus*
3495	S1M10000047A07	*Staphylococcus aureus*
3496	S1M10000047A08	*Staphylococcus aureus*
3497	S1M10000047A09	*Staphylococcus aureus*
3498	S1M10000047A10	*Staphylococcus aureus*
3499	S1M10000047A11	*Staphylococcus aureus*
3500	S1M10000047A12	*Staphylococcus aureus*
3501	S1M10000047B02	*Staphylococcus aureus*
3502	S1M10000047B04	*Staphylococcus aureus*
3503	S1M10000047B05	*Staphylococcus aureus*
3504	S1M10000047B06	*Staphylococcus aureus*
3505	S1M10000047B08	*Staphylococcus aureus*
3506	S1M10000047B09	*Staphylococcus aureus*
3507	S1M10000047B10	*Staphylococcus aureus*
3508	S1M10000047B12	*Staphylococcus aureus*
3509	S1M10000047C01	*Staphylococcus aureus*
3510	S1M10000047C02	*Staphylococcus aureus*
3511	S1M10000047C03	*Staphylococcus aureus*
3512	S1M10000047C04	*Staphylococcus aureus*
3513	S1M10000047C06	*Staphylococcus aureus*
3514	S1M10000047C08	*Staphylococcus aureus*
3515	S1M10000047C09	*Staphylococcus aureus*
3516	S1M10000047C11	*Staphylococcus aureus*
3517	S1M10000047C12	*Staphylococcus aureus*
3518	S1M10000047D02	*Staphylococcus aureus*
3519	S1M10000047D03	*Staphylococcus aureus*
3520	S1M10000047D04	*Staphylococcus aureus*
3521	S1M10000047D05	*Staphylococcus aureus*
3522	S1M10000047D09	*Staphylococcus aureus*
3523	S1M10000047D10	*Staphylococcus aureus*
3524	S1M10000047D11	*Staphylococcus aureus*
3525	S1M10000047D12	*Staphylococcus aureus*
3526	S1M10000047E01	*Staphylococcus aureus*
3527	S1M10000047E02	*Staphylococcus aureus*
3528	S1M10000047E03	*Staphylococcus aureus*
3529	S1M10000047E04	*Staphylococcus aureus*
3530	S1M10000047E05	*Staphylococcus aureus*

SeqID	Clone name	Organism
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3532	S1M10000047E08	*Staphylococcus aureus*
3533	S1M10000047E09	*Staphylococcus aureus*
3534	S1M10000047E10	*Staphylococcus aureus*
3535	S1M10000047E11	*Staphylococcus aureus*
3536	S1M10000047E12	*Staphylococcus aureus*
3537	S1M10000047F02	*Staphylococcus aureus*
3538	S1M10000047F03	*Staphylococcus aureus*
3539	S1M10000047F04	*Staphylococcus aureus*
3540	S1M10000047F05	*Staphylococcus aureus*
3541	S1M10000047F06	*Staphylococcus aureus*
3542	S1M10000047F07	*Staphylococcus aureus*
3543	S1M10000047F08	*Staphylococcus aureus*
3544	S1M10000047F09	*Staphylococcus aureus*
3545	S1M10000047F10	*Staphylococcus aureus*
3546	S1M10000047F11	*Staphylococcus aureus*
3547	S1M10000047F12	*Staphylococcus aureus*
3548	S1M10000047G01	*Staphylococcus aureus*
3549	S1M10000047G02	*Staphylococcus aureus*
3550	S1M10000047G04	*Staphylococcus aureus*
3551	S1M10000047G05	*Staphylococcus aureus*
3552	S1M10000047G06	*Staphylococcus aureus*
3553	S1M10000047G07	*Staphylococcus aureus*
3554	S1M10000047G08	*Staphylococcus aureus*
3555	S1M10000047G09	*Staphylococcus aureus*
3556	S1M10000047G10	*Staphylococcus aureus*
3557	S1M10000047H03	*Staphylococcus aureus*
3558	S1M10000047H04	*Staphylococcus aureus*
3559	S1M10000047H05	*Staphylococcus aureus*
3560	S1M10000047H06	*Staphylococcus aureus*
3561	S1M10000047H07	*Staphylococcus aureus*
3562	S1M10000047H08	*Staphylococcus aureus*
3563	S1M10000047H09	*Staphylococcus aureus*
3564	S1M10000047H11	*Staphylococcus aureus*
3565	S1M10000048A02	*Staphylococcus aureus*
3566	S1M10000048A03	*Staphylococcus aureus*
3567	S1M10000048A04	*Staphylococcus aureus*
3568	S1M10000048A05	*Staphylococcus aureus*
3569	S1M10000048A06	*Staphylococcus aureus*
3570	S1M10000048A07	*Staphylococcus aureus*
3571	S1M10000048A09	*Staphylococcus aureus*
3572	S1M10000048A10	*Staphylococcus aureus*
3573	S1M10000048A11	*Staphylococcus aureus*
3574	S1M10000048A12	*Staphylococcus aureus*
3575	S1M10000048B02	*Staphylococcus aureus*
3576	S1M10000048B05	*Staphylococcus aureus*
3577	S1M10000048B08	*Staphylococcus aureus*

SeqID	Clone name	Organism
3578	S1M10000048B10	*Staphylococcus aureus*
3579	S1M10000048B11	*Staphylococcus aureus*
3580	S1M10000048B12	*Staphylococcus aureus*
3581	S1M10000048C01	*Staphylococcus aureus*
3582	S1M10000048C02	*Staphylococcus aureus*
3583	S1M10000048C03	*Staphylococcus aureus*
3584	S1M10000048C05	*Staphylococcus aureus*
3585	S1M10000048C06	*Staphylococcus aureus*
3586	S1M10000048C07	*Staphylococcus aureus*
3587	S1M10000048C08	*Staphylococcus aureus*
3588	S1M10000048C09	*Staphylococcus aureus*
3589	S1M10000048C11	*Staphylococcus aureus*
3590	S1M10000048D02	*Staphylococcus aureus*
3591	S1M10000048D08	*Staphylococcus aureus*
3592	S1M10000048D09	*Staphylococcus aureus*
3593	S1M10000048D10	*Staphylococcus aureus*
3594	S1M10000048D12	*Staphylococcus aureus*
3595	S1M10000048E02	*Staphylococcus aureus*
3596	S1M10000048E03	*Staphylococcus aureus*
3597	S1M10000048E04	*Staphylococcus aureus*
3598	S1M10000048E06	*Staphylococcus aureus*
3599	S1M10000048E07	*Staphylococcus aureus*
3600	S1M10000048E08	*Staphylococcus aureus*
3601	S1M10000048E10	*Staphylococcus aureus*
3602	S1M10000048F02	*Staphylococcus aureus*
3603	S1M10000048F07	*Staphylococcus aureus*
3604	S1M10000048F08	*Staphylococcus aureus*
3605	S1M10000048F09	*Staphylococcus aureus*
3606	S1M10000048F11	*Staphylococcus aureus*
3607	S1M10000048F12	*Staphylococcus aureus*
3608	S1M10000048G02	*Staphylococcus aureus*
3609	S1M10000048G03	*Staphylococcus aureus*
3610	S1M10000048G04	*Staphylococcus aureus*
3611	S1M10000048G05	*Staphylococcus aureus*
3612	S1M10000048G07	*Staphylococcus aureus*
3613	S1M10000048G10	*Staphylococcus aureus*
3614	S1M10000048G11	*Staphylococcus aureus*
3615	S1M10000048H01	*Staphylococcus aureus*
3616	S1M10000048H02	*Staphylococcus aureus*
3617	S1M10000048H03	*Staphylococcus aureus*
3618	S1M10000048H04	*Staphylococcus aureus*
3619	S1M10000048H05	*Staphylococcus aureus*
3620	S1M10000048H07	*Staphylococcus aureus*
3621	S1M10000048H08	*Staphylococcus aureus*
3622	S1M10000048H09	*Staphylococcus aureus*
3623	S1M10000048H10	*Staphylococcus aureus*
3624	S1M10000048H11	*Staphylococcus aureus*

SeqID	Clone name	Organism
3625	S1M10000009E10	*Staphylococcus aureus*
3626	S1M10000001F01	*Staphylococcus aureus*
3627	S1M10000006B12	*Staphylococcus aureus*
3628	S1M10000003D09	*Staphylococcus aureus*
3629	S1M10000001D11	*Staphylococcus aureus*
3630	S1M10000003B07	*Staphylococcus aureus*
3631	S1M10000002A07	*Staphylococcus aureus*
3632	S1M10000003F11	*Staphylococcus aureus*
3633	S1M10000047C07	*Staphylococcus aureus*
3634	S1M10000013F10	*Staphylococcus aureus*
3635	S1M10000014D11	*Staphylococcus aureus*
3636	S1M10000015F05	*Staphylococcus aureus*
3637	S1M10000048D01	*Staphylococcus aureus*
3638	S1M10000011C03	*Staphylococcus aureus*
3639	S1M10000012F03	*Staphylococcus aureus*
3640	S1M10000002F07	*Staphylococcus aureus*
3641	S1M10000048G01	*Staphylococcus aureus*
3642	S1M10000009G12	*Staphylococcus aureus*
3643	S1M10000012D05	*Staphylococcus aureus*
3644	S1M10000014D07	*Staphylococcus aureus*
3645	S1M10000047C05	*Staphylococcus aureus*
3646	S1M10000018D08*	*Staphylococcus aureus*
3647	S1M10000047B01	*Staphylococcus aureus*
3648	S1M10000047H10	*Staphylococcus aureus*
3649	S1M10000001A04	*Staphylococcus aureus*
3650	S1M10000016E01	*Staphylococcus aureus*
3651	S1M10000017E12	*Staphylococcus aureus*
3652	S1M10000019B01	*Staphylococcus aureus*
3653	S1M10000048F03	*Staphylococcus aureus*
3654	S1M10000034A07	*Staphylococcus aureus*
3655	S1M10000023G01	*Staphylococcus aureus*
3656	S1M10000021G12	*Staphylococcus aureus*
3657	S1M10000024E04	*Staphylococcus aureus*
3658	S1M10000028H08	*Staphylococcus aureus*
3659	S1M10000022B07	*Staphylococcus aureus*
3660	S1M10000003A05	*Staphylococcus aureus*
3661	S1M10000003A09	*Staphylococcus aureus*
3662	S1M10000003E01	*Staphylococcus aureus*
3663	S1M10000004C11	*Staphylococcus aureus*
3664	S1M10000007E08	*Staphylococcus aureus*
3665	S1M10000021G06	*Staphylococcus aureus*
3666	S1M10000024C06	*Staphylococcus aureus*
3667	S1M10000024D01	*Staphylococcus aureus*
3668	S1M10000027D07	*Staphylococcus aureus*
3669	S1M10000027E03	*Staphylococcus aureus*
3670	S1M10000027G01	*Staphylococcus aureus*
3671	S1M10000029A03	*Staphylococcus aureus*

SeqID	Clone name	Organism
3672	S1M10000032B10	*Staphylococcus aureus*
3673	S1M10000032C07	*Staphylococcus aureus*
3674	S1M10000038D04	*Staphylococcus aureus*
3675	S1M10000047D07	*Staphylococcus aureus*
3676	S1M10000048B03	*Staphylococcus aureus*
3677	S1M10000048B06	*Staphylococcus aureus*
3678	S1M10000048C10	*Staphylococcus aureus*
3679	S1M10000048F05	*Staphylococcus aureus*
3680	S4M10000001C01	*Salmonella typhimurium*
3681	S4M10000002B06	*Salmonella typhimurium*
3682	S4M10000002B09	*Salmonella typhimurium*
3683	S4M10000002G04	*Salmonella typhimurium*
3684	S4M10000002G08	*Salmonella typhimurium*
3685	S4M10000005G05	*Salmonella typhimurium*
3686	S4M10000005H02	*Salmonella typhimurium*
3687	S4M10000006A06	*Salmonella typhimurium*
3688	S4M10000006A08	*Salmonella typhimurium*
3689	S4M10000006C05	*Salmonella typhimurium*
3690	S4M10000006F08	*Salmonella typhimurium*
3691	S4M10000007G01	*Salmonella typhimurium*
3692	S4M10000008C08	*Salmonella typhimurium*
3693	S4M10000008H10	*Salmonella typhimurium*
3694	S4M10000009A05	*Salmonella typhimurium*
3695	S4M10000010B05	*Salmonella typhimurium*
3696	S4M10000010D04	*Salmonella typhimurium*
3697	S4M10000010H04	*Salmonella typhimurium*
3698	S4M10000011D08	*Salmonella typhimurium*
3699	S4M10000011E08	*Salmonella typhimurium*
3700	S4M10000012B06	*Salmonella typhimurium*
3701	S4M10000012B12	*Salmonella typhimurium*
3702	S4M10000012D02	*Salmonella typhimurium*
3703	S4M10000013H02	*Salmonella typhimurium*
3704	S4M10000014B05	*Salmonella typhimurium*
3705	S4M10000014D04	*Salmonella typhimurium*
3706	S4M10000014D07	*Salmonella typhimurium*
3707	S4M10000014H02	*Salmonella typhimurium*
3708	S4M10000015B11	*Salmonella typhimurium*
3709	S4M10000015E09	*Salmonella typhimurium*
3710	S4M10000016A02	*Salmonella typhimurium*
3711	S4M10000018D09	*Salmonella typhimurium*
3712	S4M10000018E10	*Salmonella typhimurium*
3713	S4M10000018F10	*Salmonella typhimurium*
3714	S4M10000018G03	*Salmonella typhimurium*
3715	S4M10000018H04	*Salmonella typhimurium*
3716	S4M10000019F05	*Salmonella typhimurium*
3717	S4M10000019G04	*Salmonella typhimurium*
3718	S4M10000019G05	*Salmonella typhimurium*

SeqID	Clone name	Organism
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3720	S4M10000020A04	*Salmonella typhimurium*
3721	S4M10000020F05	*Salmonella typhimurium*
3722	S4M10000020G10	*Salmonella typhimurium*
3723	S4M10000022D04	*Salmonella typhimurium*
3724	S4M10000022D12	*Salmonella typhimurium*
3725	S4M10000022E12	*Salmonella typhimurium*
3726	S4M10000022G07	*Salmonella typhimurium*
3727	S4M10000022H06	*Salmonella typhimurium*
3728	S4M10000023F01	*Salmonella typhimurium*
3729	S4M10000024B02	*Salmonella typhimurium*
3730	S4M10000024C06	*Salmonella typhimurium*
3731	S4M10000024C11	*Salmonella typhimurium*
3732	S4M10000024F08	*Salmonella typhimurium*
3733	S4M10000024G01	*Salmonella typhimurium*
3734	S4M10000024G04	*Salmonella typhimurium*
3735	S4M10000024G09	*Salmonella typhimurium*
3736	S4M10000024H02	*Salmonella typhimurium*
3737	S4M10000025A11	*Salmonella typhimurium*
3738	S4M10000025E02	*Salmonella typhimurium*
3739	S4M10000025E05	*Salmonella typhimurium*
3740	S4M10000025H07	*Salmonella typhimurium*
3741	S4M10000026C10	*Salmonella typhimurium*
3742	S4M10000026D04	*Salmonella typhimurium*
3743	S4M10000026E06	*Salmonella typhimurium*
3744	S4M10000026E12	*Salmonella typhimurium*
3745	S4M10000027C10	*Salmonella typhimurium*
3746	S4M10000027E02	*Salmonella typhimurium*
3747	S4M10000029B12	*Salmonella typhimurium*
3748	S4M10000029D12	*Salmonella typhimurium*
3749	S4M10000030D03	*Salmonella typhimurium*
3750	S4M10000030F07	*Salmonella typhimurium*
3751	S4M10000030G11	*Salmonella typhimurium*
3752	S4M10000032B12	*Salmonella typhimurium*
3753	S4M10000033F08	*Salmonella typhimurium*
3754	S4M10000033G05	*Salmonella typhimurium*
3755	S4M10000033G09	*Salmonella typhimurium*
3756	S4M10000034A02	*Salmonella typhimurium*
3757	S4M10000034A09	*Salmonella typhimurium*
3758	S4M10000034D06	*Salmonella typhimurium*
3759	S4M10000034H05	*Salmonella typhimurium*
3760	S4M10000034H09	*Salmonella typhimurium*
3761	S4M10000035B01	*Salmonella typhimurium*
3762	S4M10000035D01	*Salmonella typhimurium*
3763	S4M10000035D02	*Salmonella typhimurium*
3764	S4M10000035E03	*Salmonella typhimurium*
3765	S4M10000035F02	*Salmonella typhimurium*

SeqID	Clone name	Organism
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3767	S4M10000036D07	*Salmonella typhimurium*
3768	S4M10000036F07	*Salmonella typhimurium*
3769	S4M10000037A04	*Salmonella typhimurium*
3770	S4M10000037A10	*Salmonella typhimurium*
3771	S4M10000037E10	*Salmonella typhimurium*
3772	S4M10000037H09	*Salmonella typhimurium*
3773	S4M10000001H01	*Salmonella typhimurium*
3774	S4M10000002F06	*Salmonella typhimurium*
3775	S4M10000008D01	*Salmonella typhimurium*
3776	S4M10000009G11	*Salmonella typhimurium*
3777	S4M10000011F09	*Salmonella typhimurium*
3778	S4M10000020F08	*Salmonella typhimurium*
3779	S4M10000021E07	*Salmonella typhimurium*
3780	S4M10000022B05	*Salmonella typhimurium*
3781	S4M10000025H11	*Salmonella typhimurium*
3782	S4M10000026B10	*Salmonella typhimurium*
3783	S4M10000026E03	*Salmonella typhimurium*
3784	S4M10000029A03	*Salmonella typhimurium*
3785	S4M10000029C11	*Salmonella typhimurium*
3786	S4M10000030F06	*Salmonella typhimurium*
3787	S4M10000032F03	*Salmonella typhimurium*
3788	S4M10000032G01	*Salmonella typhimurium*
3789	S4M10000034C05	*Salmonella typhimurium*
3790	S4M10000034H04	*Salmonella typhimurium*
3791	S4M10000035A09	*Salmonella typhimurium*
3792	S4M10000035B06	*Salmonella typhimurium*
3793	S4M10000035F01	*Salmonella typhimurium*
3794	S4M10000037A08	*Salmonella typhimurium*
3795	S4M10000037E03	*Salmonella typhimurium*

TABLE IB

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000001A02	8	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001A06	9	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001B01	10	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001B02	11	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000001B02	11	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000001B02	11	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000001B05	12	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000001B06	13	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000001B08	14	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001B10	15	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001C02	16	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000001C09	17	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000001D02	18	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000001D04	19	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000001D04	19	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000001D04	19	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000001D05	20	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000001D05	20	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000001D09	21	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001D09	21	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001E01	22	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000001E01	22	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000001E02	23	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000001E03	24	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001E03	24	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001E04	25	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001E08	26	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000001E09	27	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001E09	27	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001F02	28	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000001F04	29	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000001F06	30	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001F07	31	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000001G02	32	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001G03	33	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001G03	33	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001G04	34	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000001G05	35	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000001H02	36	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000001H03	37	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001H03	37	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001H04	38	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000001H04	38	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000001H04	38	EFA102554	5002	EFA1c0022_orf_19p	10532

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000004A04	39	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000004A04	39	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000004C03	40	EFA100478	4880	EFA1c0012_orf_2p	10486
E3M10000004D01	41	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000004D01	41	EFA101413	4938	#N/A	#N/A
E3M10000004D01	41	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000004D02	42	EFA102022	4974	EFA1c0044_orf_106p	10881
E3M10000004D02	42	EFA102023	4975	EFA1c0044_orf_107p	10882
E3M10000004D10	43	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000004D10	43	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000004E11	44	EFA101086	4910	EFA1c0040_orf_90p	10763
E3M10000004F08	45	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000004F08	45	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000004F10	46	EFA101086	4910	EFA1c0040_orf_90p	10763
E3M10000004G01	47	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000004H11	48	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000004H11	48	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005A07	49	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005B01	50	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000005B01	50	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000005B08	51	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005B08	51	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005C01	52	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000005C03	53	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005C04	54	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000005C04	54	EFA102453	4993	EFA1c0045_orf_203p	10931
E3M10000005C04	54	EFA102728	5006	EFA1c0045_orf_93p	10948
E3M10000005D03	55	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005D04	56	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000005D10	57	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005D10	57	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005E01	58	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005E01	58	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005E02	59	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005E02	59	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005E03	60	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005E08	61	EFA101403	4932	EFA1c0033_orf_54p	10662
E3M10000005F07	62	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000005F10	63	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005F10	63	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005G05	64	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005G05	64	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005H04	65	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000006B03	66	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000006B03	66	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000006C01	67	EFA101416	4941	EFA1c0022_orf_17p	10530

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000006C01	67	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000006C12	68	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000006C12	68	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000006D03	69	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000006D03	69	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000006E11	70	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000006E11	70	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000006F04	71	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000006F04	71	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000006G04	72	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000006G04	72	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000006G12	73	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000006G12	73	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000006H09	74	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000007A02	75	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007A02	75	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007B02	76	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007B02	76	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007B03	77	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007B03	77	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007C03	78	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000007C03	78	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000007C04	79	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000007D03	80	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007D03	80	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007E05	81	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000007E05	81	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000007E05	81	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000007F01	82	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007F01	82	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007F06	83	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007F06	83	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007G01	84	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007G01	84	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000008C03	85	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000008C08	86	EFA101536	4946	EFA1c0042_orf_46p	10823
E3M10000008C09	87	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000008D08	88	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000008E02	89	EFA100783	4895	EFA1c0042_orf_141p	10811
E3M10000008G05	90	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000008G05	90	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000008G09	91	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000008G09	91	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000008H02	92	EFA101695	4954	EFA1c0031_orf_6p	10629
E3M10000009C07	93	EFA103508	5029	EFA1c0033_orf_95p	10672
E3M10000009C09	94	EFA100870	4899	EFA1c0031_orf_36p	10627

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000009D01	95	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000009E02	96	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000009E02	96	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000009E03	97	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000009E05	98	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000009G02	99	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000010C08	100	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000010D05	101	EFA100757	4894	EFA1c0044_orf_27p	10897
E3M10000010F01	102	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000010G05	103	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000010G07	104	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000010G09	105	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000010G10	106	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000010H02	107	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000011A09	108	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000011B03	109	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000011B09	110	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000011C07	111	EFA101790	4959	EFA1c0042_orf_111p	10803
E3M10000011D03	112	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000011D03	112	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000011H02	113	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000011H05	114	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000012B01	115	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000012B02	116	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000012B07	117	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000012B07	117	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000012B07	117	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000012B08	118	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000012C01	119	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000012D10	120	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000012E08	121	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000012F05	122	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000012F06	123	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000012F07	124	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000012F07	124	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000012F10	125	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000012F10	125	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000012G02	126	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000012G07	127	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000012G07	127	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000013A06	128	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000013A07	129	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000013C05	130	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000013C05	130	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000013D02	131	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000013D08	132	EFA101415	4940	EFA1c0022_orf_16p	10529

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000013D10	133	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000013D10	133	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000013E02	134	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000013E08	135	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000013F05	136	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000013F12	137	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000013F12	137	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000013G10	138	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000013H03	139	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000013H05	140	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000013H10	141	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000014B12	142	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000014B12	142	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000014B12	142	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000014E12	143	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000014E12	143	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000014G09	144	EFA100991	4905	EFA1c0035_orf_60p	10681
E3M10000014G09	144	EFA103033	5016	EFA1c0035_orf_60p	10681
E3M10000015B04	145	EFA100065	4863	EFA1c0042_orf_14p	10813
E3M10000015B12	146	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000015E12	147	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000015E12	147	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000016A03	148	EFA101753	4957	EFA1c0022_orf_50p	10552
E3M10000016A04	149	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000016C11	150	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000016C11	150	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000016D03	151	EFA102774	5009	EFA1c0044_orf_25p	10896
E3M10000016F06	152	EFA102205	4983	EFA1c0041_orf_115p	10769
E3M10000016F10	153	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000016F10	153	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000016H05	154	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000016H10	155	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000017A09	156	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000017A09	156	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000017D09	157	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000018A07	158	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000018C02	159	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000018E01	160	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000018G09	161	EFA101583	4949	EFA1c0026_orf_23p	10593
E3M10000018H06	162	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000019B06	163	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000019D02	164	EFA102022	4974	EFA1c0044_orf_106p	10881
E3M10000019E03	165	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000019E03	165	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000019E04	166	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000020G04	167	EFA100870	4899	EFA1c0031_orf_36p	10627

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000020H05	168	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000021A08	169	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000021A08	169	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000021A11	170	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000021B10	171	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000021C03	172	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000021C04	173	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000021C08	174	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000021D04	175	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000021D04	175	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000021E10	176	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000021G04	177	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000021G10	178	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000021G11	179	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000021H11	180	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000022A04	181	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022A11	182	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000022B04	183	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022B05	184	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022B05	184	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000022B07	185	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000022C05	186	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000022C05	186	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000022C06	187	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000022C09	188	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000022D04	189	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000022F05	190	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000022F06	191	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000022F06	191	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000022F08	192	EFA101410	4935	EFA1c0022_orf_12p	10525
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E3M10000022G12	194	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000023A03	195	EFA101413	4938	#N/A	#N/A
E3M10000023A06	196	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000023A07	197	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000023A09	198	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000023B02	199	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000023B02	199	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000023B06	200	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000023C03	201	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000023C03	201	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000023C04	202	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000023C06	203	EFA101413	4938	#N/A	#N/A
E3M10000023C08	204	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000023C09	205	EFA101159	4916	EFA1c0022_orf_2p	10543

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000023C09	205	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000023D02	206	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000023D04	207	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000023D10	208	EFA101413	4938	#N/A	#N/A
E3M10000023E04	209	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000023E07	210	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000023E09	211	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000023F02	212	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000023F10	213	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000023G02	214	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000023G04	215	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000023G10	216	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000023H08	217	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000024A03	218	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000024A04	219	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000024A08	220	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000024A08	220	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000024C06	221	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000025A06	222	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000025B01	223	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000025B01	223	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000025B03	224	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000025B03	224	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000025B05	225	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000025B10	226	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000025C01	227	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000025C04	228	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000025C05	229	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000025C05	229	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000025C07	230	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000025C08	231	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000025C08	231	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000025C09	232	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000025C11	233	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000025D01	234	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000025D01	234	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000025D10	235	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000025E07	236	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000025E08	237	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000025E12	238	EFA102728	5006	EFA1c0045_orf_93p	10948
E3M10000025F04	239	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000025F04	239	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000025F06	240	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000025F06	240	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000025F06	240	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000025F08	241	EFA103038	5017	EFA1c0030_orf_17p	10613

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000025F10	243	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000025F11	244	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000025F12	245	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000025G02	246	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000025G07	247	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000025G09	248	EFA102185	4980	EFA1c0045_orf_95p	10950
E3M10000027A02	249	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000027A07	250	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027A09	251	EFA101413	4938	#N/A	#N/A
E3M10000027A09	251	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000027B07	252	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000027B08	253	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027B09	254	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000027B09	254	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000027C02	255	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000027C03	256	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027C08	257	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000027D03	258	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000027D03	258	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000027D05	259	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000027D08	260	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000027D10	261	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000027G01	262	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000027G08	263	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000027H04	264	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027H07	265	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000027H07	265	EFA101162	4919	EFA1c0022_orf_5p	10555
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E3M10000028A03	267	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000028A04	268	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000028A04	268	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000028A05	269	EFA101080	4909	#N/A	#N/A
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E3M10000028A06	270	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000028A08	271	EFA101424	4943	EFA1c0041_orf_39p	10784
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E3M10000028B01	272	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000028B02	273	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028B02	273	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028B03	274	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000028B04	275	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000028B05	276	EFA101424	4943	EFA1c0041_orf_39p	10784
E3M10000028B05	276	EFA101425	4944	EFA1c0041_orf_40p	10785
E3M10000028B06	277	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000028B07	278	EFA101160	4917	EFA1c0022_orf_3p	10549

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000028C01	280	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028C01	280	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028C02	281	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028C02	281	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028C04	282	EFA101322	4927	EFA1c0030_orf_57p	10620
E3M10000028C05	283	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000028C06	284	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000028C07	285	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000028C08	286	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028C08	286	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028D01	287	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000028D01	287	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000028D02	288	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000028D05	289	EFA101080	4909	#N/A	#N/A
E3M10000028D06	290	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000028D08	291	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000028E01	292	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000028E04	293	EFA101370	4931	EFA1c0040_orf_103p	10738
E3M10000028E07	294	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028F02	295	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000028F03	296	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000028F03	296	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000028F03	296	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000028F04	297	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000028F04	297	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000028F05	298	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000028F06	299	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000028F07	300	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000028G05	301	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000028G06	302	EFA100748	4892	EFA1c0011_orf_10p	10483
E3M10000028G07	303	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000028G07	303	EFA101411	4936	EFA1c0022_orf_13p	10526
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E3M10000029A02	306	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000029A04	307	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000029A05	308	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000029A10	309	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000029A11	310	EFA101413	4938	#N/A	#N/A
E3M10000029B01	311	EFA103295	5024	EFA1c0032_orf_1p	10633
E3M10000029B02	312	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000029B05	313	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000029B06	314	EFA100914	4900	EFA1c0024_orf_9p	10579
E3M10000029B08	315	EFA102338	4987	EFA1c0032_orf_8p	10651
E3M10000029B11	316	EFA100397	4877	EFA1c0041_orf_148p	10773

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000029B12	317	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000029C01	318	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000029C02	319	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000029C03	320	EFA102253	4984	EFA1c0038_orf_85p	10727
E3M10000029C04	321	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000029C05	322	EFA100399	4878	EFA1c0041_orf_104p	10766
E3M10000029C06	323	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000029C06	323	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000029C07	324	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000029C07	324	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000029C08	325	EFA101868	4966	EFA1c0042_orf_69p	10829
E3M10000029C09	326	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000029C10	327	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029C12	328	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000029D01	329	EFA101080	4909	#N/A	#N/A
E3M10000029D03	330	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000029D04	331	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029D05	332	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000029D06	333	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000029D06	333	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000029D08	334	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000029D12	335	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000029E01	336	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000029E02	337	EFA102051	4976	#N/A	#N/A
E3M10000029E03	338	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000029E05	339	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000029E07	340	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000029E08	341	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000029E09	342	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029E12	343	EFA100397	4877	EFA1c0041_orf_148p	10773
E3M10000029F01	344	EFA100023	4862	EFA1c0017_orf_1p	10505
E3M10000029F05	345	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000029F06	346	EFA101795	4962	EFA1c0045_orf_165p	10922
E3M10000029F09	347	EFA100689	4886	EFA1c0038_orf_54p	10717
E3M10000029F10	348	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000029F11	349	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000029F12	350	EFA102282	4985	EFA1c0038_orf_89p	10729
E3M10000029G01	351	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000029G04	352	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029G05	353	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000029G07	354	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000029G08	355	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000029G09	356	EFA102201	4982	#N/A	#N/A
E3M10000029G10	357	EFA101797	4963	EFA1c0045_orf_167p	10924
E3M10000029G11	358	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000029G12	359	EFA101541	4948	EFA1c0012_orf_5p	10488

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000029H02	360	EFA101339	4928	EFA1c0040_orf_13p	10743
E3M10000029H02	360	EFA101340	4929	EFA1c0040_orf_15p	10745
E3M10000029H04	361	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000029H04	361	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000029H05	362	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000029H07	363	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000029H08	364	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000029H11	365	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000030A05	366	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030A08	367	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000030A09	368	EFA102501	4994	EFA1c0031_orf_35p	10626
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E3M10000030B03	370	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000030B04	371	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000030B05	372	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030B06	373	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000030B07	374	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000030B08	375	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030B10	376	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000030B11	377	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000030B12	378	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000030B12	378	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000030C03	379	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000030C04	380	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000030C12	381	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000030D02	382	EFA102350	4988	EFA1c0032_orf_19p	10632
E3M10000030D05	383	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000030D08	384	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000030D09	385	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000030D10	386	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030D12	387	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000030E01	388	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000030E01	388	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000030E02	389	EFA100329	4875	EFA1c0041_orf_35p	10782
E3M10000030E04	390	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000030E08	391	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000030E09	392	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000030E10	393	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030F01	394	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000030F04	395	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000030F06	396	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000030F07	397	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030F10	398	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000030F12	399	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000030G01	400	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000030G03	401	EFA100023	4862	EFA1c0017_orf_1p	10505

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000030G08	403	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030G09	404	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000030G12	405	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000030H03	406	EFA101258	4926	EFA1c0045_orf_160p	10918
E3M10000030H04	407	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000030H06	408	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000030H07	409	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000030H08	410	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030H10	411	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000030H11	412	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000031A02	413	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000031A06	414	EFA100970	4903	EFA1c0044_orf_98p	10906
E3M10000031A07	415	EFA102201	4982	#N/A	#N/A
E3M10000031A08	416	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000031B02	417	EFA100289	4872	EFA1c0042_orf_139p	10810
E3M10000031B03	418	EFA100426	4879	EFA1c0036_orf_59p	10702
E3M10000031B04	419	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000031B09	420	EFA102183	4979	EFA1c0045_orf_97p	10952
E3M10000031B10	421	EFA101253	4924	EFA1c0043_orf_178p	10852
E3M10000031B11	422	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000031B12	423	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000031C01	424	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000031C04	425	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000031C06	426	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000031C10	427	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000031C11	428	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000031C12	429	EFA100668	4885	EFA1c0035_orf_58p	10679
E3M10000031D03	430	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000031D04	431	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000031D08	432	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000031E03	433	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000031E09	434	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000031F02	435	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000031F02	435	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000031F04	436	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000031F07	437	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000031F09	438	EFA102764	5008	EFA1c0008_orf_3p	10478
E3M10000031F11	439	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000031F11	439	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000031G03	440	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000031G04	441	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000031G05	442	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000031G06	443	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000031G07	444	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000031G08	445	EFA100295	4873	EFA1c0021_orf_15p	10517

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000031H05	447	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000031H06	448	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000031H07	449	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000031H08	450	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000031H10	451	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000031H11	452	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000031H11	452	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000032A02	453	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000032A04	454	EFA101670	4950	EFA1c0019_orf_20p	10511
E3M10000032A06	455	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000032A07	456	EFA101670	4950	EFA1c0019_orf_20p	10511
E3M10000032A08	457	EFA100329	4875	EFA1c0041_orf_35p	10782
E3M10000032A09	458	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000032A10	459	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000032A11	460	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000032A11	460	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000032B03	461	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000032B04	462	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000032B07	463	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000032B08	464	EFA102698	5005	EFA1c0045_orf_115p	10909
E3M10000032B09	465	EFA102051	4976	#N/A	#N/A
E3M10000032B11	466	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000032B12	467	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000032C01	468	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000032C02	469	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000032C03	470	EFA103348	5025	EFA1c0043_orf_67p	10873
E3M10000032C04	471	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000032C06	472	EFA101150	4915	EFA1c0038_orf_57p	10719
E3M10000032C09	473	EFA100740	4889	EFA1c0022_orf_22p	10536
E3M10000032C11	474	EFA102501	4994	EFA1c0031_orf_35p	10626
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E3M10000032D01	476	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000032D02	477	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000032D03	478	EFA100399	4878	EFA1c0041_orf_104p	10766
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E3M10000032E04	482	EFA101792	4961	EFA1c0042_orf_113p	10805
E3M10000032E04	482	EFA103786	5031	EFA1c0042_orf_114p	10806
E3M10000032E05	483	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000032E08	484	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000032E10	485	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000032E10	485	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000032E11	486	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000032E12	487	EFA102326	4986	#N/A	#N/A

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000032F02	488	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000032F03	489	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000032F05	490	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000032F07	491	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000032F08	492	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000032F11	493	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000032F12	494	EFA102201	4982	#N/A	#N/A
E3M10000032G01	495	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000032G02	496	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000032G04	497	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000032G05	498	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000032G06	499	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000032G07	500	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000032H05	501	EFA100200	4869	EFA1c0041_orf_88p	10798
E3M10000032H06	502	EFA101833	4965	EFA1c0038_orf_61p	10720
E3M10000032H08	503	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000032H09	504	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000032H10	505	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000033A03	506	EFA101253	4924	EFA1c0043_orf_178p	10852
E3M10000033A04	507	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000033A05	508	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000033A06	509	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000033A07	510	EFA102774	5009	EFA1c0044_orf_25p	10896
E3M10000033A08	511	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000033A11	512	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000033B01	513	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000033B02	514	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000033B04	515	EFA101765	4958	EFA1c0025_orf_33p	10587
E3M10000033B05	516	EFA102541	4998	EFA1c0028_orf_3p	10602
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E3M10000033B08	518	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000033B09	519	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000033C01	520	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000033C02	521	EFA103174	5021	EFA1c0036_orf_120p	10689
E3M10000033C05	522	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000033C05	522	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000033C09	523	EFA100811	4898	EFA1c0022_orf_33p	10546
E3M10000033C10	524	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000033C10	524	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000033C11	525	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000033C12	526	EFA102389	4992	EFA1c0044_orf_83p	10904
E3M10000033D01	527	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000033D04	528	EFA101682	4951	EFA1c0041_orf_53p	10789
E3M10000033D05	529	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000033D06	530	EFA100641	4883	EFA1c0041_orf_57p	10793

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000033D09	531	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000033D10	532	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000033D11	533	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000033E02	534	EFA101477	4945	EFA1c0043_orf_224p	10861
E3M10000033E03	535	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000033E03	535	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000033E04	536	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000033E05	537	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000033E07	538	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033E08	539	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000033E09	540	EFA100617	4882	EFA1c0040_orf_93p	10764
E3M10000033E11	541	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000033F01	542	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033F03	543	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000033F04	544	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000033F05	545	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000033F07	546	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033F08	547	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000033F10	548	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000033F12	549	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000033F12	549	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000033G01	550	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000033G02	551	EFA102813	5013	EFA1c0043_orf_9p	10878
E3M10000033G03	552	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000033G04	553	EFA102326	4986	#N/A	#N/A
E3M10000033G06	554	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000033G07	555	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000033G08	556	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000033G09	557	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000033G12	558	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000033H02	559	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000033H04	560	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000033H05	561	EFA100741	4890	EFA1c0022_orf_21p	10535
E3M10000033H07	562	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033H08	563	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000033H09	564	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000033H10	565	EFA101079	4908	#N/A	#N/A
E3M10000033H11	566	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000034A02	567	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000034A03	568	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000034A04	569	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000034B02	570	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000034B04	571	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000034C04	572	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000034D01	573	EFA100704	4887	EFA1c0010_orf_4p	10482

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000034E01	575	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000034E04	576	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000034F02	577	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000034F03	578	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000034F04	579	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000034G02	580	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000034G03	581	EFA100740	4889	EFA1c0022_orf_22p	10536
E3M10000034H02	582	EFA101257	4925	EFA1c0045_orf_159p	10917
E3M10000034H03	583	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000035A02	584	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000035A04	585	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035A05	586	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000035A06	587	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035A08	588	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035A09	589	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000035A11	590	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000035B01	591	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000035B03	592	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035B06	593	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000035B07	594	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035B08	595	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000035B10	596	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000035B11	597	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035B12	598	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035C01	599	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035C03	600	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000035C04	601	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035C05	602	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000035C06	603	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000035C07	604	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000035C08	605	EFA100741	4890	EFA1c0022_orf_21p	10535
E3M10000035C08	605	EFA100742	4891	EFA1c0022_orf_20p	10534
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E3M10000035C11	607	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035C12	608	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035D02	609	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000035D03	610	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000035D04	611	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000035D05	612	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000035D10	613	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035D11	614	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000035E03	615	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000035E04	616	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000035E05	617	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000035E07	618	EFA100919	4901	EFA1c0013_orf_12p	10491

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000035E09	620	EFA100312	4874	EFA1c0032_orf_28p	10641
E3M10000035E10	621	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000035E11	622	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000035E12	623	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035F01	624	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000035F02	625	EFA101925	4971	EFA1c0044_orf_19p	10893
E3M10000035F03	626	EFA100312	4874	EFA1c0032_orf_28p	10641
E3M10000035F06	627	EFA101080	4909	#N/A	#N/A
E3M10000035F07	628	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000035F08	629	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035F09	630	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000035F09	630	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000035F11	631	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035F12	632	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000035G02	633	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000035G02	633	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000035G04	634	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000035G05	635	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000035G08	636	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000035G09	637	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000035G09	637	EFA103508	5029	EFA1c0033_orf_95p	10672
E3M10000035G10	638	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035G11	639	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000035H03	640	EFA101080	4909	#N/A	#N/A
E3M10000035H06	641	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000035H09	642	EFA102501	4994	EFA1c0031_orf_35p	10626
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E3M10000035H11	643	EFA101258	4926	EFA1c0045_orf_160p	10918
E3M10000036A03	644	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000036A04	645	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000036A05	646	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000036A06	647	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000036A07	648	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000036A08	649	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000036A09	650	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000036A10	651	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000036B01	652	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036B03	653	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000036B06	654	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036B07	655	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000036B08	656	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000036B09	657	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000036B11	658	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000036B12	659	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036B12	659	EFA101163	4920	EFA1c0022_orf_6p	10557

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000036C03	661	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000036C06	662	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036C07	663	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000036C08	664	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000036C09	665	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000036C10	666	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000036C11	667	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000036D03	668	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000036D04	669	EFA102201	4982	#N/A	#N/A
E3M10000036D06	670	EFA100740	4889	EFA1c0022_orf_22p	10536
E3M10000036D08	671	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000036D09	672	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000036D10	673	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036D11	674	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000036D12	675	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036E01	676	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036E04	677	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036E05	678	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000036E07	679	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000036E08	680	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000036F03	681	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000036F04	682	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000036F05	683	EFA101792	4961	EFA1c0042_orf_113p	10805
E3M10000036F08	684	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036F09	685	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000036F10	686	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036F12	687	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000036G01	688	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000036G01	688	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000036G02	689	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036G03	690	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000036G04	691	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036G06	692	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000036G10	693	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036H02	694	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000036H03	695	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000036H04	696	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000036H05	697	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000036H06	698	EFA101162	4919	EFA1c0022_orf_5p	10555
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E3M10000036H08	700	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000036H09	701	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036H10	702	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000037A03	703	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000037A06	704	EFA100870	4899	EFA1c0031_orf_36p	10627

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000037A09	706	EFA100756	4893	EFA1c0024_orf_39p	10575
E3M10000037A10	707	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000037B02	708	EFA100641	4883	EFA1c0041_orf_57p	10793
E3M10000037B02	708	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000037B07	709	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000037B08	710	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000037B11	711	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000037C01	712	EFA101080	4909	#N/A	#N/A
E3M10000037C02	713	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000037C04	714	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000037C05	715	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000037C07	716	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000037C07	716	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000037C11	717	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000037C12	718	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000037D02	719	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000037D03	720	EFA100795	4896	EFA1c0043_orf_229p	10863
E3M10000037D03	720	EFA103081	5020	EFA1c0043_orf_228p	10862
E3M10000037D04	721	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037D05	722	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000037D06	723	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000037D09	724	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000037D09	724	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000037D11	725	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037E01	726	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000037E02	727	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000037E03	728	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000037E05	729	EFA101080	4909	#N/A	#N/A
E3M10000037E07	730	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037E08	731	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000037E10	732	EFA101253	4924	EFA1c0043_orf_178p	10852
E3M10000037E12	733	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000037F01	734	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000037F02	735	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000037F06	736	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037F07	737	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037F12	738	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000037G01	739	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000037G02	740	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000037G03	741	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000037G05	742	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000037G06	743	EFA103295	5024	EFA1c0032_orf_1p	10633
E3M10000037G07	744	EFA101541	4948	EFA1c0012_orf_5p	10488
E3M10000037G08	745	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000037G10	746	EFA101412	4937	EFA1c0022_orf_14p	10527

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000037G11	747	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000037H02	748	EFA101413	4938	#N/A	#N/A
E3M10000037H05	749	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000037H07	750	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000037H10	751	EFA101080	4909	#N/A	#N/A
E3M10000037H11	752	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000038A02	753	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000038A03	754	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000038A05	755	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000038A06	756	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000038A07	757	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000038A09	758	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000038A10	759	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000038A11	760	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000038B02	761	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000038B03	762	EFA102389	4992	EFA1c0044_orf_83p	10904
E3M10000038B04	763	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000038B05	764	EFA100795	4896	EFA1c0043_orf_229p	10863
E3M10000038B05	764	EFA103081	5020	EFA1c0043_orf_228p	10862
E3M10000038B07	765	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000038B08	766	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038B09	767	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000038B11	768	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000038C02	769	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000038C03	770	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000038C05	771	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000038C07	772	EFA101963	4972	EFA1c0043_orf_162p	10848
E3M10000038C10	773	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000038C12	774	EFA101080	4909	#N/A	#N/A
E3M10000038D01	775	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038D02	776	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000038D04	777	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038D08	778	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038D10	779	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000038D11	780	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000038D12	781	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038E02	782	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000038E03	783	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000038E04	784	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038E05	785	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000038E07	786	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000038E08	787	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000038E11	788	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000038F02	789	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000038F04	790	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000038F05	791	EFA101160	4917	EFA1c0022_orf_3p	10549

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000038F06	792	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000038F07	793	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000038F09	794	EFA102185	4980	EFA1c0045_orf_95p	10950
E3M10000038F10	795	EFA101080	4909	#N/A	#N/A
E3M10000038F11	796	EFA100740	4889	EFA1c0022_orf_22p	10536
E3M10000038G02	797	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000038G03	798	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000038G06	799	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000038G07	800	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000038G07	800	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000038G11	801	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000038H02	802	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000038H05	803	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038H06	804	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000038H07	805	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000038H08	806	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000038H09	807	EFA102802	5012	EFA1c0043_orf_18p	10854
E3M10000038H10	808	EFA101541	4948	EFA1c0012_orf_5p	10488
E3M10000039A02	809	EFA101736	4955	EFA1c0041_orf_14p	10775
E3M10000039A02	809	EFA101737	4956	EFA1c0041_orf_15p	10778
E3M10000039A06	810	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000039A07	811	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000039A08	812	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039A10	813	EFA101257	4925	EFA1c0045_orf_159p	10917
E3M10000039A11	814	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000039B01	815	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000039B03	816	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000039B04	817	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000039B04	817	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000039B06	818	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000039B07	819	EFA102110	4978	EFA1c0042_orf_99p	10841
E3M10000039B08	820	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000039B09	821	EFA101792	4961	EFA1c0042_orf_113p	10805
E3M10000039B11	822	EFA101080	4909	#N/A	#N/A
E3M10000039C02	823	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000039C04	824	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039C05	825	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000039C06	826	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000039C07	827	EFA101791	4960	EFA1c0042_orf_112p	10804
E3M10000039C07	827	EFA101792	4961	EFA1c0042_orf_113p	10805
E3M10000039C08	828	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000039C09	829	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000039C10	830	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039D02	831	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000039D03	832	EFA102655	5003	EFA1c0039_orf_25p	10733

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000039D06	834	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000039E01	835	EFA102201	4982	#N/A	#N/A
E3M10000039E02	836	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000039E03	837	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000039E05	838	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000039E07	839	EFA103295	5024	EFA1c0032_orf_1p	10633
E3M10000039E08	840	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000039F01	841	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000039F02	842	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000039F03	843	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000039F03	843	EFA103375	5027	EFA1c0033_orf_40p	10660
E3M10000039F06	844	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000039F07	845	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000039F08	846	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039G01	847	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000039G02	848	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000039G05	849	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000039G07	850	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000039G09	851	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000039G10	852	EFA101682	4951	EFA1c0041_orf_53p	10789
E3M10000039H02	853	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000039H07	854	EFA101080	4909	#N/A	#N/A
E3M10000039H08	855	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000039H10	856	EFA101413	4938	#N/A	#N/A
E3M10000039H11	857	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000039H11	857	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000040A03	858	EFA101123	4913	EFA1c0040_orf_22p	10748
E3M10000040A05	859	EFA101080	4909	#N/A	#N/A
E3M10000040A07	860	EFA100157	4865	EFA1c0034_orf_63p	10673
E3M10000040A09	861	EFA102502	4995	EFA1c0031_orf_36p	10627
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E3M10000040A11	863	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000040B01	864	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000040B02	865	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000040B05	866	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000040B05	866	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000040B06	867	EFA102518	4997	EFA1c0032_orf_46p	10647
E3M10000040B08	868	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000040B09	869	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000040B10	870	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000040B11	871	EFA102764	5008	EFA1c0008_orf_3p	10478
E3M10000040B12	872	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000040C02	873	EFA101080	4909	#N/A	#N/A
E3M10000040C05	874	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000040C06	875	EFA102091	4977	EFA1c0010_orf_3p	10481

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000040C08	877	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000040C09	878	EFA100165	4866	EFA1c0032_orf_23p	10637
E3M10000040C09	878	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000040C10	879	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000040C11	880	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000040C12	881	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000040D03	882	EFA102201	4982	#N/A	#N/A
E3M10000040D04	883	EFA101080	4909	#N/A	#N/A
E3M10000040D08	884	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000040D12	885	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000040E02	886	EFA102051	4976	#N/A	#N/A
E3M10000040E10	887	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000040E11	888	EFA103039	5018	EFA1c0043_orf_16p	10850
E3M10000040E12	889	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000040F01	890	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000040F03	891	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000040F08	892	EFA101080	4909	#N/A	#N/A
E3M10000040F09	893	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000040F10	894	EFA102051	4976	#N/A	#N/A
E3M10000040G01	895	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000040G02	896	EFA101424	4943	EFA1c0041_orf_39p	10784
E3M10000040G02	896	EFA101425	4944	EFA1c0041_orf_40p	10785
E3M10000040G04	897	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000040G05	898	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000040G07	899	EFA101079	4908	#N/A	#N/A
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E3M10000040G08	900	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000040G09	901	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000040G11	902	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000040H02	903	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000040H03	904	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000040H04	905	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000040H04	905	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000040H05	906	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000040H05	906	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000040H09	907	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000040H09	907	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041A03	908	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000041A05	909	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000041A08	910	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041A09	911	EFA101354	4930	EFA1c0032_orf_69p	10648
E3M10000041A10	912	EFA100001	4861	EFA1c0030_orf_3p	10618
E3M10000041A11	913	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000041A11	913	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000041B02	914	EFA102656	5004	EFA1c0039_orf_26p	10734

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E3M10000041B05	916	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041B06	917	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041B08	918	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000041B09	919	EFA101924	4970	EFA1c0044_orf_18p	10891
E3M10000041B09	919	EFA101925	4971	EFA1c0044_orf_19p	10893
E3M10000041B10	920	EFA101080	4909	#N/A	#N/A
E3M10000041B11	921	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000041B11	921	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041B12	922	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000041C01	923	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000041C07	924	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000041C08	925	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000041C09	926	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000041C10	927	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000041C11	928	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000041C12	929	EFA100798	4897	EFA1c0042_orf_160p	10818
E3M10000041D02	930	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000041D03	931	EFA101060	4907	EFA1c0038_orf_73p	10722
E3M10000041D04	932	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000041D04	932	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000041D05	933	EFA101080	4909	#N/A	#N/A
E3M10000041D06	934	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000041D08	935	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041D09	936	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000041D10	937	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000041D11	938	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041D12	939	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000041E02	940	EFA101797	4963	EFA1c0045_orf_167p	10924
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E3M10000041E05	942	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000041E07	943	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041E10	944	EFA100704	4887	EFA1c0010_orf_4p	10482
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E3M10000041F03	946	EFA102503	4996	EFA1c0032_orf_32p	10643
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E3M10000041F06	948	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000041F07	949	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000041F08	950	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000041F09	951	EFA101417	4942	EFA1c0022_orf_18p	10531
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E3M10000041G02	954	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000041G03	955	EFA102253	4984	EFA1c0038_orf_85p	10727
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E3M10000041G08	959	EFA100704	4887	EFA1c0010_orf_4p	10482
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E3M10000041G10	961	EFA100394	4876	EFA1c0034_orf_6p	10675
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E3M10000041H06	965	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000041H07	966	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000041H08	967	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000041H09	968	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000041H10	969	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000041H11	970	EFA102253	4984	EFA1c0038_orf_85p	10727
E3M10000042A03	971	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000042A03	971	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000042A08	972	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000042A10	973	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000042B01	974	EFA101404	4933	EFA1c0033_orf_55p	10663
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E3M10000042B08	977	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000042B09	978	EFA101797	4963	EFA1c0045_orf_167p	10924
E3M10000042B10	979	EFA101121	4912	EFA1c0036_orf_112p	10686
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E3M10000042C02	981	EFA101150	4915	EFA1c0038_orf_57p	10719
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E3M10000042C04	983	EFA102656	5004	EFA1c0039_orf_26p	10734
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E3M10000042D02	986	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000042D03	987	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000042D06	988	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000042D09	989	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000042D11	990	EFA101412	4937	EFA1c0022_orf_14p	10527
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E3M10000042G08	998	EFA102780	5010	EFA1c0045_orf_101p	10908
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E3M10000043A02	1004	EFA101799	4964	EFA1c0045_orf_169p	10926
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E3M10000043A09	1008	EFA101414	4939	EFA1c0022_orf_15p	10528
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E3M10000043B03	1013	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000043B06	1014	EFA101404	4933	EFA1c0033_orf_55p	10663
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E3M10000043E03	1028	EFA100397	4877	EFA1c0041_orf_148p	10773
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E3M10000043F08	1036	EFA101121	4912	EFA1c0036_orf_112p	10686
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K1M10000007F01	1057	KPN104183	5041	KPN1c1646_orf_2p	11650
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K1M10000008C02	1058	KPN107626	5051	#N/A	#N/A
K1M10000008C10	1059	KPN101729	5036	KPN1c1566_orf_1p	11647
K1M10000008G10	1060	KPN106840	5050	KPN1c2087_orf_1p	11664
K1M10000009D04	1061	KPN107776	5052	KPN1c4041_orf_1p	11771
K1M10000013E04	1062	KPN105779	5047	KPN1c4012_orf_1p	11770
K1M10000020B02	1065	KPN101729	5036	KPN1c1566_orf_1p	11647
K1M10000022C10	1067	KPN100854	5033	KPN1c0845_orf_1p	11630
K1M10000030C07	1070	KPN104716	5045	KPN1c3094_orf_5p	11757
K1M10000030E07	1071	KPN104538	5044	KPN1c2918_orf_2p	11726
K1M10000032E11	1073	KPN101729	5036	KPN1c1566_orf_1p	11647
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P1M10000040D04	1145	PA0378	5062	#N/A	#N/A
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P1M10000040E10	1147	PA2128	5100	#N/A	#N/A
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P1M10000053E07	1178	PA4254	5170	#N/A	#N/A
P1M10000053F08	1179	PA1270	5082	#N/A	#N/A
P1M10000055A11	1180	PA5076	5204	#N/A	#N/A
P1M10000055C08	1181	PA1493	5088	#N/A	#N/A
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P1M10000056C07	1183	PA1360	5084	#N/A	#N/A
P1M10000056F05	1184	PA4258	5173	#N/A	#N/A
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P1M10000058B07	1187	PA5436	5215	#N/A	#N/A
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P1M10000059B10	1189	PA4269	5179	#N/A	#N/A
P1M10000059B11	1190	PA0934	5077	#N/A	#N/A
P1M10000059D11	1191	PA4027	5149	#N/A	#N/A
P1M10000059H08	1192	PA4027	5149	#N/A	#N/A
P1M10000059H09	1193	PA4271	5180	#N/A	#N/A
P1M10000060E03	1194	PA0423	5067	#N/A	#N/A
P1M10000060H02	1195	PA0221	5057	#N/A	#N/A
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P1M10000061B04	1197	PA2726	5119	#N/A	#N/A
P1M10000061E04	1198	PA4244	5160	#N/A	#N/A
P1M10000061F04	1199	PA3522	5136	#N/A	#N/A
P1M10000062A12	1200	PA4598	5194	#N/A	#N/A
P1M10000062C03	1201	PA0321	5059	#N/A	#N/A
P1M10000062C04	1202	PA4254	5170	#N/A	#N/A
P1M10000062C07	1203	PA4251	5167	#N/A	#N/A
P1M10000062C12	1204	PA5316	5212	#N/A	#N/A
P1M10000062D07	1205	PA4247	5163	#N/A	#N/A
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P1M10000065A04	1222	PA3522	5136	#N/A	#N/A
P1M10000065B07	1223	PA4347	5184	#N/A	#N/A
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P1M10000065D06	1226	PA4347	5184	#N/A	#N/A
P1M10000065F01	1227	PA2494	5111	#N/A	#N/A
P1M10000065G06	1228	PA0423	5067	#N/A	#N/A
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P1M10000067A05	1233	PA3876	5144	#N/A	#N/A
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P1M10000067A06	1234	PA0419	5066	#N/A	#N/A
P1M10000067A08	1235	PA0600	5071	#N/A	#N/A
P1M10000067C04	1236	PA3845	5142	#N/A	#N/A
P1M10000067C06	1237	PA4433	5188	#N/A	#N/A
P1M10000067D05	1238	PA3479	5134	#N/A	#N/A
P1M10000067F05	1239	PA3643	5137	#N/A	#N/A
P1M10000067G05	1240	PA5199	5207	#N/A	#N/A
P1M10000068A09	1241	PA0353	5061	#N/A	#N/A
P1M10000068D04	1242	PA5388	5213	#N/A	#N/A
P1M10000068F04	1243	PA4237	5158	#N/A	#N/A
P1M10000068F08	1244	PA5193	5206	#N/A	#N/A
P1M10000068G01	1245	PA3716	5140	#N/A	#N/A
P1M10000068H05	1246	PA4268	5178	#N/A	#N/A
P1M10000069D09	1247	PA4246	5162	#N/A	#N/A
P1M10000069G06	1248	PA4246	5162	#N/A	#N/A
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P1M10000070B10	1251	PA5393	5214	#N/A	#N/A
P1M10000070C06	1252	PA4237	5158	#N/A	#N/A
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P1M10000070G06	1255	PA3374	5133	#N/A	#N/A
P1M10000070G12	1256	PA3121	5127	#N/A	#N/A
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P1M10000071A03	1258	PA4251	5167	#N/A	#N/A
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P1M10000071F01	1261	PA0506	5070	#N/A	#N/A
P1M10000073A06	1262	PA4246	5162	#N/A	#N/A
P1M10000073B10	1263	PA5248	5210	#N/A	#N/A
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P1M10000073D09	1265	PA1918	5094	#N/A	#N/A
P1M10000073G03	1266	PA5248	5210	#N/A	#N/A
P1M10000074B01	1267	PA4771	5199	#N/A	#N/A
P1M10000074B04	1268	PA1684	5091	#N/A	#N/A
P1M10000074E04	1269	PA0120	5054	#N/A	#N/A
P1M10000074E09	1270	PA3479	5134	#N/A	#N/A
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P1M10000074G12	1272	PA4244	5160	#N/A	#N/A
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P1M10000075G05	1276	PA3709	5139	#N/A	#N/A
P1M10000076D05	1277	PA1876	5093	#N/A	#N/A
P1M10000076D10	1278	PA1636	5090	#N/A	#N/A
P1M10000077A08	1279	PA3479	5134	#N/A	#N/A
P1M10000077C08	1280	PA1019	5079	#N/A	#N/A
P1M10000077E04	1281	PA3522	5136	#N/A	#N/A
P1M10000077H05	1282	PA4246	5162	#N/A	#N/A
P1M10000079A10	1283	PA4576	5193	#N/A	#N/A
P1M10000079B10	1284	PA4576	5193	#N/A	#N/A
P1M10000079C10	1285	PA4576	5193	#N/A	#N/A
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P1M10000079D10	1287	PA5490	5217	#N/A	#N/A
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P1M10000080B01	1289	PA3866	5143	#N/A	#N/A
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P1M10000081D12	1294	PA3006	5121	#N/A	#N/A
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P1M10000082A05	1297	PA0401	5063	#N/A	#N/A
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P1M10000083A11	1302	PA3006	5121	#N/A	#N/A
P1M10000083B01	1303	PA4271	5180	#N/A	#N/A
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P1M10000083C12	1306	PA3006	5121	#N/A	#N/A
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P1M10000084D03	1308	PA3006	5121	#N/A	#N/A
P1M10000084E04	1309	PA5493	5218	#N/A	#N/A
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P1M10000084F08	1311	PA4271	5180	#N/A	#N/A
P1M10000085D06	1312	PA3006	5121	#N/A	#N/A
P1M10000086A02	1313	PA4413	5187	#N/A	#N/A
P1M10000086B01	1314	PA4158	5157	#N/A	#N/A
P1M10000086D02	1315	PA2641	5115	#N/A	#N/A
P1M10000086E05	1316	PA3006	5121	#N/A	#N/A
P1M10000087A11	1317	PA4268	5178	#N/A	#N/A
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P1M10000088A07	1322	PA2742	5120	#N/A	#N/A
P1M10000088D06	1323	PA2108	5099	#N/A	#N/A
P1M10000089C08	1324	PA3048	5125	#N/A	#N/A
P1M10000089D11	1325	PA4268	5178	#N/A	#N/A
P1M10000089G08	1326	PA2461	5108	#N/A	#N/A
P1M10000090B11	1327	PA3153	5128	#N/A	#N/A
P1M10000090F06	1328	PA2313	5105	#N/A	#N/A
P1M10000090F08	1329	PA4258	5173	#N/A	#N/A
P1M10000090F08	1329	PA4259	5174	#N/A	#N/A
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P1M10000091E09	1331	PA5316	5212	#N/A	#N/A
P1M10000091G10	1332	PA2742	5120	#N/A	#N/A
P1M10000092B02	1333	PA2641	5115	#N/A	#N/A
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P1M10000092D09	1335	PA2128	5100	#N/A	#N/A
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P1M10000093A03	1338	PA5088	5205	#N/A	#N/A
P1M10000093B09	1339	PA3703	5138	#N/A	#N/A
P1M10000093C08	1340	PA1868	5092	#N/A	#N/A
P1M10000093E09	1341	PA4332	5183	#N/A	#N/A
P1M10000093F03	1342	PA2101	5098	#N/A	#N/A
P1M10000093H07	1343	PA4665	5195	#N/A	#N/A
P1M10000094F04	1344	PA4268	5178	#N/A	#N/A
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P1M10000095C01	1346	PA2488	5110	#N/A	#N/A
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P1M10000095E04	1348	PA4363	5185	#N/A	#N/A
P1M10000095G04	1349	PA4256	5171	#N/A	#N/A
P1M10000096E04	1350	PA0353	5061	#N/A	#N/A
P1M10000096E12	1351	PA4246	5162	#N/A	#N/A
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S1M10000001A05	1354	SAU201508	5819	SAU2c0432_orf_19p	12947
S1M10000001A08	1355	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000001A09	1356	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000001A10	1357	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000001C06	1358	SAU102939	5747	#N/A	#N/A
S1M10000001D01	1359	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000001D02	1360	SAU100527	5285	SAU1c0037_orf_101p	12341
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S1M10000001D06	1361	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000001D07	1362	SAU101360	5431	SAU1c0044_orf_109p	12555

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000001E04	1364	SAU102284	5635	SAU1c0038_orf_5p	12389
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S1M10000001E05	1365	SAU102939	5747	#N/A	#N/A
S1M10000001E09	1366	SAU201752	5832	SAU2c0436_orf_19p	12963
S1M10000001E10	1367	SAU103038	5757	#N/A	#N/A
S1M10000001E11	1368	SAU302513	5906	SAU3c1298_orf_1p	13085
S1M10000001F02	1369	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000001F04	1370	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000001F08	1371	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000001F09	1372	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000001F10	1373	SAU102602	5708	SAU1c0032_orf_5p	12249
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S1M10000001G07	1376	SAU102939	5747	#N/A	#N/A
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S1M10000002A10	1381	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000002A10	1381	SAU301148	5888	#N/A	#N/A
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S1M10000002B01	1383	SAU102602	5708	SAU1c0032_orf_5p	12249
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S1M10000002B04	1385	SAU101907	5574	SAU1c0040_orf_79p	12442
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S1M10000002C11	1394	SAU202267	5848	SAU2c0204_orf_2p	12727
S1M10000002C11	1394	SAU202781	5853	SAU2c0109_orf_2p	12718
S1M10000002C11	1394	SAU203001	5859	SAU2c0412_orf_15p	12894
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S1M10000002C11	1394	SAU302699	5910	SAU3c1408_orf_3p	13115
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000002D03	1398	SAU102631	5721	SAU1c0045_orf_94p	12712
S1M10000002D05	1399	SAU202930	5856	SAU2c0396_orf_3p	12871
S1M10000002D07	1400	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000002D07	1400	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000002D08	1401	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000002D10	1402	SAU102939	5747	#N/A	#N/A
S1M10000002D12	1403	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000002E01	1404	SAU101616	5495	SAU1c0040_orf_32p	12432
S1M10000002E02	1405	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000002E07	1406	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000002E07	1406	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000002F01	1410	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000002F02	1411	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000002F04	1412	SAU102939	5747	#N/A	#N/A
S1M10000002F09	1413	SAU302513	5906	SAU3c1298_orf_1p	13085
S1M10000002F12	1414	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000002G01	1415	SAU102939	5747	#N/A	#N/A
S1M10000002G03	1416	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000002G05	1417	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000002G06	1418	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000002G07	1419	SAU103038	5757	#N/A	#N/A
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S1M10000002G09	1421	SAU102939	5747	#N/A	#N/A
S1M10000002G10	1422	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000002G11	1423	SAU102939	5747	#N/A	#N/A
S1M10000002G12	1424	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000003A01	1425	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000003A01	1425	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000003A01	1425	SAU301148	5888	#N/A	#N/A
S1M10000003A02	1426	SAU101624	5497	SAU1c0040_orf_25p	12429
S1M10000003A03	1427	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000003A04	1428	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000003A06	1429	SAU101266	5408	SAU1c0042_orf_117p	12490
S1M10000003A07	1430	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000003A08	1431	SAU102939	5747	#N/A	#N/A
S1M10000003A10	1432	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000003A11	1433	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000003B06	1434	SAU102007	5590	SAU1c0040_orf_108p	12428
S1M10000003B08	1435	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000003B09	1436	SAU100771	5325	SAU1c0043_orf_49p	12545

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000003C06	1438	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000003C07	1439	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000003C10	1440	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000003C12	1441	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000003D05	1442	SAU102939	5747	#N/A	#N/A
S1M10000003D06	1443	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000003D08	1444	SAU100793	5329	SAU1c0028_orf_52p	12188
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S1M10000003E07	1446	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000003E09	1447	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000003E10	1448	SAU101674	5508	SAU1c0044_orf_226p	12594
S1M10000003E11	1449	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000003F02	1450	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000003F05	1451	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000003F06	1452	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000003F07	1453	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000003F08	1454	SAU102939	5747	#N/A	#N/A
S1M10000003F12	1455	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000003G03	1456	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000003G04	1457	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000003G04	1457	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000003G04	1457	SAU301148	5888	#N/A	#N/A
S1M10000003G08	1458	SAU102939	5747	#N/A	#N/A
S1M10000003G10	1459	SAU102939	5747	#N/A	#N/A
S1M10000004A04	1460	SAU102631	5721	SAU1c0045_orf_94p	12712
S1M10000004A06	1461	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000004A07	1462	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000004A11	1463	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000004A12	1464	SAU102132	5605	SAU1c0027_orf_19p	12177
S1M10000004B03	1465	SAU102610	5714	SAU1c0041_orf_53p	12474
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S1M10000004B06	1467	SAU102939	5747	#N/A	#N/A
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S1M10000004B09	1469	SAU101476	5459	SAU1c0032_orf_69p	12254
S1M10000004B11	1470	SAU101495	5467	SAU1c0037_orf_65p	12360
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S1M10000004C02	1472	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M10000004C02	1472	SAU301148	5888	#N/A	#N/A
S1M10000004C03	1473	SAU102939	5747	#N/A	#N/A
S1M10000004C06	1474	SAU102883	5741	SAU1c0045_orf_38p	12702
S1M10000004C07	1475	SAU102939	5747	#N/A	#N/A
S1M10000004C08	1476	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000004C08	1476	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000004C09	1477	SAU201810	5836	SAU2c0308_orf_2p	12769

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000004C10	1478	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000004C10	1478	SAU101286	5413	SAU1c0034_orf_67p	12292
S1M10000004C10	1478	SAU302931	5913	SAU3c1507_orf_10p	13155
S1M10000004C12	1479	SAU102007	5590	SAU1c0040_orf_108p	12428
S1M10000004D01	1480	SAU101301	5416	SAU1c0044_orf_114p	12558
S1M10000004D01	1480	SAU101302	5417	SAU1c0044_orf_115p	12559
S1M10000004D03	1481	SAU102390	5657	SAU1c0033_orf_38p	12269
S1M10000004D03	1481	SAU201333	5810	SAU2c0418_orf_8p	12905
S1M10000004D04	1482	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000004D04	1482	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000004D06	1483	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000004D07	1484	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000004D07	1484	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000004D07	1484	SAU301148	5888	#N/A	#N/A
S1M10000004D08	1485	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000004D10	1486	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000004D12	1487	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000004D12	1487	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000004E03	1488	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000004E04	1489	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000004E06	1490	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000004E07	1491	SAU101476	5459	SAU1c0032_orf_69p	12254
S1M10000004E11	1492	SAU102939	5747	#N/A	#N/A
S1M10000004E12	1493	SAU101996	5584	SAU1c0040_orf_99p	12456
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S1M10000004F02	1495	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000004F06	1496	SAU201611	5825	SAU2c0440_orf_14p	12973
S1M10000004F07	1497	SAU102764	5734	SAU1c0044_orf_56p	12625
S1M10000004F08	1498	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000004F08	1498	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000004F09	1499	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000004F09	1499	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000004F09	1499	SAU301148	5888	#N/A	#N/A
S1M10000004F12	1500	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000004G01	1501	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000004G01	1501	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000004G01	1501	SAU301148	5888	#N/A	#N/A
S1M10000004G02	1502	SAU102939	5747	#N/A	#N/A
S1M10000004G03	1503	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000004G05	1504	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000004G06	1505	SAU102939	5747	#N/A	#N/A
S1M10000004G07	1506	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000004G07	1506	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000004G09	1507	SAU101869	5566	SAU1c0036_orf_24p	12321

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000005A01	1509	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005A01	1509	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000005A01	1509	SAU301148	5888	#N/A	#N/A
S1M10000005A03	1510	SAU101090	5380	SAU1c0028_orf_8p	12191
S1M10000005A05	1511	SAU102939	5747	#N/A	#N/A
S1M10000005A06	1512	SAU102939	5747	#N/A	#N/A
S1M10000005A07	1513	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000005A08	1514	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005A08	1514	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000005A08	1514	SAU301148	5888	#N/A	#N/A
S1M10000005A09	1515	SAU103038	5757	#N/A	#N/A
S1M10000005A10	1516	SAU101239	5402	SAU1c0044_orf_15p	12570
S1M10000005A10	1516	SAU101240	5403	SAU1c0044_orf_16p	12573
S1M10000005A11	1517	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000005B02	1518	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000005B04	1519	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000005B07	1520	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005B07	1520	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000005B07	1520	SAU301148	5888	#N/A	#N/A
S1M10000005B08	1521	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000005B09	1522	SAU102422	5666	SAU1c0030_orf_22p	12207
S1M10000005B12	1523	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000005B12	1523	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000005C01	1524	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005C01	1524	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000005C01	1524	SAU301148	5888	#N/A	#N/A
S1M10000005C05	1525	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000005C06	1526	SAU100885	5348	SAU1c0038_orf_38p	12376
S1M10000005C09	1527	SAU302513	5906	SAU3c1298_orf_1p	13085
S1M10000005C11	1528	SAU101495	5467	SAU1c0037_orf_65p	12360
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S1M10000005D03	1531	SAU101907	5574	SAU1c0040_orf_79p	12442
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S1M10000005D05	1533	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000005D06	1534	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000005D06	1534	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000005D07	1535	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000005D08	1536	SAU101624	5497	SAU1c0040_orf_25p	12429
S1M10000005D09	1537	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000005D11	1538	SAU100158	5238	SAU1c0040_orf_80p	12443
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S1M10000005E01	1540	SAU100542	5288	SAU1c0043_orf_210p	12532
S1M10000005E02	1541	SAU102631	5721	SAU1c0045_orf_94p	12712

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000005E05	1542	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000005E05	1542	SAU301148	5888	#N/A	#N/A
S1M10000005E06	1543	SAU102939	5747	#N/A	#N/A
S1M10000005E07	1544	SAU102939	5747	#N/A	#N/A
S1M10000005E08	1545	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005E08	1545	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000005E08	1545	SAU301148	5888	#N/A	#N/A
S1M10000005E10	1546	SAU102939	5747	#N/A	#N/A
S1M10000005E11	1547	SAU100381	5265	SAU1c0033_orf_9p	12276
S1M10000005E12	1548	SAU102939	5747	#N/A	#N/A
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S1M10000005F02	1549	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000005F03	1550	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000005F03	1550	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000005F04	1551	SAU102044	5593	SAU1c0039_orf_65p	12414
S1M10000005F04	1551	SAU102046	5594	SAU1c0039_orf_66p	12415
S1M10000005F04	1551	SAU201961	5840	#N/A	#N/A
S1M10000006A03	1552	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006A03	1552	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006A03	1552	SAU301148	5888	#N/A	#N/A
S1M10000006A04	1553	SAU101271	5411	SAU1c0037_orf_90p	12366
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S1M10000006A07	1555	SAU100952	5358	SAU1c0043_orf_182p	12523
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S1M10000006B10	1563	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000006B11	1564	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000006C02	1565	SAU102939	5747	#N/A	#N/A
S1M10000006C04	1566	SAU102287	5637	SAU1c0038_orf_7p	12398
S1M10000006C06	1567	SAU102486	5687	SAU1c0039_orf_93p	12420
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S1M10000006C07	1568	SAU100157	5237	SAU1c0040_orf_81p	12444
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000006C10	1570	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006C10	1570	SAU301148	5888	#N/A	#N/A
S1M10000006D03	1571	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000006D05	1572	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006D05	1572	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006D05	1572	SAU301148	5888	#N/A	#N/A
S1M10000006D06	1573	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006D06	1573	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000006D07	1574	SAU102936	5746	SAU1c0037_orf_57p	12356
S1M10000006D08	1575	SAU102939	5747	#N/A	#N/A
S1M10000006E02	1576	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006E02	1576	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006E02	1576	SAU301148	5888	#N/A	#N/A
S1M10000006E03	1577	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000006E04	1578	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000006E07	1579	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006E07	1579	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006E07	1579	SAU301148	5888	#N/A	#N/A
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S1M10000006F01	1581	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000006F02	1582	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000006F03	1583	SAU102294	5639	SAU1c0044_orf_288p	12610
S1M10000006F03	1583	SAU301080	5885	SAU3c1287_orf_1p	13083
S1M10000006F04	1584	SAU100964	5363	SAU1c0044_orf_86p	12641
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S1M10000006G02	1586	SAU101833	5555	SAU1c0038_orf_34p	12373
S1M10000006G03	1587	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000006G05	1588	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000006G06	1589	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000006G07	1590	SAU101612	5493	SAU1c0044_orf_7p	12637
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S1M10000006G09	1591	SAU102939	5747	#N/A	#N/A
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S1M10000007A02	1594	SAU102939	5747	#N/A	#N/A
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S1M10000007B02	1596	SAU202872	5854	SAU2c0393_orf_6p	12866
S1M10000007B11	1597	SAU101476	5459	SAU1c0032_orf_69p	12254
S1M10000007C02	1598	SAU102939	5747	#N/A	#N/A
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S1M10000007C05	1600	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000007C06	1601	SAU101652	5503	SAU1c0042_orf_123p	12492
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000007D11	1609	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000007E04	1610	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000007E04	1610	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000007E07	1612	SAU101365	5432	SAU1c0044_orf_112p	12556
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S1M10000007F02	1614	SAU101685	5512	SAU1c0023_orf_11p	12152
S1M10000007F04	1615	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000007F08	1616	SAU100794	5330	SAU1c0028_orf_53p	12189
S1M10000007F09	1617	SAU202930	5856	SAU2c0396_orf_3p	12871
S1M10000007F10	1618	SAU101791	5532	SAU1c0032_orf_12p	12216
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S1M10000007G05	1623	SAU101907	5574	SAU1c0040_orf_79p	12442
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S1M10000008A09	1630	SAU100741	5318	SAU1c0039_orf_48p	12409
S1M10000008A12	1631	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000008B03	1632	SAU103144	5761	SAU1c0045_orf_15p	12663
S1M10000008B04	1633	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M10000008B04	1633	SAU301148	5888	#N/A	#N/A
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S1M10000008B08	1635	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000008B09	1636	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000008B10	1637	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000008C05	1638	SAU102939	5747	#N/A	#N/A
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S1M10000008D09	1644	SAU103038	5757	#N/A	#N/A
S1M10000008E05	1645	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000008E08	1646	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000008E09	1647	SAU101343	5425	SAU1c0044_orf_40p	12619
S1M10000008E10	1648	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000008F01	1649	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000008F01	1649	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000008F02	1650	SAU102007	5590	SAU1c0040_orf_108p	12428
S1M10000008F03	1651	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000008F06	1652	SAU100741	5318	SAU1c0039_orf_48p	12409
S1M10000008F08	1653	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000008F09	1654	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000008F09	1654	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000008F09	1654	SAU301148	5888	#N/A	#N/A
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S1M10000008F11	1656	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000008G02	1657	SAU201167	5803	SAU2c0407_orf_5p	12887
S1M10000008G03	1658	SAU101637	5500	SAU1c0029_orf_8p	12201
S1M10000008G05	1659	SAU102870	5738	SAU1c0026_orf_17p	12170
S1M10000009A02	1660	SAU101159	5387	SAU1c0036_orf_46p	12331
S1M10000009A04	1661	SAU102979	5750	SAU1c0043_orf_227p	12536
S1M10000009A07	1662	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000009A08	1663	SAU100658	5303	SAU1c0038_orf_59p	12388
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S1M10000009A09	1664	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000009A10	1665	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000009A11	1666	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000009B01	1667	SAU201506	5818	SAU2c0432_orf_18p	12946
S1M10000009B02	1668	SAU101159	5387	SAU1c0036_orf_46p	12331
S1M10000009B03	1669	SAU201506	5818	SAU2c0432_orf_18p	12946
S1M10000009B04	1670	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000009B05	1671	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000009B06	1672	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000009B07	1673	SAU201952	5839	SAU2c0457_orf_10p	13020
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S1M10000009B10	1674	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000009B11	1675	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000009B12	1676	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000009C01	1677	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000009C01	1677	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000009C02	1678	SAU102418	5664	SAU1c0030_orf_18p	12205
S1M10000009C05	1679	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000009C06	1680	SAU102613	5715	SAU1c0041_orf_55p	12475
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000009C10	1684	SAU102336	5646	SAU1c0045_orf_146p	12659
S1M10000009C11	1685	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000009D01	1686	SAU102262	5627	SAU1c0032_orf_58p	12248
S1M10000009D02	1687	SAU100355	5263	SAU1c0023_orf_6p	12155
S1M10000009D03	1688	SAU102418	5664	SAU1c0030_orf_18p	12205
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S1M10000009E08	1696	SAU201539	5821	SAU2c0431_orf_15p	12943
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S1M10000009G05	1710	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000009G06	1711	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000009G07	1712	SAU200468	5781	SAU2c0429_orf_19p	12937
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S1M10000009G10	1714	SAU100646	5302	SAU1c0025_orf_5p	12168
S1M10000009G11	1715	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000009H01	1716	SAU201506	5818	SAU2c0432_orf_18p	12946
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S1M10000009H03	1718	SAU201654	5829	SAU2c0442_orf_12p	12982
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000009H07	1720	SAU102297	5640	SAU1c0045_orf_41p	12704
S1M10000009H09	1721	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000009H11	1722	SAU101801	5541	#N/A	#N/A
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S1M10000011A03	1724	SAU101271	5411	SAU1c0037_orf_90p	12366
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S1M10000011B02	1728	SAU101541	5472	SAU1c0037_orf_128p	12344
S1M10000011B03	1729	SAU101849	5559	SAU1c0044_orf_148p	12567
S1M10000011B04	1730	SAU101574	5486	SAU1c0044_orf_213p	12588
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S1M10000011C01	1732	SAU101447	5454	SAU1c0045_orf_244p	12683
S1M10000011C05	1733	SAU100432	5271	SAU1c0040_orf_88p	12450
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S1M10000011D01	1735	SAU101293	5414	SAU1c0044_orf_61p	12631
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S1M10000011D04	1737	SAU102280	5632	SAU1c0038_orf_3p	12378
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S1M10000011G03	1747	SAU302626	5907	SAU3c1367_orf_3p	13105
S1M10000011G04	1748	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000011G05	1749	SAU102350	5649	SAU1c0040_orf_36p	12433
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S1M10000011H01	1751	SAU201558	5823	SAU2c0434_orf_5p	12954
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S1M10000012A08	1756	SAU101630	5498	SAU1c0039_orf_4p	12410
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000012B01	1760	SAU100751	5321	SAU1c0036_orf_59p	12335
S1M10000012B05	1761	SAU101573	5485	SAU1c0044_orf_212p	12587
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S1M10000012B07	1763	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000012B07	1763	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000012B11	1764	SAU102551	5698	SAU1c0045_orf_206p	12672
S1M10000012C01	1765	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000012C03	1766	SAU100776	5327	SAU1c0041_orf_72p	12482
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S1M10000012C12	1771	SAU101781	5528	SAU1c0037_orf_43p	12353
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S1M10000012D07	1774	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000012D08	1775	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000012D09	1776	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000012D12	1777	SAU102620	5718	SAU1c0041_orf_62p	12479
S1M10000012D12	1777	SAU102621	5719	SAU1c0041_orf_63p	12480
S1M10000012D12	1777	SAU202006	5842	SAU2c0456_orf_20p	13018
S1M10000012E01	1778	SAU100733	5314	SAU1c0044_orf_254p	12602
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S1M10000012E08	1782	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000012E12	1783	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M10000012E12	1783	SAU301148	5888	#N/A	#N/A
S1M10000012F04	1784	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000012F07	1785	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000012F07	1785	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000012F08	1786	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000012F09	1787	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000012F10	1788	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000012F11	1789	SAU101781	5528	SAU1c0037_orf_43p	12353
S1M10000012F12	1790	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000012F12	1790	SAU202174	5845	SAU2c0412_orf_3p	12895

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000012G03	1793	SAU201301	5809	SAU2c0416_orf_17p	12899
S1M10000012G06	1794	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000012G07	1795	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000012G07	1795	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000012G08	1796	SAU102593	5704	SAU1c0041_orf_39p	12463
S1M10000012G10	1797	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000012H05	1798	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000012H08	1799	SAU202186	5847	SAU2c0222_orf_1p	12731
S1M10000012H09	1800	SAU100227	5244	SAU1c0043_orf_188p	12525
S1M10000012H10	1801	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000012H10	1801	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000012H10	1801	SAU101751	5521	SAU1c0040_orf_86p	12448
S1M10000012H11	1802	SAU301118	5886	SAU3c1305_orf_3p	13086
S1M10000013A02	1803	SAU102674	5730	SAU1c0024_orf_12p	12156
S1M10000013A03	1804	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000013A05	1805	SAU102450	5675	SAU1c0045_orf_21p	12675
S1M10000013A07	1806	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000013A08	1807	SAU101143	5383	SAU1c0042_orf_159p	12502
S1M10000013A09	1808	SAU101567	5481	SAU1c0022_orf_10p	12144
S1M10000013A09	1808	SAU200030	5772	SAU2c0282_orf_3p	12745
S1M10000013A10	1809	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000013A11	1810	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000013A12	1811	SAU100690	5309	#N/A	#N/A
S1M10000013B02	1812	SAU100433	5272	SAU1c0040_orf_87p	12449
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S1M10000013B04	1814	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000013B05	1815	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000013B06	1816	SAU100118	5229	SAU1c0015_orf_13p	12125
S1M10000013B07	1817	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000013B11	1819	SAU103042	5758	#N/A	#N/A
S1M10000013C03	1820	SAU101781	5528	SAU1c0037_orf_43p	12353
S1M10000013C05	1821	SAU101038	5372	SAU1c0043_orf_180p	12521
S1M10000013C07	1822	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000013C08	1823	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000013C09	1824	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000013C10	1825	SAU100736	5316	SAU1c0038_orf_64p	12391
S1M10000013C11	1826	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000013C12	1827	SAU103038	5757	#N/A	#N/A
S1M10000013D08	1828	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000013D09	1829	SAU102669	5728	SAU1c0024_orf_7p	12160
S1M10000013D09	1829	SAU302956	5915	SAU3c1513_orf_9p	13161

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000013E01	1831	SAU102674	5730	SAU1c0024_orf_12p	12156
S1M10000013E02	1832	SAU101184	5391	SAU1c0035_orf_80p	12305
S1M10000013E04	1833	SAU101802	5542	SAU1c0032_orf_22p	12227
S1M10000013E06	1834	SAU101833	5555	SAU1c0038_orf_34p	12373
S1M10000013E08	1835	SAU100831	5335	SAU1c0038_orf_93p	12403
S1M10000013E09	1836	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000013E10	1837	SAU101801	5541	#N/A	#N/A
S1M10000013F02	1838	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000013F03	1839	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000013F06	1840	SAU103038	5757	#N/A	#N/A
S1M10000013F07	1841	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000013F08	1842	SAU100961	5360	SAU1c0044_orf_83p	12638
S1M10000013F09	1843	SAU101398	5442	SAU1c0036_orf_33p	12324
S1M10000013F12	1844	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000013G01	1845	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000013G04	1846	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000013G05	1847	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000013G05	1847	SAU102242	5618	SAU1c0043_orf_26p	12540
S1M10000013G06	1848	SAU102380	5654	SAU1c0033_orf_29p	12265
S1M10000013G07	1849	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000013G10	1850	SAU201539	5821	SAU2c0431_orf_15p	12943
S1M10000013G11	1851	SAU101890	5570	SAU1c0034_orf_29p	12280
S1M10000013G12	1852	SAU100843	5339	SAU1c0036_orf_40p	12328
S1M10000013H03	1853	SAU100690	5309	#N/A	#N/A
S1M10000013H04	1854	SAU102450	5675	SAU1c0045_orf_21p	12675
S1M10000013H05	1855	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000013H07	1856	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000013H09	1857	SAU100444	5275	SAU1c0038_orf_67p	12392
S1M10000013H09	1857	SAU200721	5791	SAU2c0339_orf_5p	12797
S1M10000013H10	1858	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000013H11	1859	SAU100690	5309	#N/A	#N/A
S1M10000014A02	1860	SAU200564	5784	SAU2c0324_orf_6p	12780
S1M10000014A03	1861	SAU101310	5418	SAU1c0044_orf_125p	12562
S1M10000014A05	1862	SAU101991	5582	SAU1c0040_orf_94p	12454
S1M10000014A07	1863	SAU101526	5470	SAU1c0027_orf_32p	12179
S1M10000014A08	1864	SAU103038	5757	#N/A	#N/A
S1M10000014A11	1865	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000014A12	1866	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000014B01	1867	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000014B02	1868	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000014B02	1868	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000014B03	1869	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000014B04	1870	SAU100778	5328	SAU1c0043_orf_140p	12514
S1M10000014B05	1871	SAU102476	5682	SAU1c0026_orf_33p	12175
S1M10000014B06	1872	SAU101199	5395	SAU1c0035_orf_62p	12302

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000014B11	1876	SAU102534	5696	#N/A	#N/A
S1M10000014B12	1877	SAU102534	5696	#N/A	#N/A
S1M10000014C01	1878	SAU101575	5487	SAU1c0044_orf_214p	12589
S1M10000014C05	1879	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000014C06	1880	SAU100305	5256	SAU1c0038_orf_77p	12397
S1M10000014C07	1881	SAU101801	5541	#N/A	#N/A
S1M10000014C09	1882	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000014C09	1882	SAU102881	5740	SAU1c0032_orf_4p	12242
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S1M10000014C12	1885	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000014C12	1885	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000014D03	1886	SAU100885	5348	SAU1c0038_orf_38p	12376
S1M10000014D06	1887	SAU100305	5256	SAU1c0038_orf_77p	12397
S1M10000014D08	1888	SAU101752	5522	SAU1c0040_orf_85p	12447
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S1M10000014E01	1891	SAU101794	5535	#N/A	#N/A
S1M10000014E04	1892	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000014E05	1893	SAU101565	5480	SAU1c0022_orf_8p	12151
S1M10000014E07	1894	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000014E07	1894	SAU100659	5304	SAU1c0038_orf_60p	12390
S1M10000014E08	1895	SAU202176	5846	SAU2c0412_orf_3p	12895
S1M10000014E09	1896	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000014E09	1896	SAU300269	5869	#N/A	#N/A
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S1M10000014E12	1898	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000014E12	1898	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000014F02	1899	SAU100128	5231	#N/A	#N/A
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S1M10000014F03	1900	SAU102200	5611	SAU1c0045_orf_168p	12665
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S1M10000014F04	1901	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000014F05	1902	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000014F08	1903	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000014F09	1904	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000014F09	1904	SAU300269	5869	#N/A	#N/A
S1M10000014F10	1905	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000014G02	1906	SAU102054	5596	SAU1c0039_orf_74p	12417
S1M10000014G04	1907	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000014G06	1908	SAU100275	5252	SAU1c0036_orf_15p	12314

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000014G08	1910	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000014G12	1911	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000014H02	1912	SAU100242	5246	SAU1c0036_orf_5p	12336
S1M10000014H03	1913	SAU102264	5628	SAU1c0032_orf_60p	12250
S1M10000014H04	1914	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000014H05	1915	SAU102116	5602	SAU1c0027_orf_5p	12180
S1M10000014H06	1916	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000014H07	1917	SAU103038	5757	#N/A	#N/A
S1M10000014H08	1918	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000014H11	1919	SAU102534	5696	#N/A	#N/A
S1M10000015A02	1920	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000015A03	1921	SAU102388	5655	SAU1c0033_orf_35p	12267
S1M10000015A05	1922	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000015A06	1923	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000015A09	1924	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000015A10	1925	SAU103038	5757	#N/A	#N/A
S1M10000015A11	1926	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000015A12	1927	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000015B02	1928	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000015B05	1929	SAU103038	5757	#N/A	#N/A
S1M10000015B08	1930	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000015B08	1930	SAU101792	5533	SAU1c0032_orf_13p	12217
S1M10000015B09	1931	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000015B09	1931	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000015B09	1931	SAU302685	5908	SAU3c1403_orf_1p	13113
S1M10000015B10	1932	SAU102308	5642	SAU1c0045_orf_50p	12706
S1M10000015C01	1933	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000015C02	1934	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000015C03	1935	SAU102390	5657	SAU1c0033_orf_38p	12269
S1M10000015C03	1935	SAU201333	5810	SAU2c0418_orf_8p	12905
S1M10000015C05	1936	SAU100690	5309	#N/A	#N/A
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S1M10000015C10	1939	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000015C12	1940	SAU100305	5256	SAU1c0038_orf_77p	12397
S1M10000015D02	1941	SAU100794	5330	SAU1c0028_orf_53p	12189
S1M10000015D03	1942	SAU102032	5591	SAU1c0029_orf_47p	12198
S1M10000015D04	1943	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000015D05	1944	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000015D06	1945	SAU100736	5316	SAU1c0038_orf_64p	12391
S1M10000015D12	1946	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000015E02	1947	SAU102390	5657	SAU1c0033_orf_38p	12269
S1M10000015E02	1947	SAU201333	5810	SAU2c0418_orf_8p	12905
S1M10000015E03	1948	SAU200468	5781	SAU2c0429_orf_19p	12937

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000015E07	1950	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000015E09	1951	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000015E10	1952	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000015E11	1953	SAU102286	5636	SAU1c0038_orf_6p	12393
S1M10000015E11	1953	SAU102287	5637	SAU1c0038_orf_7p	12398
S1M10000015E12	1954	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000015F01	1955	SAU100123	5230	SAU1c0043_orf_189p	12526
S1M10000015F01	1955	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000015F01	1955	SAU103159	5762	SAU1c0045_orf_204p	12670
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S1M10000015F03	1957	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000015F04	1958	SAU201403	5815	SAU2c0423_orf_3p	12913
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S1M10000015F07	1960	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000015F08	1961	SAU102102	5600	SAU1c0045_orf_340p	12696
S1M10000015F09	1962	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000015F09	1962	SAU101801	5541	#N/A	#N/A
S1M10000015F10	1963	SAU100114	5228	SAU1c0043_orf_225p	12535
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S1M10000015G02	1965	SAU200058	5773	SAU2c0134_orf_1p	12719
S1M10000015G02	1965	SAU200059	5774	SAU2c0134_orf_3p	12720
S1M10000015G03	1966	SAU101070	5376	SAU1c0034_orf_60p	12291
S1M10000015G04	1967	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000015G05	1968	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000015G06	1969	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000015G07	1970	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000015G08	1971	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000015G09	1972	SAU102143	5607	SAU1c0041_orf_14p	12458
S1M10000015G09	1972	SAU102144	5608	SAU1c0041_orf_15p	12459
S1M10000015G10	1973	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000015G11	1974	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000015H04	1975	SAU101801	5541	#N/A	#N/A
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S1M10000015H06	1976	SAU201385	5814	#N/A	#N/A
S1M10000016A03	1977	SAU101803	5543	SAU1c0032_orf_23p	12228
S1M10000016A03	1977	SAU101804	5544	#N/A	#N/A
S1M10000016A04	1978	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000016A04	1978	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000016A06	1979	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000016A07	1980	SAU100932	5356	SAU1c0044_orf_308p	12615
S1M10000016A09	1981	SAU101067	5375	SAU1c0034_orf_58p	12290
S1M10000016A09	1981	SAU300732	5877	SAU3c1116_orf_1p	13061
S1M10000016A10	1982	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000016A12	1983	SAU100522	5284	SAU1c0044_orf_249p	12599

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000016B02	1984	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000016B05	1985	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000016B06	1986	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000016B06	1986	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000016B07	1987	SAU103077	5759	SAU1c0039_orf_44p	12408
S1M10000016B08	1988	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000016B09	1989	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000016B10	1990	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000016B11	1991	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000016B12	1992	SAU101794	5535	#N/A	#N/A
S1M10000016B12	1992	SAU101795	5536	SAU1c0032_orf_15p	12219
S1M10000016C01	1993	SAU100845	5340	SAU1c0036_orf_41p	12329
S1M10000016C02	1994	SAU102049	5595	SAU1c0039_orf_68p	12416
S1M10000016C04	1995	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000016C05	1996	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000016C06	1997	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000016C06	1997	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000016C06	1997	SAU301148	5888	#N/A	#N/A
S1M10000016C08	1998	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000016C09	1999	SAU102233	5616	SAU1c0043_orf_20p	12531
S1M10000016C10	2000	SAU201513	5820	SAU2c0432_orf_10p	12944
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S1M10000016C11	2001	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000016C12	2002	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000016D01	2003	SAU102355	5651	SAU1c0040_orf_40p	12435
S1M10000016D02	2004	SAU200242	5777	SAU2c0250_orf_2p	12734
S1M10000016D04	2005	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000016D05	2006	SAU100770	5324	#N/A	#N/A
S1M10000016D06	2007	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000016D08	2008	SAU101070	5376	SAU1c0034_orf_60p	12291
S1M10000016D09	2009	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000016D10	2010	SAU201513	5820	SAU2c0432_orf_10p	12944
S1M10000016D10	2010	SAU203196	5861	SAU2c0432_orf_11p	12945
S1M10000016D11	2011	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000016E04	2012	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000016E05	2013	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000016E06	2014	SAU102639	5724	#N/A	#N/A
S1M10000016E07	2015	SAU102636	5722	SAU1c0045_orf_101p	12650
S1M10000016E07	2015	SAU102637	5723	SAU1c0045_orf_102p	12651
S1M10000016E08	2016	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000016E09	2017	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000016E10	2018	SAU102983	5751	SAU1c0045_orf_224p	12676
S1M10000016E11	2019	SAU102281	5633	SAU1c0038_orf_4p	12384
S1M10000016E12	2020	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000016F02	2021	SAU102113	5601	SAU1c0027_orf_2p	12178
S1M10000016F02	2021	SAU301223	5889	SAU3c1345_orf_3p	13090

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000016F03	2022	SAU101864	5562	SAU1c0044_orf_163p	12572
S1M10000016F05	2023	SAU201168	5804	SAU2c0407_orf_8p	12889
S1M10000016F06	2024	SAU102407	5662	#N/A	#N/A
S1M10000016F08	2025	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000016F09	2026	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000016F11	2027	SAU102113	5601	SAU1c0027_orf_2p	12178
S1M10000016F11	2027	SAU301223	5889	SAU3c1345_orf_3p	13090
S1M10000016G01	2028	SAU102434	5669	SAU1c0045_orf_36p	12700
S1M10000016G03	2029	SAU101300	5415	SAU1c0044_orf_113p	12557
S1M10000016G03	2029	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000016G04	2030	SAU102450	5675	SAU1c0045_orf_21p	12675
S1M10000016G05	2031	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000016H03	2032	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000016H04	2033	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000016H08	2034	SAU101067	5375	SAU1c0034_orf_58p	12290
S1M10000016H08	2034	SAU300732	5877	SAU3c1116_orf_1p	13061
S1M10000016H10	2035	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000017A02	2036	SAU101866	5564	SAU1c0036_orf_21p	12319
S1M10000017A03	2037	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000017A03	2037	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000017A04	2038	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000017A08	2039	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000017A11	2040	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000017A12	2041	SAU301357	5893	SAU3c1394_orf_2p	13111
S1M10000017B02	2042	SAU102242	5618	SAU1c0043_orf_26p	12540
S1M10000017B05	2043	SAU302513	5906	SAU3c1298_orf_1p	13085
S1M10000017B07	2044	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000017B08	2045	SAU101546	5475	SAU1c0037_orf_133p	12349
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S1M10000017B10	2047	SAU101754	5523	SAU1c0040_orf_84p	12446
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S1M10000017B12	2049	SAU201375	5811	SAU2c0426_orf_4p	12926
S1M10000017C01	2050	SAU101224	5397	SAU1c0044_orf_98p	12647
S1M10000017C03	2051	SAU101910	5576	SAU1c0040_orf_76p	12440
S1M10000017C05	2052	SAU200657	5789	#N/A	#N/A
S1M10000017C08	2053	SAU101890	5570	SAU1c0034_orf_29p	12280
S1M10000017C09	2054	SAU101398	5442	SAU1c0036_orf_33p	12324
S1M10000017C10	2055	SAU102614	5716	SAU1c0041_orf_56p	12476
S1M10000017C10	2055	SAU102615	5717	SAU1c0041_orf_57p	12477
S1M10000017C11	2056	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000017C11	2056	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000017C12	2057	SAU101782	5529	SAU1c0037_orf_44p	12354
S1M10000017C12	2057	SAU200994	5802	SAU2c0428_orf_4p	12935
S1M10000017D03	2058	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000017D09	2059	SAU101799	5539	SAU1c0032_orf_19p	12223
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000017E05	2062	SAU102334	5645	SAU1c0045_orf_144p	12658
S1M10000017E08	2063	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000017E11	2064	SAU102883	5741	SAU1c0045_orf_38p	12702
S1M10000017F01	2065	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000017F04	2066	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000017F04	2066	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000017F05	2067	SAU102541	5697	SAU1c0045_orf_195p	12668
S1M10000017F06	2068	SAU102356	5652	SAU1c0040_orf_41p	12436
S1M10000017F11	2069	SAU101463	5458	SAU1c0045_orf_232p	12679
S1M10000017G02	2070	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000017G05	2071	SAU102259	5624	SAU1c0032_orf_55p	12245
S1M10000017G06	2072	SAU200565	5785	SAU2c0324_orf_7p	12781
S1M10000018A03	2073	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000018A03	2073	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000018A04	2074	SAU102142	5606	SAU1c0041_orf_13p	12457
S1M10000018A05	2075	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000018A05	2075	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000018A06	2076	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000018A08	2077	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000018A08	2077	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000018A09	2078	SAU102142	5606	SAU1c0041_orf_13p	12457
S1M10000018A10	2079	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000018A11	2080	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000018A11	2080	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000018B02	2081	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000018B02	2081	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000018B03	2082	SAU101839	5556	SAU1c0042_orf_12p	12495
S1M10000018B05	2083	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000018B09	2084	SAU100836	5336	SAU1c0031_orf_13p	12212
S1M10000018B09	2084	SAU202731	5850	#N/A	#N/A
S1M10000018B10	2085	SAU100401	5268	SAU1c0044_orf_174p	12576
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S1M10000018B11	2086	SAU100658	5303	SAU1c0038_orf_59p	12388
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S1M10000018C03	2089	SAU100778	5328	SAU1c0043_orf_140p	12514
S1M10000018C04	2090	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000018C05	2091	SAU103038	5757	#N/A	#N/A
S1M10000018C06	2092	SAU100684	5306	SAU1c0044_orf_68p	12632
S1M10000018C08	2093	SAU102256	5622	SAU1c0032_orf_52p	12243
S1M10000018C08	2093	SAU102257	5623	SAU1c0032_orf_53p	12244
S1M10000018C09	2094	SAU101065	5374	SAU1c0034_orf_56p	12289
S1M10000018C09	2094	SAU102068	5599	SAU1c0034_orf_55p	12288
S1M10000018C10	2095	SAU100112	5227	SAU1c0044_orf_70p	12634

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000018C12	2097	SAU101948	5579	SAU1c0045_orf_69p	12709
S1M10000018D01	2098	SAU101452	5455	SAU1c0045_orf_247p	12684
S1M10000018D02	2099	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000018D02	2099	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000018D03	2100	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000018D04	2101	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000018D09	2102	SAU101067	5375	SAU1c0034_orf_58p	12290
S1M10000018D10	2103	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000018D11	2104	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000018D12	2105	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000018E01	2106	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000018E02	2107	SAU100265	5249	SAU1c0014_orf_11p	12122
S1M10000018E03	2108	SAU102420	5665	SAU1c0030_orf_20p	12206
S1M10000018E04	2109	SAU102035	5592	SAU1c0029_orf_50p	12199
S1M10000018E05	2110	SAU100596	5295	SAU1c0043_orf_63p	12548
S1M10000018E08	2111	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000018E09	2112	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000018E11	2113	SAU101799	5539	SAU1c0032_orf_19p	12223
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S1M10000018F03	2115	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000018F04	2116	SAU102396	5660	SAU1c0033_orf_43p	12272
S1M10000018F04	2116	SAU301118	5886	SAU3c1305_orf_3p	13086
S1M10000018F07	2117	SAU102629	5720	SAU1c0041_orf_71p	12481
S1M10000018F09	2118	SAU101810	5549	SAU1c0032_orf_28p	12233
S1M10000018F09	2118	SAU300110	5865	SAU3c0533_orf_2p	13031
S1M10000018F10	2119	SAU100432	5271	SAU1c0040_orf_88p	12450
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S1M10000018G08	2124	SAU102200	5611	SAU1c0045_orf_168p	12665
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S1M10000018G10	2126	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000018G10	2126	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000018G12	2127	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000018H01	2128	SAU101663	5506	SAU1c0033_orf_14p	12261
S1M10000018H02	2129	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000018H02	2129	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000018H07	2130	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000018H09	2131	SAU101622	5496	SAU1c0040_orf_27p	12430
S1M10000018H10	2132	SAU100157	5237	SAU1c0040_orf_81p	12444

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000019A03	2134	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000019A05	2135	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000019A06	2136	SAU101311	5419	SAU1c0044_orf_126p	12563
S1M10000019A07	2137	SAU101727	5516	SAU1c0016_orf_6p	12133
S1M10000019A07	2137	SAU101728	5517	SAU1c0016_orf_5p	12132
S1M10000019A09	2138	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000019A11	2139	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000019A12	2140	SAU102693	5731	SAU1c0044_orf_58p	12627
S1M10000019A12	2140	SAU102694	5732	SAU1c0044_orf_59p	12628
S1M10000019B03	2141	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000019B04	2142	SAU100899	5351	SAU1c0034_orf_11p	12277
S1M10000019B04	2142	SAU100901	5352	SAU1c0034_orf_13p	12278
S1M10000019B07	2143	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000019B08	2144	SAU102422	5666	SAU1c0030_orf_22p	12207
S1M10000019B08	2144	SAU102423	5667	SAU1c0030_orf_23p	12208
S1M10000019B09	2145	SAU100182	5241	SAU1c0037_orf_82p	12362
S1M10000019B09	2145	SAU100251	5248	SAU1c0037_orf_83p	12363
S1M10000019B10	2146	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000019B11	2147	SAU100879	5345	SAU1c0041_orf_82p	12483
S1M10000019B12	2148	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000019C01	2149	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000019C04	2150	SAU103175	5764	SAU1c0045_orf_269p	12687
S1M10000019C04	2150	SAU301472	5897	SAU3c1431_orf_4p	13124
S1M10000019C05	2151	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000019C06	2152	SAU101790	5531	SAU1c0032_orf_11p	12215
S1M10000019C06	2152	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000019C07	2153	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000019C08	2154	SAU202126	5844	SAU2c0045_orf_1p	12714
S1M10000019C11	2155	SAU100301	5254	SAU1c0040_orf_91p	12452
S1M10000019C12	2156	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000019D01	2157	SAU102270	5631	SAU1c0032_orf_65p	12253
S1M10000019D02	2158	SAU101145	5384	SAU1c0035_orf_43p	12299
S1M10000019D04	2159	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000019D05	2160	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000019D06	2161	SAU102526	5692	SAU1c0045_orf_299p	12691
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S1M10000019D09	2163	SAU102639	5724	#N/A	#N/A
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S1M10000019E01	2165	SAU100961	5360	SAU1c0044_orf_83p	12638
S1M10000019E01	2165	SAU100962	5361	SAU1c0044_orf_84p	12639
S1M10000019E02	2166	SAU101624	5497	SAU1c0040_orf_25p	12429
S1M10000019E07	2167	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000019F01	2168	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000019F05	2169	SAU101612	5493	SAU1c0044_orf_7p	12637
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000019F09	2172	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000019F11	2173	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000019G04	2174	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000019G07	2175	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000019G09	2176	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000019G10	2177	SAU101235	5400	SAU1c0044_orf_11p	12561
S1M10000019G10	2177	SAU101236	5401	SAU1c0044_orf_12p	12564
S1M10000019G11	2178	SAU101802	5542	SAU1c0032_orf_22p	12227
S1M10000019H05	2179	SAU101802	5542	SAU1c0032_orf_22p	12227
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S1M10000020A05	2181	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000020A06	2182	SAU101801	5541	#N/A	#N/A
S1M10000020A07	2183	SAU101567	5481	SAU1c0022_orf_10p	12144
S1M10000020A07	2183	SAU200030	5772	SAU2c0282_orf_3p	12745
S1M10000020A11	2184	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000020A12	2185	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000020B02	2186	SAU100475	5276	SAU1c0036_orf_61p	12337
S1M10000020B03	2187	SAU100059	5224	SAU1c0045_orf_10p	12652
S1M10000020B05	2188	SAU301133	5887	SAU3c1311_orf_3p	13087
S1M10000020B06	2189	SAU100747	5320	SAU1c0044_orf_235p	12597
S1M10000020B07	2190	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000020B09	2191	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000020B12	2192	SAU102143	5607	SAU1c0041_orf_14p	12458
S1M10000020C09	2193	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000020C10	2194	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000020C10	2194	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000020C11	2195	SAU101452	5455	SAU1c0045_orf_247p	12684
S1M10000020D03	2196	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000020D04	2197	SAU102481	5685	SAU1c0039_orf_99p	12422
S1M10000020D06	2198	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000020D07	2199	SAU100198	5243	SAU1c0009_orf_1p	12120
S1M10000020D08	2200	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000020D09	2201	SAU102939	5747	#N/A	#N/A
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S1M10000020E01	2203	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000020E03	2204	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000020E04	2205	SAU101805	5545	SAU1c0032_orf_24p	12229
S1M10000020E06	2206	SAU102162	5609	SAU1c0041_orf_27p	12462
S1M10000020E08	2207	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000020E11	2208	SAU101876	5567	SAU1c0025_orf_9p	12169
S1M10000020E12	2209	SAU200657	5789	#N/A	#N/A
S1M10000020F01	2210	SAU101592	5490	SAU1c0039_orf_37p	12406
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000020F06	2212	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000020F07	2213	SAU200731	5793	SAU2c0352_orf_2p	12808
S1M10000020F09	2214	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000020F11	2215	SAU101663	5506	SAU1c0033_orf_14p	12261
S1M10000020F11	2215	SAU101664	5507	SAU1c0033_orf_15p	12262
S1M10000020F12	2216	SAU100745	5319	SAU1c0044_orf_233p	12596
S1M10000020G01	2217	SAU102905	5742	SAU1c0033_orf_45p	12273
S1M10000020G05	2218	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000020G07	2219	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000020G08	2220	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000020G09	2221	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000020G10	2222	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000020G10	2222	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000020G11	2223	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000020G12	2224	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000020H01	2225	SAU202039	5843	SAU2c0452_orf_20p	13009
S1M10000020H02	2226	SAU101754	5523	SAU1c0040_orf_84p	12446
S1M10000020H04	2227	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000020H06	2228	SAU101541	5472	SAU1c0037_orf_128p	12344
S1M10000020H08	2229	SAU201558	5823	SAU2c0434_orf_5p	12954
S1M10000020H10	2230	SAU101754	5523	SAU1c0040_orf_84p	12446
S1M10000020H11	2231	SAU100053	5222	SAU1c0020_orf_1p	12143
S1M10000021A04	2232	SAU200752	5795	SAU2c0354_orf_5p	12809
S1M10000021A04	2232	SAU300975	5880	SAU3c1240_orf_3p	13075
S1M10000021A05	2233	SAU101408	5445	SAU1c0035_orf_93p	12308
S1M10000021A06	2234	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000021A07	2235	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000021A07	2235	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000021A08	2236	SAU101183	5390	SAU1c0035_orf_79p	12304
S1M10000021A09	2237	SAU102933	5744	SAU1c0039_orf_62p	12412
S1M10000021A09	2237	SAU201184	5805	SAU2c0351_orf_19p	12807
S1M10000021A10	2238	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000021B05	2239	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000021B05	2239	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000021B06	2240	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000021B07	2241	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000021B10	2242	SAU101772	5526	SAU1c0037_orf_34p	12351
S1M10000021C04	2243	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000021C05	2244	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000021C07	2245	SAU202968	5858	SAU2c0407_orf_2p	12886
S1M10000021C08	2246	SAU102575	5700	SAU1c0044_orf_283p	12609
S1M10000021C10	2247	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000021C11	2248	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000021C12	2249	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000021D01	2250	SAU102503	5691	SAU1c0045_orf_274p	12690

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000021D03	2251	SAU101286	5413	SAU1c0034_orf_67p	12292
S1M10000021D04	2252	SAU100858	5341	SAU1c0038_orf_86p	12401
S1M10000021D04	2252	SAU100859	5342	SAU1c0038_orf_87p	12402
S1M10000021D06	2253	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000021D09	2254	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000021D10	2255	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000021E01	2256	SAU101655	5505	SAU1c0042_orf_125p	12494
S1M10000021E02	2257	SAU102200	5611	SAU1c0045_orf_168p	12665
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S1M10000021E03	2258	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000021E05	2259	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000021E06	2260	SAU102663	5727	SAU1c0024_orf_2p	12158
S1M10000021E09	2261	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000021E12	2262	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000021F02	2263	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000021F04	2264	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000021F04	2264	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000021F05	2265	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000021F06	2266	SAU101235	5400	SAU1c0044_orf_11p	12561
S1M10000021F07	2267	SAU101383	5438	SAU1c0022_orf_20p	12147
S1M10000021F09	2268	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000021F09	2268	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000021F11	2269	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000021G01	2270	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000021G03	2271	SAU301357	5893	SAU3c1394_orf_2p	13111
S1M10000021G08	2272	SAU100714	5312	SAU1c0044_orf_74p	12635
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S1M10000021H04	2273	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000021H05	2274	SAU300131	5866	SAU3c0560_orf_2p	13034
S1M10000021H07	2275	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000021H08	2276	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000021H11	2277	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000022A02	2278	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000022A02	2278	SAU301230	5890	SAU3c1347_orf_6p	13092
S1M10000022A03	2279	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000022A05	2280	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000022A08	2281	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000022A09	2282	SAU102939	5747	#N/A	#N/A
S1M10000022A12	2283	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000022B02	2284	SAU100865	5343	SAU1c0044_orf_99p	12648
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S1M10000022B03	2285	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000022B05	2286	SAU100920	5354	SAU1c0038_orf_75p	12395
S1M10000022B06	2287	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000022B08	2288	SAU102292	5638	SAU1c0038_orf_10p	12368

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000022B10	2290	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000022B11	2291	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000022B12	2292	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000022C02	2293	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000022C03	2294	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000022C04	2295	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000022C06	2296	SAU100246	5247	SAU1c0042_orf_130p	12496
S1M10000022C06	2296	SAU300998	5881	SAU3c1253_orf_3p	13077
S1M10000022C07	2297	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000022C08	2298	SAU100528	5286	SAU1c0042_orf_87p	12507
S1M10000022C08	2298	SAU103115	5760	SAU1c0042_orf_88p	12508
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S1M10000022D06	2302	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000022D07	2303	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000022D08	2304	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000022D09	2305	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000022D11	2306	SAU101447	5454	SAU1c0045_orf_244p	12683
S1M10000022E01	2307	SAU200601	5787	#N/A	#N/A
S1M10000022E03	2308	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000022E05	2309	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000022E09	2310	SAU101235	5400	SAU1c0044_orf_11p	12561
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S1M10000022F06	2312	SAU101868	5565	SAU1c0036_orf_23p	12320
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S1M10000022F08	2314	SAU100414	5270	SAU1c0022_orf_24p	12148
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S1M10000022H03	2321	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000022H05	2322	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000022H06	2323	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000022H07	2324	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000022H08	2325	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000022H11	2326	SAU101610	5492	SAU1c0044_orf_5p	12629
S1M10000023A05	2327	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000023A09	2328	SAU101340	5423	SAU1c0038_orf_82p	12400
S1M10000023A11	2329	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000023A12	2330	SAU101651	5502	SAU1c0042_orf_122p	12491
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000023B03	2332	SAU101652	5503	SAU1c0042_orf_123p	12492
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S1M10000023B07	2333	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000023B08	2334	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000023B08	2334	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000023B09	2335	SAU101340	5423	SAU1c0038_orf_82p	12400
S1M10000023B10	2336	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000023B11	2337	SAU102613	5715	SAU1c0041_orf_55p	12475
S1M10000023B12	2338	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000023B12	2338	SAU301148	5888	#N/A	#N/A
S1M10000023C02	2339	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000023C02	2339	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000023C10	2340	SAU102554	5699	SAU1c0045_orf_209p	12673
S1M10000023C11	2341	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000023C12	2342	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000023D01	2343	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000023D03	2344	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000023D04	2345	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000023D07	2346	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000023D08	2347	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000023D09	2348	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000023D10	2349	SAU100963	5362	SAU1c0044_orf_85p	12640
S1M10000023D12	2350	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000023E01	2351	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000023E04	2352	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000023E07	2353	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000023E10	2354	SAU203293	5862	SAU2c0441_orf_21p	12979
S1M10000023E11	2355	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000023F04	2356	SAU101736	5518	SAU1c0043_orf_166p	12519
S1M10000023F04	2356	SAU101737	5519	SAU1c0043_orf_165p	12518
S1M10000023F07	2357	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000023F08	2358	SAU102883	5741	SAU1c0045_orf_38p	12702
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S1M10000023F11	2360	SAU100617	5300	SAU1c0035_orf_102p	12295
S1M10000023F12	2361	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000023G02	2362	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000023G03	2363	SAU101996	5584	SAU1c0040_orf_99p	12456
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S1M10000023G07	2365	SAU301054	5884	#N/A	#N/A
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S1M10000023G11	2368	SAU102613	5715	SAU1c0041_orf_55p	12475
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S1M10000023H06	2370	SAU100158	5238	SAU1c0040_orf_80p	12443
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000024A02	2374	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000024A04	2375	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000024A07	2376	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000024A08	2377	SAU101231	5399	SAU1c0035_orf_6p	12303
S1M10000024A11	2378	SAU103226	5768	SAU1c0045_orf_95p	12713
S1M10000024B05	2379	SAU102418	5664	SAU1c0030_orf_18p	12205
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S1M10000024B08	2381	SAU100601	5296	SAU1c0044_orf_313p	12616
S1M10000024B09	2382	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000024B10	2383	SAU101265	5407	#N/A	#N/A
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S1M10000024C04	2385	SAU101862	5561	SAU1c0044_orf_161p	12571
S1M10000024C07	2386	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000024D02	2387	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000024D03	2388	SAU100714	5312	SAU1c0044_orf_74p	12635
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S1M10000024D10	2389	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000024D11	2390	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000024E03	2391	SAU201571	5824	SAU2c0447_orf_17p	12997
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S1M10000024E06	2393	SAU102418	5664	SAU1c0030_orf_18p	12205
S1M10000024E07	2394	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000024E08	2395	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000024F02	2396	SAU101447	5454	SAU1c0045_orf_244p	12683
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S1M10000024F05	2398	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000024F08	2399	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000024F10	2400	SAU200468	5781	SAU2c0429_orf_19p	12937
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S1M10000024G08	2404	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000024G10	2405	SAU202176	5846	SAU2c0412_orf_3p	12895
S1M10000024G12	2406	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000024H02	2407	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000024H04	2408	SAU100770	5324	#N/A	#N/A
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S1M10000024H08	2410	SAU102002	5587	SAU1c0040_orf_103p	12425
S1M10000024H08	2410	SAU102003	5588	SAU1c0040_orf_104p	12426
S1M10000025A03	2411	SAU101247	5405	SAU1c0043_orf_136p	12512
S1M10000025A08	2412	SAU102766	5735	#N/A	#N/A
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S1M10000025A10	2414	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000025A10	2414	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000025A10	2414	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000025B01	2415	SAU101655	5505	SAU1c0042_orf_125p	12494
S1M10000025B02	2416	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000025B03	2417	SAU101385	5439	SAU1c0038_orf_50p	12385
S1M10000025B05	2418	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000025B05	2418	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000025B05	2418	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000025B06	2419	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000025B09	2420	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000025B12	2421	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000025C01	2422	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000025C03	2423	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000025C05	2424	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000025C09	2425	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000025C09	2425	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000025C10	2426	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000025C11	2427	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000025D01	2428	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000025D03	2429	SAU101771	5525	SAU1c0037_orf_33p	12350
S1M10000025D03	2429	SAU101772	5526	SAU1c0037_orf_34p	12351
S1M10000025D04	2430	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000025D06	2431	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000025D08	2432	SAU102598	5705	SAU1c0041_orf_43p	12464
S1M10000025D08	2432	SAU102599	5706	SAU1c0041_orf_45p	12466
S1M10000025D08	2432	SAU103191	5765	SAU1c0041_orf_44p	12465
S1M10000025D09	2433	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000025D10	2434	SAU102200	5611	SAU1c0045_orf_168p	12665
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S1M10000025E01	2435	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000025E04	2436	SAU100389	5266	SAU1c0034_orf_14p	12279
S1M10000025E09	2437	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000025E11	2438	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000025F03	2439	SAU102297	5640	SAU1c0045_orf_41p	12704
S1M10000025F05	2440	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000025F05	2440	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000025F08	2441	SAU200685	5790	SAU2c0344_orf_9p	12801
S1M10000025F09	2442	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000025F10	2443	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000025F12	2444	SAU102200	5611	SAU1c0045_orf_168p	12665
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S1M10000025G04	2445	SAU300617	5874	SAU3c1046_orf_2p	13056
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000025H05	2448	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000025H06	2449	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000025H07	2450	SAU200752	5795	SAU2c0354_orf_5p	12809
S1M10000025H07	2450	SAU300975	5880	SAU3c1240_orf_3p	13075
S1M10000025H10	2451	SAU100590	5293	SAU1c0013_orf_5p	12121
S1M10000025H10	2451	SAU301268	5891	SAU3c1364_orf_2p	13102
S1M10000026A02	2452	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000026A04	2453	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000026A05	2454	SAU200934	5799	SAU2c0375_orf_9p	12842
S1M10000026A06	2455	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000026A07	2456	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000026A08	2457	SAU100266	5250	SAU1c0032_orf_75p	12256
S1M10000026A09	2458	SAU102452	5676	SAU1c0045_orf_20p	12674
S1M10000026A09	2458	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000026A10	2459	SAU100970	5365	SAU1c0043_orf_197p	12529
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S1M10000026A11	2460	SAU102260	5625	SAU1c0032_orf_56p	12246
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S1M10000026A11	2460	SAU300868	5879	#N/A	#N/A
S1M10000026B02	2461	SAU101907	5574	SAU1c0040_orf_79p	12442
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S1M10000026B05	2463	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000026B06	2464	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000026B07	2465	SAU101341	5424	SAU1c0044_orf_38p	12618
S1M10000026B07	2465	SAU301275	5892	SAU3c1365_orf_2p	13103
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S1M10000026B12	2468	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000026C01	2469	SAU100266	5250	SAU1c0032_orf_75p	12256
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S1M10000026C12	2474	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000026D04	2475	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000026D05	2476	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000026D06	2477	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000026D07	2478	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000026D08	2479	SAU100690	5309	#N/A	#N/A
S1M10000026D10	2480	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000026D12	2481	SAU100546	5289	SAU1c0032_orf_2p	12235
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S1M10000026E07	2483	SAU102939	5747	#N/A	#N/A
S1M10000026E09	2484	SAU102001	5586	SAU1c0040_orf_102p	12424
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000026E11	2486	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000026E12	2487	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000026F01	2488	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000026F03	2489	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000026F03	2489	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000026F04	2490	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000026F05	2491	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000026F06	2492	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000026F07	2493	SAU101869	5566	SAU1c0036_orf_24p	12321
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S1M10000026F11	2497	SAU102939	5747	#N/A	#N/A
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S1M10000026G07	2504	SAU100886	5349	SAU1c0018_orf_16p	12139
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S1M10000026H01	2508	SAU101652	5503	SAU1c0042_orf_123p	12492
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S1M10000027A08	2518	SAU101772	5526	SAU1c0037_orf_34p	12351
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S1M10000027B04	2520	SAU102939	5747	#N/A	#N/A
S1M10000027B06	2521	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000027B07	2522	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000027B08	2523	SAU101807	5547	SAU1c0032_orf_26p	12231
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S1M10000027C04	2527	SAU201236	5808	SAU2c0409_orf_10p	12891
S1M10000027C05	2528	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000027C06	2529	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000027C08	2530	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000027C09	2531	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000027D02	2532	SAU101652	5503	SAU1c0042_orf_123p	12492
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S1M10000027D03	2533	SAU100300	5253	SAU1c0040_orf_90p	12451
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S1M10000027D06	2535	SAU202708	5849	SAU2c0385_orf_1p	12855
S1M10000027D08	2536	SAU100714	5312	SAU1c0044_orf_74p	12635
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S1M10000027E08	2543	SAU201571	5824	SAU2c0447_orf_17p	12997
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S1M10000027E11	2545	SAU101551	5477	SAU1c0043_orf_67p	12550
S1M10000027F01	2546	SAU103038	5757	#N/A	#N/A
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S1M10000027F09	2551	SAU100858	5341	SAU1c0038_orf_86p	12401
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S1M10000027G04	2553	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000027G05	2554	SAU102526	5692	SAU1c0045_orf_299p	12691
S1M10000027G06	2555	SAU202708	5849	SAU2c0385_orf_1p	12855
S1M10000027G07	2556	SAU102265	5629	SAU1c0032_orf_61p	12251
S1M10000027G09	2557	SAU101807	5547	SAU1c0032_orf_26p	12231
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S1M10000027H04	2560	SAU101777	5527	SAU1c0037_orf_39p	12352
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S1M10000027H08	2564	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000027H09	2565	SAU101382	5437	SAU1c0022_orf_19p	12146
S1M10000027H10	2566	SAU100158	5238	SAU1c0040_orf_80p	12443
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S1M10000028A04	2569	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000028A06	2570	SAU100478	5277	SAU1c0044_orf_265p	12605
S1M10000028A06	2570	SAU100996	5366	SAU1c0044_orf_266p	12606
S1M10000028A08	2571	SAU102054	5596	SAU1c0039_orf_74p	12417
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S1M10000028B03	2574	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000028B04	2575	SAU102764	5734	SAU1c0044_orf_56p	12625
S1M10000028B05	2576	SAU101869	5566	SAU1c0036_orf_24p	12321
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S1M10000028B08	2578	SAU100158	5238	SAU1c0040_orf_80p	12443
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S1M10000028C02	2580	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000028C04	2581	SAU101381	5436	SAU1c0022_orf_18p	12145
S1M10000028C05	2582	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000028C05	2582	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000028C05	2582	SAU200297	5778	SAU2c0274_orf_2p	12739
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S1M10000028C08	2584	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000028D03	2585	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000028D04	2586	SAU101381	5436	SAU1c0022_orf_18p	12145
S1M10000028D06	2587	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000028D07	2588	SAU101271	5411	SAU1c0037_orf_90p	12366
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S1M10000028D09	2590	SAU100158	5238	SAU1c0040_orf_80p	12443
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S1M10000028F01	2594	SAU101086	5379	SAU1c0034_orf_43p	12285
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S1M10000028F05	2597	SAU100301	5254	SAU1c0040_orf_91p	12452
S1M10000028F05	2597	SAU100302	5255	SAU1c0040_orf_92p	12453
S1M10000028F06	2598	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000028F06	2598	SAU202756	5852	SAU2c0470_orf_1p	13027
S1M10000028F07	2599	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000028G01	2600	SAU102554	5699	SAU1c0045_orf_209p	12673
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S1M10000028G04	2603	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000028G05	2604	SAU100690	5309	#N/A	#N/A
S1M10000028G06	2605	SAU101865	5563	SAU1c0036_orf_20p	12318
S1M10000028G08	2606	SAU101341	5424	SAU1c0044_orf_38p	12618
S1M10000028G08	2606	SAU301275	5892	SAU3c1365_orf_2p	13103
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S1M10000028H04	2608	SAU103038	5757	#N/A	#N/A
S1M10000028H05	2609	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000029A02	2610	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000029A04	2611	SAU100489	5278	SAU1c0044_orf_133p	12566
S1M10000029A04	2611	SAU100557	5291	SAU1c0044_orf_132p	12565
S1M10000029A09	2612	SAU101495	5467	SAU1c0037_orf_65p	12360
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S1M10000029A11	2614	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000029A12	2615	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000029B02	2616	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000029B03	2617	SAU201225	5807	SAU2c0412_orf_5p	12896
S1M10000029B04	2618	SAU201621	5828	SAU2c0437_orf_4p	12966
S1M10000029B05	2619	SAU100355	5263	SAU1c0023_orf_6p	12155
S1M10000029B06	2620	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000029B08	2621	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000029B10	2622	SAU101891	5571	SAU1c0034_orf_30p	12281
S1M10000029C02	2623	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029C03	2624	SAU100690	5309	#N/A	#N/A
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S1M10000029C07	2626	SAU102222	5613	SAU1c0043_orf_12p	12511
S1M10000029C09	2627	SAU101495	5467	SAU1c0037_orf_65p	12360
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S1M10000029C12	2629	SAU100859	5342	SAU1c0038_orf_87p	12402
S1M10000029D02	2630	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000029D05	2631	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000029D09	2632	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000029D10	2633	SAU101891	5571	SAU1c0034_orf_30p	12281
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S1M10000029E02	2635	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000029E05	2636	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000029E10	2637	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029E11	2638	SAU101271	5411	SAU1c0037_orf_90p	12366
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S1M10000029F02	2640	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029F02	2640	SAU101286	5413	SAU1c0034_orf_67p	12292
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S1M10000029F10	2643	SAU102621	5719	SAU1c0041_orf_63p	12480
S1M10000029F11	2644	SAU102883	5741	SAU1c0045_orf_38p	12702
S1M10000029F12	2645	SAU102603	5709	SAU1c0041_orf_48p	12469
S1M10000029F12	2645	SAU102609	5713	SAU1c0041_orf_52p	12473
S1M10000029G01	2646	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000029G02	2647	SAU101622	5496	SAU1c0040_orf_27p	12430
S1M10000029G03	2648	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000029G05	2649	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000029G07	2650	SAU101622	5496	SAU1c0040_orf_27p	12430
S1M10000029G08	2651	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000029G12	2652	SAU101270	5410	SAU1c0037_orf_89p	12365
S1M10000029H01	2653	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000029H05	2654	SAU102613	5715	SAU1c0041_orf_55p	12475
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S1M10000029H08	2656	SAU101271	5411	SAU1c0037_orf_90p	12366
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S1M10000029H10	2658	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000030A02	2659	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000030A05	2660	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000030A09	2661	SAU101242	5404	SAU1c0044_orf_18p	12578
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S1M10000030A11	2663	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000030B02	2664	SAU101573	5485	SAU1c0044_orf_212p	12587
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S1M10000030B09	2667	SAU301898	5904	SAU3c1079_orf_1p	13057
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S1M10000030C03	2669	SAU102629	5720	SAU1c0041_orf_71p	12481
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S1M10000030C09	2673	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000030C10	2674	SAU301592	5898	SAU3c1467_orf_2p	13137
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S1M10000030D02	2677	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000030D03	2678	SAU100731	5313	SAU1c0044_orf_252p	12601
S1M10000030D05	2679	SAU102222	5613	SAU1c0043_orf_12p	12511
S1M10000030D06	2680	SAU102392	5658	SAU1c0033_orf_40p	12270
S1M10000030D06	2680	SAU201541	5822	SAU2c0431_orf_14p	12942
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S1M10000029F12	2645	SAU102603	5709	SAU1c0041_orf_48p	12469
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S1M10000029G12	2652	SAU101270	5410	SAU1c0037_orf_89p	12365
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S1M10000029H10	2658	SAU101271	5411	SAU1c0037_orf_90p	12366
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S1M10000030A10	2662	SAU101092	5381	SAU1c0028_orf_9p	12192
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S1M10000030D11	2684	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000030E02	2685	SAU100731	5313	SAU1c0044_orf_252p	12601
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S1M10000030G03	2695	SAU101752	5522	SAU1c0040_orf_85p	12447
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S1M10000030G08	2698	SAU100546	5289	SAU1c0032_orf_2p	12235
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S1M10000030G10	2700	SAU102453	5677	SAU1c0045_orf_19p	12669
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S1M10000030G12	2702	SAU201197	5806	SAU2c0429_orf_2p	12938
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S1M10000030H02	2704	SAU200392	5780	SAU2c0298_orf_3p	12755
S1M10000030H03	2705	SAU102162	5609	SAU1c0041_orf_27p	12462
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S1M10000031A03	2709	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000031A08	2710	SAU101641	5501	SAU1c0029_orf_12p	12193
S1M10000031A10	2711	SAU102242	5618	SAU1c0043_orf_26p	12540
S1M10000031B01	2712	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000031B02	2713	SAU102602	5708	SAU1c0032_orf_5p	12249
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S1M10000031B11	2715	SAU101262	5406	SAU1c0042_orf_113p	12488
S1M10000031B12	2716	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000031C04	2717	SAU100062	5225	SAU1c0035_orf_98p	12309
S1M10000031C04	2717	SAU100231	5245	#N/A	#N/A
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S1M10000031C09	2719	SAU102117	5603	SAU1c0027_orf_6p	12181
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S1M10000031D07	2722	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000031D08	2723	SAU101891	5571	SAU1c0034_orf_30p	12281
S1M10000031D09	2724	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000031E02	2725	SAU101350	5429	SAU1c0042_orf_109p	12487
S1M10000031E03	2726	SAU101267	5409	SAU1c0037_orf_86p	12364
S1M10000031E03	2726	SAU300719	5876	SAU3c1108_orf_3p	13059
S1M10000031E04	2727	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000031E07	2728	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000031E08	2729	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000031E10	2730	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000031E12	2731	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000031F02	2732	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000031F02	2732	SAU101801	5541	#N/A	#N/A
S1M10000031F03	2733	SAU101791	5532	SAU1c0032_orf_12p	12216
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S1M10000031F05	2735	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000031F08	2736	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000031F10	2737	SAU102593	5704	SAU1c0041_orf_39p	12463
S1M10000031F11	2738	SAU102469	5679	SAU1c0026_orf_25p	12172
S1M10000031F12	2739	SAU102593	5704	SAU1c0041_orf_39p	12463
S1M10000031G02	2740	SAU101797	5537	SAU1c0032_orf_17p	12221
S1M10000031G03	2741	SAU101679	5509	SAU1c0044_orf_222p	12593
S1M10000031G04	2742	SAU103198	5766	#N/A	#N/A
S1M10000031G06	2743	SAU101907	5574	SAU1c0040_orf_79p	12442
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S1M10000031G10	2745	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000031G11	2746	SAU100118	5229	SAU1c0015_orf_13p	12125
S1M10000031H01	2747	SAU103144	5761	SAU1c0045_orf_15p	12663
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S1M10000032A03	2752	SAU202039	5843	SAU2c0452_orf_20p	13009
S1M10000032A05	2753	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000032A06	2754	SAU100610	5298	SAU1c0034_orf_71p	12294
S1M10000032A07	2755	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000032A08	2756	SAU102142	5606	SAU1c0041_orf_13p	12457
S1M10000032A08	2756	SAU102143	5607	SAU1c0041_orf_14p	12458
S1M10000032A10	2757	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000032B01	2758	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000032B05	2759	SAU102607	5712	SAU1c0041_orf_51p	12472
S1M10000032B05	2759	SAU102944	5749	SAU1c0041_orf_47p	12468
S1M10000032B07	2760	SAU100157	5237	SAU1c0040_orf_81p	12444
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000032C01	2764	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032C03	2765	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000032C04	2766	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000032C05	2767	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000032C09	2768	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032C10	2769	SAU201615	5826	SAU2c0440_orf_10p	12972
S1M10000032C11	2770	SAU102863	5737	#N/A	#N/A
S1M10000032C12	2771	SAU102863	5737	#N/A	#N/A
S1M10000032D03	2772	SAU100613	5299	SAU1c0015_orf_14p	12126
S1M10000032D06	2773	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000032D07	2774	SAU200468	5781	SAU2c0429_orf_19p	12937
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S1M10000032D11	2776	SAU100128	5231	#N/A	#N/A
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S1M10000032E02	2777	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000032E03	2778	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000032E04	2779	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000032E06	2780	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000032E08	2781	SAU102281	5633	SAU1c0038_orf_4p	12384
S1M10000032E09	2782	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000032E10	2783	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000032E11	2784	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000032E12	2785	SAU101999	5585	SAU1c0040_orf_101p	12423
S1M10000032F01	2786	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000032F01	2786	SAU102002	5587	SAU1c0040_orf_103p	12425
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S1M10000032F05	2788	SAU101339	5422	SAU1c0038_orf_81p	12399
S1M10000032F10	2789	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000032F10	2789	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000032F11	2790	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000032F12	2791	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000032G02	2792	SAU100710	5311	SAU1c0043_orf_54p	12546
S1M10000032G02	2792	SAU200628	5788	SAU2c0334_orf_4p	12790
S1M10000032G03	2793	SAU100813	5334	SAU1c0036_orf_29p	12322
S1M10000032G04	2794	SAU101904	5573	SAU1c0044_orf_36p	12617
S1M10000032G06	2795	SAU101509	5469	SAU1c0039_orf_81p	12418
S1M10000032G08	2796	SAU101752	5522	SAU1c0040_orf_85p	12447
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S1M10000032H01	2799	SAU101445	5452	SAU1c0038_orf_47p	12382
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000032H09	2802	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032H11	2803	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000033A02	2804	SAU201775	5835	SAU2c0446_orf_4p	12996
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S1M10000033A07	2805	SAU200949	5800	SAU2c0380_orf_11p	12846
S1M10000033A08	2806	SAU101231	5399	SAU1c0035_orf_6p	12303
S1M10000033A10	2807	SAU202039	5843	SAU2c0452_orf_20p	13009
S1M10000033B02	2808	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000033B07	2809	SAU102044	5593	SAU1c0039_orf_65p	12414
S1M10000033B08	2810	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000033B11	2811	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000033B11	2811	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000033B12	2812	SAU101104	5382	SAU1c0029_orf_20p	12195
S1M10000033B12	2812	SAU103010	5753	SAU1c0029_orf_19p	12194
S1M10000033C04	2813	SAU102933	5744	SAU1c0039_orf_62p	12412
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S1M10000033D03	2815	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000033D04	2816	SAU100745	5319	SAU1c0044_orf_233p	12596
S1M10000033D05	2817	SAU100301	5254	SAU1c0040_orf_91p	12452
S1M10000033D06	2818	SAU102113	5601	SAU1c0027_orf_2p	12178
S1M10000033D10	2819	SAU100813	5334	SAU1c0036_orf_29p	12322
S1M10000033D12	2820	SAU101360	5431	SAU1c0044_orf_109p	12555
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S1M10000033F03	2825	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000033F06	2826	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000033F07	2827	SAU102044	5593	SAU1c0039_orf_65p	12414
S1M10000033F09	2828	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000033F11	2829	SAU100689	5308	SAU1c0036_orf_2p	12323
S1M10000033G05	2830	SAU101904	5573	SAU1c0044_orf_36p	12617
S1M10000033G07	2831	SAU101824	5554	SAU1c0038_orf_26p	12371
S1M10000033G09	2832	SAU102380	5654	SAU1c0033_orf_29p	12265
S1M10000033G10	2833	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000033G10	2833	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000033G11	2834	SAU101968	5581	SAU1c0028_orf_43p	12187
S1M10000033G12	2835	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000033H01	2836	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000033H02	2837	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000033H03	2838	SAU101833	5555	SAU1c0038_orf_34p	12373
S1M10000033H07	2839	SAU101996	5584	SAU1c0040_orf_99p	12456

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S1M10000033H09	2841	SAU100710	5311	SAU1c0043_orf_54p	12546
S1M10000033H10	2842	SAU100690	5309	#N/A	#N/A
S1M10000033H11	2843	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000034A02	2844	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000034A03	2845	SAU102939	5747	#N/A	#N/A
S1M10000034A04	2846	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000034A05	2847	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000034A08	2848	SAU101020	5368	SAU1c0045_orf_86p	12710
S1M10000034A09	2849	SAU100773	5326	SAU1c0038_orf_39p	12377
S1M10000034A11	2850	SAU102389	5656	SAU1c0033_orf_36p	12268
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S1M10000034B03	2852	SAU101907	5574	SAU1c0040_orf_79p	12442
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S1M10000034B09	2857	SAU101909	5575	SAU1c0040_orf_77p	12441
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S1M10000034B12	2859	SAU200593	5786	SAU2c0327_orf_1p	12784
S1M10000034C02	2860	SAU100557	5291	SAU1c0044_orf_132p	12565
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S1M10000034C12	2864	SAU100859	5342	SAU1c0038_orf_87p	12402
S1M10000034D01	2865	SAU100414	5270	SAU1c0022_orf_24p	12148
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S1M10000034D12	2872	SAU101632	5499	SAU1c0039_orf_3p	12407
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S1M10000034E04	2875	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000034E05	2876	SAU100738	5317	SAU1c0044_orf_52p	12624
S1M10000034E06	2877	SAU100347	5262	SAU1c0036_orf_56p	12334
S1M10000034E06	2877	SAU100443	5274	SAU1c0036_orf_55p	12333
S1M10000034E07	2878	SAU100617	5300	SAU1c0035_orf_102p	12295
S1M10000034E10	2879	SAU102401	5661	SAU1c0030_orf_4p	12209
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S1M10000034E12	2881	SAU200960	5801	SAU2c0377_orf_5p	12843
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S1M10000034F03	2884	SAU201971	5841	SAU2c0455_orf_17p	13015
S1M10000034F03	2884	SAU301363	5894	#N/A	#N/A
S1M10000034F04	2885	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000034F05	2886	SAU101630	5498	SAU1c0039_orf_4p	12410
S1M10000034F07	2887	SAU101175	5388	SAU1c0031_orf_1p	12213
S1M10000034F08	2888	SAU202736	5851	SAU2c0426_orf_7p	12927
S1M10000034F09	2889	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000034F10	2890	SAU102350	5649	SAU1c0040_orf_36p	12433
S1M10000034F12	2891	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000034G02	2892	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000034G03	2893	SAU101198	5394	SAU1c0035_orf_61p	12301
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S1M10000034G08	2896	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000034G09	2897	SAU102294	5639	SAU1c0044_orf_288p	12610
S1M10000034G09	2897	SAU201775	5835	SAU2c0446_orf_4p	12996
S1M10000034G11	2898	SAU200558	5782	SAU2c0322_orf_5p	12777
S1M10000034G12	2899	SAU100557	5291	SAU1c0044_orf_132p	12565
S1M10000034H01	2900	SAU101293	5414	SAU1c0044_orf_61p	12631
S1M10000034H02	2901	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000034H03	2902	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000034H06	2903	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000034H07	2904	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000034H08	2905	SAU200740	5794	SAU2c0340_orf_3p	12798
S1M10000034H09	2906	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000034H10	2907	SAU102422	5666	SAU1c0030_orf_22p	12207
S1M10000035A03	2908	SAU101360	5431	SAU1c0044_orf_109p	12555
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S1M10000035A09	2910	SAU101350	5429	SAU1c0042_orf_109p	12487
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S1M10000035A10	2911	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000035A11	2912	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000035A12	2913	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000035A12	2913	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000035A12	2913	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000035B01	2914	SAU102584	5702	SAU1c0043_orf_239p	12537
S1M10000035B03	2915	SAU102246	5619	SAU1c0043_orf_30p	12542
S1M10000035B04	2916	SAU102246	5619	SAU1c0043_orf_30p	12542
S1M10000035B08	2917	SAU103232	5769	SAU1c0045_orf_341p	12697
S1M10000035B11	2918	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000035C01	2919	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000035C02	2920	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000035C04	2921	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000035C06	2922	SAU101497	5468	SAU1c0037_orf_66p	12361
S1M10000035C11	2923	SAU101752	5522	SAU1c0040_orf_85p	12447

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000035D06	2926	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000035D09	2927	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000035D12	2928	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000035E02	2929	SAU102883	5741	SAU1c0045_orf_38p	12702
S1M10000035E03	2930	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000035E04	2931	SAU103025	5755	SAU1c0029_orf_9p	12202
S1M10000035E08	2932	SAU100690	5309	#N/A	#N/A
S1M10000035E09	2933	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000035E12	2934	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000035F03	2935	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000035F03	2935	SAU202882	5855	SAU2c0381_orf_3p	12848
S1M10000035F04	2936	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000035F09	2937	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000035F12	2938	SAU101427	5447	SAU1c0042_orf_144p	12500
S1M10000035F12	2938	SAU103204	5767	SAU1c0042_orf_143p	12499
S1M10000035G02	2939	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000035G09	2940	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000035G11	2941	SAU101344	5426	SAU1c0044_orf_41p	12620
S1M10000035G12	2942	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000035H01	2943	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000035H07	2944	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000035H07	2944	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000035H07	2944	SAU200297	5778	SAU2c0274_orf_2p	12739
S1M10000035H08	2945	SAU101772	5526	SAU1c0037_orf_34p	12351
S1M10000035H09	2946	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000035H09	2946	SAU301004	5882	SAU3c1255_orf_1p	13079
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S1M10000035H11	2948	SAU101344	5426	SAU1c0044_orf_41p	12620
S1M10000036A02	2949	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000036A03	2950	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000036A04	2951	SAU200994	5802	SAU2c0428_orf_4p	12935
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S1M10000036A08	2953	SAU101220	5396	SAU1c0044_orf_94p	12645
S1M10000036A11	2954	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000036A12	2955	SAU100813	5334	SAU1c0036_orf_29p	12322
S1M10000036B04	2956	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000036B04	2956	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000036B06	2957	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000036B07	2958	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000036B08	2959	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000036B11	2960	SAU102059	5597	SAU1c0034_orf_51p	12286
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S1M10000036C04	2964	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000036C05	2965	SAU100497	5280	SAU1c0018_orf_3p	12140
S1M10000036C06	2966	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000036C07	2967	SAU101800	5540	SAU1c0032_orf_20p	12225
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S1M10000036C09	2968	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000036C09	2968	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000036C09	2968	SAU302685	5908	SAU3c1403_orf_1p	13113
S1M10000036C10	2969	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000036C10	2969	SAU101751	5521	SAU1c0040_orf_86p	12448
S1M10000036D02	2970	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000036D03	2971	SAU103038	5757	#N/A	#N/A
S1M10000036D06	2972	SAU103024	5754	SAU1c0029_orf_6p	12200
S1M10000036D08	2973	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000036D10	2974	SAU102933	5744	SAU1c0039_orf_62p	12412
S1M10000036D11	2975	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000036D11	2975	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000036D12	2976	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000036E06	2977	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000036E06	2977	SAU202756	5852	SAU2c0470_orf_1p	13027
S1M10000036E08	2978	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000036E11	2979	SAU101343	5425	SAU1c0044_orf_40p	12619
S1M10000036F06	2980	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000036F07	2981	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000036F08	2982	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000036F09	2983	SAU100532	5287	SAU1c0044_orf_198p	12580
S1M10000036F10	2984	SAU101586	5489	SAU1c0044_orf_242p	12598
S1M10000036F11	2985	SAU201506	5818	SAU2c0432_orf_18p	12946
S1M10000036G03	2986	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000036G07	2987	SAU102355	5651	SAU1c0040_orf_40p	12435
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S1M10000036H02	2991	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000036H03	2992	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000036H04	2993	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000036H05	2994	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000036H06	2995	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000036H08	2996	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000036H11	2997	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000037A02	2998	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000037A02	2998	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000037A03	2999	SAU100128	5231	#N/A	#N/A
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000037A08	3001	SAU102669	5728	SAU1c0024_orf_7p	12160
S1M10000037A09	3002	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000037A09	3002	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000037A11	3003	SAU101436	5449	SAU1c0028_orf_23p	12183
S1M10000037A12	3004	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000037B03	3005	SAU101999	5585	SAU1c0040_orf_101p	12423
S1M10000037B04	3006	SAU100767	5323	SAU1c0044_orf_192p	12579
S1M10000037B05	3007	SAU102578	5701	SAU1c0039_orf_61p	12411
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S1M10000037B06	3008	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000037B07	3009	SAU101915	5577	SAU1c0040_orf_72p	12439
S1M10000037B08	3010	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000037B10	3011	SAU101346	5427	SAU1c0044_orf_43p	12621
S1M10000037B11	3012	SAU101399	5443	SAU1c0036_orf_34p	12325
S1M10000037B12	3013	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000037C05	3014	SAU101482	5461	SAU1c0015_orf_10p	12123
S1M10000037C06	3015	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000037C07	3016	SAU101641	5501	SAU1c0029_orf_12p	12193
S1M10000037C08	3017	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000037C09	3018	SAU101818	5553	SAU1c0038_orf_20p	12369
S1M10000037C10	3019	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000037D04	3020	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000037D05	3021	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000037D06	3022	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000037D09	3023	SAU102246	5619	SAU1c0043_orf_30p	12542
S1M10000037D12	3024	SAU101999	5585	SAU1c0040_orf_101p	12423
S1M10000037E02	3025	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000037E02	3025	SAU102448	5673	SAU1c0045_orf_23p	12681
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S1M10000037E06	3027	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000037E08	3028	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000037E08	3028	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000037E09	3029	SAU102049	5595	SAU1c0039_orf_68p	12416
S1M10000037E10	3030	SAU101444	5451	SAU1c0038_orf_46p	12381
S1M10000037E11	3031	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000037E12	3032	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000037F02	3033	SAU100776	5327	SAU1c0041_orf_72p	12482
S1M10000037F03	3034	SAU101339	5422	SAU1c0038_orf_81p	12399
S1M10000037F04	3035	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000037F05	3036	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000037F06	3037	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000037F06	3037	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000037F07	3038	SAU100793	5329	SAU1c0028_orf_52p	12188
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000037F09	3040	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000037F10	3041	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000037G01	3042	SAU102502	5690	SAU1c0045_orf_273p	12689
S1M10000037G01	3042	SAU102503	5691	SAU1c0045_orf_274p	12690
S1M10000037G02	3043	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000037G03	3044	SAU101344	5426	SAU1c0044_orf_41p	12620
S1M10000037G06	3045	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000037G07	3046	SAU103038	5757	#N/A	#N/A
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S1M10000037G10	3048	SAU100062	5225	SAU1c0035_orf_98p	12309
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S1M10000037H05	3051	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000037H07	3052	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000037H08	3053	SAU200928	5798	SAU2c0365_orf_5p	12815
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S1M10000037H11	3055	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000038A04	3056	SAU101275	5412	SAU1c0044_orf_257p	12604
S1M10000038A07	3057	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000038A08	3058	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000038A09	3059	SAU100307	5257	SAU1c0036_orf_134p	12313
S1M10000038A11	3060	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000038A12	3061	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000038B01	3062	SAU101483	5462	SAU1c0015_orf_11p	12124
S1M10000038B03	3063	SAU101360	5431	SAU1c0044_orf_109p	12555
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S1M10000038C08	3071	SAU102132	5605	SAU1c0027_orf_19p	12177
S1M10000038C10	3072	SAU101346	5427	SAU1c0044_orf_43p	12621
S1M10000038C10	3072	SAU101347	5428	SAU1c0044_orf_44p	12622
S1M10000038C11	3073	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000038C12	3074	SAU101792	5533	SAU1c0032_orf_13p	12217
S1M10000038D02	3075	SAU101842	5557	SAU1c0042_orf_9p	12510
S1M10000038D05	3076	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000038D07	3077	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000038D08	3078	SAU101341	5424	SAU1c0044_orf_38p	12618
S1M10000038D08	3078	SAU301275	5892	SAU3c1365_orf_2p	13103
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000038D12	3082	SAU100752	5322	SAU1c0043_orf_183p	12524
S1M10000038D12	3082	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000038E01	3083	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000038E02	3084	SAU101842	5557	SAU1c0042_orf_9p	12510
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S1M10000038E04	3086	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000038E05	3087	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000038E06	3088	SAU102231	5614	SAU1c0043_orf_18p	12527
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S1M10000038E07	3089	SAU200593	5786	SAU2c0327_orf_1p	12784
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S1M10000038E12	3091	SAU100838	5337	SAU1c0031_orf_12p	12211
S1M10000038E12	3091	SAU100839	5338	SAU1c0031_orf_11p	12210
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S1M10000038F04	3093	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000038F04	3093	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000038F05	3094	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000038F05	3094	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000038F06	3095	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000038F08	3096	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000038F09	3097	SAU201666	5830	SAU2c0442_orf_11p	12981
S1M10000038F10	3098	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000038F11	3099	SAU100747	5320	SAU1c0044_orf_235p	12597
S1M10000038F12	3100	SAU202039	5843	SAU2c0452_orf_20p	13009
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S1M10000038G04	3103	SAU100475	5276	SAU1c0036_orf_61p	12337
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S1M10000038G11	3107	SAU100123	5230	SAU1c0043_orf_189p	12526
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S1M10000038G12	3108	SAU101184	5391	SAU1c0035_orf_80p	12305
S1M10000038H03	3109	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000038H07	3110	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000038H09	3111	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000038H11	3112	SAU101452	5455	SAU1c0045_orf_247p	12684
S1M10000039A02	3113	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000039A02	3113	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000039A05	3114	SAU100964	5363	SAU1c0044_orf_86p	12641
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S1M10000039A07	3115	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000039A08	3116	SAU100522	5284	SAU1c0044_orf_249p	12599

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000039A12	3118	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000039B02	3119	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000039B02	3119	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000039B06	3120	SAU102350	5649	SAU1c0040_orf_36p	12433
S1M10000039B07	3121	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000039B10	3122	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000039B12	3123	SAU301118	5886	SAU3c1305_orf_3p	13086
S1M10000039C04	3124	SAU102252	5621	SAU1c0032_orf_48p	12241
S1M10000039C06	3125	SAU100633	5301	SAU1c0043_orf_147p	12515
S1M10000039C07	3126	SAU200657	5789	#N/A	#N/A
S1M10000039C08	3127	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000039C09	3128	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000039C10	3129	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000039C11	3130	SAU200657	5789	#N/A	#N/A
S1M10000039D02	3131	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000039D09	3132	SAU102294	5639	SAU1c0044_orf_288p	12610
S1M10000039D09	3132	SAU301080	5885	SAU3c1287_orf_1p	13083
S1M10000039D10	3133	SAU100323	5261	SAU1c0044_orf_171p	12575
S1M10000039E01	3134	SAU102264	5628	SAU1c0032_orf_60p	12250
S1M10000039E08	3135	SAU100412	5269	SAU1c0029_orf_38p	12197
S1M10000039E09	3136	SAU100056	5223	SAU1c0044_orf_176p	12577
S1M10000039E10	3137	SAU102394	5659	SAU1c0033_orf_41p	12271
S1M10000039E10	3137	SAU301118	5886	SAU3c1305_orf_3p	13086
S1M10000039E11	3138	SAU102473	5680	SAU1c0026_orf_30p	12173
S1M10000039F02	3139	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000039F03	3140	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000039F05	3141	SAU100118	5229	SAU1c0015_orf_13p	12125
S1M10000039F07	3142	SAU102531	5694	SAU1c0045_orf_186p	12667
S1M10000039F08	3143	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000039F09	3144	SAU200157	5776	#N/A	#N/A
S1M10000039F10	3145	SAU100059	5224	SAU1c0045_orf_10p	12652
S1M10000039F12	3146	SAU101565	5480	SAU1c0022_orf_8p	12151
S1M10000039G03	3147	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000039G04	3148	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000039G07	3149	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000039G07	3149	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000039G10	3150	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000039H02	3151	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000039H02	3151	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000039H03	3152	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000039H03	3152	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000039H03	3152	SAU200297	5778	SAU2c0274_orf_2p	12739
S1M10000039H04	3153	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000039H06	3154	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000039H07	3155	SAU100793	5329	SAU1c0028_orf_52p	12188

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000039H08	3156	SAU102440	5671	SAU1c0045_orf_30p	12692
S1M10000040A04	3157	SAU100040	5221	SAU1c0043_orf_217p	12533
S1M10000040A05	3158	SAU102671	5729	SAU1c0024_orf_9p	12161
S1M10000040A07	3159	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000040A08	3160	SAU200157	5776	#N/A	#N/A
S1M10000040A10	3161	SAU103038	5757	#N/A	#N/A
S1M10000040A11	3162	SAU101801	5541	#N/A	#N/A
S1M10000040B01	3163	SAU101461	5457	SAU1c0045_orf_234p	12680
S1M10000040B03	3164	SAU102102	5600	SAU1c0045_orf_340p	12696
S1M10000040B07	3165	SAU101432	5448	SAU1c0028_orf_27p	12184
S1M10000040B11	3166	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000040C03	3167	SAU201971	5841	SAU2c0455_orf_17p	13015
S1M10000040C03	3167	SAU301363	5894	#N/A	#N/A
S1M10000040C04	3168	SAU102551	5698	SAU1c0045_orf_206p	12672
S1M10000040C05	3169	SAU102534	5696	#N/A	#N/A
S1M10000040C06	3170	SAU101247	5405	SAU1c0043_orf_136p	12512
S1M10000040C07	3171	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000040C08	3172	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000040C10	3173	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000040C10	3173	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000040C10	3173	SAU301148	5888	#N/A	#N/A
S1M10000040C11	3174	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000040D01	3175	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000040D01	3175	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000040D03	3176	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000040D03	3176	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000040D08	3177	SAU100633	5301	SAU1c0043_orf_147p	12515
S1M10000040D09	3178	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000040D11	3179	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000040E01	3180	SAU100916	5353	SAU1c0038_orf_71p	12394
S1M10000040E02	3181	SAU101845	5558	SAU1c0042_orf_7p	12506
S1M10000040E04	3182	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000040E05	3183	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000040E06	3184	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000040E07	3185	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000040E09	3186	SAU102605	5710	SAU1c0041_orf_49p	12470
S1M10000040E10	3187	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000040E11	3188	SAU101226	5398	SAU1c0035_orf_2p	12298
S1M10000040E12	3189	SAU102503	5691	SAU1c0045_orf_274p	12690
S1M10000040E12	3189	SAU201380	5812	SAU2c0426_orf_11p	12922
S1M10000040F01	3190	SAU101226	5398	SAU1c0035_orf_2p	12298
S1M10000040F02	3191	SAU101614	5494	SAU1c0044_orf_9p	12649
S1M10000040F03	3192	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000040F04	3193	SAU100123	5230	SAU1c0043_orf_189p	12526
S1M10000040F04	3193	SAU102001	5586	SAU1c0040_orf_102p	12424

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000040F04	3193	SAU201827	5837	SAU2c0449_orf_21p	13002
S1M10000040F05	3194	SAU102232	5615	SAU1c0043_orf_19p	12530
S1M10000040F06	3195	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000040F08	3196	SAU300713	5875	SAU3c1104_orf_1p	13058
S1M10000040F09	3197	SAU101610	5492	SAU1c0044_orf_5p	12629
S1M10000040F12	3198	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000040G01	3199	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000040G02	3200	SAU200561	5783	SAU2c0324_orf_3p	12779
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S1M10000040G04	3201	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000040G07	3202	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000040G08	3203	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000040G12	3204	SAU101421	5446	SAU1c0042_orf_138p	12498
S1M10000040H02	3205	SAU100773	5326	SAU1c0038_orf_39p	12377
S1M10000040H03	3206	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000040H04	3207	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000040H05	3208	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000040H07	3209	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000040H10	3210	SAU202039	5843	SAU2c0452_orf_20p	13009
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S1M10000041B02	3212	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000041B03	3213	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000041B05	3214	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000041B06	3215	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000041B07	3216	SAU101145	5384	SAU1c0035_orf_43p	12299
S1M10000041B12	3217	SAU102725	5733	SAU1c0036_orf_68p	12338
S1M10000041C08	3218	SAU102607	5712	SAU1c0041_orf_51p	12472
S1M10000041C08	3218	SAU102944	5749	SAU1c0041_orf_47p	12468
S1M10000041C10	3219	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000041C11	3220	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000041D06	3221	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000041D07	3222	SAU102639	5724	#N/A	#N/A
S1M10000041D08	3223	SAU200030	5772	SAU2c0282_orf_3p	12745
S1M10000041D10	3224	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000041D12	3225	SAU102658	5726	SAU1c0045_orf_121p	12654
S1M10000041E03	3226	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000041E06	3227	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000041E09	3228	SAU201236	5808	SAU2c0409_orf_10p	12891
S1M10000041E12	3229	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000041F03	3230	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000041F03	3230	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000041F11	3231	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000041F12	3232	SAU102480	5684	SAU1c0039_orf_100p	12404
S1M10000041F12	3232	SAU102481	5685	SAU1c0039_orf_99p	12422
S1M10000041G01	3233	SAU100532	5287	SAU1c0044_orf_198p	12580

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000041G08	3235	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000041G10	3236	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000041G11	3237	SAU101802	5542	SAU1c0032_orf_22p	12227
S1M10000041H01	3238	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000041H04	3239	SAU100497	5280	SAU1c0018_orf_3p	12140
S1M10000041H05	3240	SAU100242	5246	SAU1c0036_orf_5p	12336
S1M10000041H07	3241	SAU102486	5687	SAU1c0039_orf_93p	12420
S1M10000041H07	3241	SAU102487	5688	SAU1c0039_orf_92p	12419
S1M10000041H08	3242	SAU301133	5887	SAU3c1311_orf_3p	13087
S1M10000041H09	3243	SAU103169	5763	SAU1c0045_orf_230p	12678
S1M10000042A04	3244	SAU201236	5808	SAU2c0409_orf_10p	12891
S1M10000042A05	3245	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000042A06	3246	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000042A07	3247	SAU100633	5301	SAU1c0043_orf_147p	12515
S1M10000042A09	3248	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000042A11	3249	SAU101815	5552	SAU1c0032_orf_33p	12238
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S1M10000042B02	3251	SAU202736	5851	SAU2c0426_orf_7p	12927
S1M10000042B03	3252	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000042B06	3253	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000042B07	3254	SAU101343	5425	SAU1c0044_orf_40p	12619
S1M10000042B08	3255	SAU100443	5274	SAU1c0036_orf_55p	12333
S1M10000042B09	3256	SAU101802	5542	SAU1c0032_orf_22p	12227
S1M10000042B10	3257	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000042B10	3257	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000042B11	3258	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000042B12	3259	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000042C02	3260	SAU100617	5300	SAU1c0035_orf_102p	12295
S1M10000042C06	3261	SAU102032	5591	SAU1c0029_orf_47p	12198
S1M10000042C10	3262	SAU101495	5467	SAU1c0037_orf_65p	12360
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S1M10000042D07	3265	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000042D10	3266	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000042D11	3267	SAU102663	5727	SAU1c0024_orf_2p	12158
S1M10000042E03	3268	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000042E06	3269	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000042E08	3270	SAU103198	5766	#N/A	#N/A
S1M10000042F01	3271	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000042F02	3272	SAU101891	5571	SAU1c0034_orf_30p	12281
S1M10000042F05	3273	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000042F06	3274	SAU100773	5326	SAU1c0038_orf_39p	12377
S1M10000042F08	3275	SAU100162	5239	SAU1c0044_orf_206p	12583
S1M10000042F09	3276	SAU100246	5247	SAU1c0042_orf_130p	12496
S1M10000042F09	3276	SAU300998	5881	SAU3c1253_orf_3p	13077

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000042F11	3278	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000042G01	3279	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000042G03	3280	SAU101220	5396	SAU1c0044_orf_94p	12645
S1M10000042G08	3281	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000042G09	3282	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000042G12	3283	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000042H05	3284	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000042H07	3285	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000042H11	3286	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000043A02	3287	SAU203001	5859	SAU2c0412_orf_15p	12894
S1M10000043A03	3288	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000043A04	3289	SAU200088	5775	SAU2c0159_orf_1p	12724
S1M10000043A06	3290	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000043A07	3291	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000043A08	3292	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000043A10	3293	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000043A11	3294	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000043A12	3295	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000043B01	3296	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000043B02	3297	SAU100059	5224	SAU1c0045_orf_10p	12652
S1M10000043B07	3298	SAU101922	5578	SAU1c0040_orf_66p	12438
S1M10000043B07	3298	SAU200345	5779	SAU2c0292_orf_3p	12751
S1M10000043B08	3299	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000043B08	3299	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000043B08	3299	SAU200297	5778	SAU2c0274_orf_2p	12739
S1M10000043B09	3300	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000043B10	3301	SAU100436	5273	SAU1c0023_orf_20p	12154
S1M10000043B12	3302	SAU102142	5606	SAU1c0041_orf_13p	12457
S1M10000043C02	3303	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000043C07	3304	SAU101784	5530	SAU1c0037_orf_46p	12355
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S1M10000043D01	3307	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000043D02	3308	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000043D04	3309	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000043D10	3310	SAU102631	5721	SAU1c0045_orf_94p	12712
S1M10000043D12	3311	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000043D12	3311	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000043E02	3312	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000043E02	3312	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000043E03	3313	SAU102032	5591	SAU1c0029_orf_47p	12198
S1M10000043E05	3314	SAU102067	5598	SAU1c0034_orf_54p	12287
S1M10000043E07	3315	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000043E08	3316	SAU101344	5426	SAU1c0044_orf_41p	12620
S1M10000043E10	3317	SAU100186	5242	SAU1c0036_orf_19p	12317

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000043E12	3319	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000043F01	3320	SAU101797	5537	SAU1c0032_orf_17p	12221
S1M10000043F01	3320	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000043F05	3321	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000043F07	3322	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000043F07	3322	SAU102448	5673	SAU1c0045_orf_23p	12681
S1M10000043F08	3323	SAU101344	5426	SAU1c0044_orf_41p	12620
S1M10000043F09	3324	SAU101801	5541	#N/A	#N/A
S1M10000043G01	3325	SAU100059	5224	SAU1c0045_orf_10p	12652
S1M10000043G04	3326	SAU102423	5667	SAU1c0030_orf_23p	12208
S1M10000043G05	3327	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000043G09	3328	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000043G09	3328	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000043G10	3329	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000043H01	3330	SAU101797	5537	SAU1c0032_orf_17p	12221
S1M10000043H01	3330	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000043H03	3331	SAU101803	5543	SAU1c0032_orf_23p	12228
S1M10000043H03	3331	SAU101804	5544	#N/A	#N/A
S1M10000043H04	3332	SAU100128	5231	#N/A	#N/A
S1M10000043H04	3332	SAU101549	5476	SAU1c0043_orf_64p	12549
S1M10000043H04	3332	SAU101576	5488	SAU1c0044_orf_105p	12554
S1M10000043H05	3333	SAU200058	5773	SAU2c0134_orf_1p	12719
S1M10000043H05	3333	SAU200059	5774	SAU2c0134_orf_3p	12720
S1M10000043H06	3334	SAU102417	5663	SAU1c0030_orf_17p	12204
S1M10000043H06	3334	SAU102863	5737	#N/A	#N/A
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S1M10000043H10	3336	SAU101024	5369	SAU1c0045_orf_90p	12711
S1M10000043H11	3337	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000044A02	3338	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000044A06	3339	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000044A08	3340	SAU101175	5388	SAU1c0031_orf_1p	12213
S1M10000044A09	3341	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000044A11	3342	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000044A12	3343	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000044B01	3344	SAU102268	5630	SAU1c0032_orf_63p	12252
S1M10000044B02	3345	SAU101968	5581	SAU1c0028_orf_43p	12187
S1M10000044B05	3346	SAU100690	5309	#N/A	#N/A
S1M10000044B06	3347	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000044B06	3347	SAU102881	5740	SAU1c0032_orf_4p	12242
S1M10000044B08	3348	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000044B11	3349	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000044B12	3350	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000044C04	3351	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000044C06	3352	SAU101614	5494	SAU1c0044_orf_9p	12649

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000044C07	3353	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000044C08	3354	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000044C11	3355	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000044C12	3356	SAU102280	5632	SAU1c0038_orf_3p	12378
S1M10000044D01	3357	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000044D01	3357	SAU102880	5739	SAU1c0032_orf_1p	12224
S1M10000044D04	3358	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000044D06	3359	SAU101300	5415	SAU1c0044_orf_113p	12557
S1M10000044D06	3359	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000044D08	3360	SAU102270	5631	SAU1c0032_orf_65p	12253
S1M10000044D09	3361	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000044D10	3362	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000044D11	3363	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000044D12	3364	SAU102231	5614	SAU1c0043_orf_18p	12527
S1M10000044D12	3364	SAU102232	5615	SAU1c0043_orf_19p	12530
S1M10000044E01	3365	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000044E02	3366	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000044E06	3367	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000044E07	3368	SAU301829	5902	SAU3c1515_orf_7p	13162
S1M10000044E09	3369	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000044E10	3370	SAU100497	5280	SAU1c0018_orf_3p	12140
S1M10000044E11	3371	SAU101270	5410	SAU1c0037_orf_89p	12365
S1M10000044F02	3372	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000044F06	3373	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000044F08	3374	SAU101262	5406	SAU1c0042_orf_113p	12488
S1M10000044F10	3375	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000044F10	3375	SAU202882	5855	SAU2c0381_orf_3p	12848
S1M10000044G02	3376	SAU102933	5744	SAU1c0039_orf_62p	12412
S1M10000044G05	3377	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000044G08	3378	SAU102601	5707	SAU1c0041_orf_46p	12467
S1M10000044G08	3378	SAU102606	5711	SAU1c0041_orf_50p	12471
S1M10000044G10	3379	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000044G10	3379	SAU202882	5855	SAU2c0381_orf_3p	12848
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S1M10000044H06	3381	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000044H06	3381	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000044H07	3382	SAU100595	5294	SAU1c0043_orf_62p	12547
S1M10000044H08	3383	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000044H09	3384	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000044H09	3384	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000044H10	3385	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000044H11	3386	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000045A02	3387	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000045A06	3388	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000045A07	3389	SAU102378	5653	SAU1c0040_orf_61p	12437

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000045A12	3391	SAU201765	5833	SAU2c0309_orf_5p	12770
S1M10000045B01	3392	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000045B02	3393	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000045B03	3394	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000045B07	3395	SAU101803	5543	SAU1c0032_orf_23p	12228
S1M10000045B10	3396	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000045B11	3397	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000045B12	3398	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000045C02	3399	SAU100690	5309	#N/A	#N/A
S1M10000045C03	3400	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000045C04	3401	SAU102286	5636	SAU1c0038_orf_6p	12393
S1M10000045C04	3401	SAU102287	5637	SAU1c0038_orf_7p	12398
S1M10000045C05	3402	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000045C07	3403	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000045C09	3404	SAU101744	5520	SAU1c0037_orf_94p	12367
S1M10000045C09	3404	SAU300191	5868	SAU3c0672_orf_1p	13037
S1M10000045D01	3405	SAU101893	5572	SAU1c0034_orf_32p	12282
S1M10000045D03	3406	SAU101599	5491	SAU1c0041_orf_5p	12478
S1M10000045D07	3407	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000045D08	3408	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000045D09	3409	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000045D10	3410	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000045D11	3411	SAU101492	5465	SAU1c0025_orf_21p	12166
S1M10000045D11	3411	SAU101493	5466	SAU1c0025_orf_22p	12167
S1M10000045D12	3412	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000045D12	3412	SAU101801	5541	#N/A	#N/A
S1M10000045E04	3413	SAU102132	5605	SAU1c0027_orf_19p	12177
S1M10000045E05	3414	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000045E08	3415	SAU201752	5832	SAU2c0436_orf_19p	12963
S1M10000045E09	3416	SAU101794	5535	#N/A	#N/A
S1M10000045E10	3417	SAU101756	5524	SAU1c0040_orf_82p	12445
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S1M10000045E12	3419	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000045F04	3420	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000045F05	3421	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000045F08	3422	SAU200657	5789	#N/A	#N/A
S1M10000045F11	3423	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000045F12	3424	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000045G03	3425	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000045G06	3426	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000045G07	3427	SAU101561	5479	SAU1c0022_orf_4p	12149
S1M10000045G08	3428	SAU100690	5309	#N/A	#N/A
S1M10000045G10	3429	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000045G12	3430	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000045H06	3431	SAU200928	5798	SAU2c0365_orf_5p	12815

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000045H11	3433	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000046A03	3434	SAU202731	5850	#N/A	#N/A
S1M10000046A04	3435	SAU100062	5225	SAU1c0035_orf_98p	12309
S1M10000046A04	3435	SAU100231	5245	#N/A	#N/A
S1M10000046A06	3436	SAU101383	5438	SAU1c0022_orf_20p	12147
S1M10000046A08	3437	SAU200994	5802	SAU2c0428_orf_4p	12935
S1M10000046A09	3438	SAU100315	5260	SAU1c0037_orf_62p	12358
S1M10000046A11	3439	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000046A11	3439	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000046A12	3440	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000046B01	3441	SAU102334	5645	SAU1c0045_orf_144p	12658
S1M10000046B03	3442	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000046B04	3443	SAU101797	5537	SAU1c0032_orf_17p	12221
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S1M10000046B07	3445	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000046B08	3446	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000046B09	3447	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000046B11	3448	SAU102541	5697	SAU1c0045_orf_195p	12668
S1M10000046B12	3449	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000046C02	3450	SAU200601	5787	#N/A	#N/A
S1M10000046C04	3451	SAU100118	5229	SAU1c0015_orf_13p	12125
S1M10000046C05	3452	SAU101159	5387	SAU1c0036_orf_46p	12331
S1M10000046C06	3453	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000046C06	3453	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000046C07	3454	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000046C08	3455	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000046C11	3456	SAU102144	5608	SAU1c0041_orf_15p	12459
S1M10000046C12	3457	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000046C12	3457	SAU100359	5264	SAU1c0032_orf_35p	12239
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S1M10000046D05	3462	SAU102602	5708	SAU1c0032_orf_5p	12249
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S1M10000046D09	3464	SAU100679	5305	SAU1c0018_orf_14p	12137
S1M10000046D10	3465	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000046D11	3466	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000046D11	3466	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000046D12	3467	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000046D12	3467	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000046E01	3468	SAU101610	5492	SAU1c0044_orf_5p	12629
S1M10000046E02	3469	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000046E04	3470	SAU101800	5540	SAU1c0032_orf_20p	12225
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000046E10	3473	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000046F01	3474	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000046F02	3475	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000046F02	3475	SAU102880	5739	SAU1c0032_orf_1p	12224
S1M10000046F05	3476	SAU102671	5729	SAU1c0024_orf_9p	12161
S1M10000046F06	3477	SAU100702	5310	SAU1c0029_orf_34p	12196
S1M10000046F06	3477	SAU300825	5878	SAU3c1171_orf_1p	13068
S1M10000046F08	3478	SAU102297	5640	SAU1c0045_orf_41p	12704
S1M10000046F09	3479	SAU100517	5282	#N/A	#N/A
S1M10000046F10	3480	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000046F12	3481	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000046G01	3482	SAU200752	5795	SAU2c0354_orf_5p	12809
S1M10000046G01	3482	SAU300975	5880	SAU3c1240_orf_3p	13075
S1M10000046G02	3483	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000046G03	3484	SAU100773	5326	SAU1c0038_orf_39p	12377
S1M10000046G04	3485	SAU100436	5273	SAU1c0023_orf_20p	12154
S1M10000046G07	3486	SAU101866	5564	SAU1c0036_orf_21p	12319
S1M10000046G09	3487	SAU102663	5727	SAU1c0024_orf_2p	12158
S1M10000046G10	3488	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000046H01	3489	SAU101445	5452	SAU1c0038_orf_47p	12382
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S1M10000046H10	3490	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000047A03	3491	SAU100157	5237	SAU1c0040_orf_81p	12444
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S1M10000047A05	3493	SAU101805	5545	SAU1c0032_orf_24p	12229
S1M10000047A06	3494	SAU201775	5835	SAU2c0446_orf_4p	12996
S1M10000047A06	3494	SAU301030	5883	SAU3c1268_orf_1p	13080
S1M10000047A07	3495	SAU101807	5547	SAU1c0032_orf_26p	12231
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S1M10000047A09	3497	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000047A10	3498	SAU100751	5321	SAU1c0036_orf_59p	12335
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S1M10000047B04	3502	SAU101366	5433	SAU1c0033_orf_2p	12266
S1M10000047B05	3503	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000047B06	3504	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000047B08	3505	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000047B09	3506	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000047B10	3507	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000047B12	3508	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000047C01	3509	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000047C02	3510	SAU101156	5386	SAU1c0036_orf_12p	12311
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000047C08	3514	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000047C09	3515	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000047C11	3516	SAU201775	5835	SAU2c0446_orf_4p	12996
S1M10000047C11	3516	SAU301030	5883	SAU3c1268_orf_1p	13080
S1M10000047C12	3517	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000047D02	3518	SAU101387	5440	SAU1c0038_orf_52p	12386
S1M10000047D03	3519	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000047D04	3520	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000047D05	3521	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000047D09	3522	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000047D10	3523	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000047D11	3524	SAU103038	5757	#N/A	#N/A
S1M10000047D12	3525	SAU101175	5388	SAU1c0031_orf_1p	12213
S1M10000047E01	3526	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000047E02	3527	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000047E03	3528	SAU102452	5676	SAU1c0045_orf_20p	12674
S1M10000047E04	3529	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000047E05	3530	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000047E06	3531	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000047E08	3532	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000047E09	3533	SAU100810	5333	SAU1c0037_orf_11p	12343
S1M10000047E10	3534	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000047E11	3535	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000047E12	3536	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000047F02	3537	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000047F03	3538	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000047F04	3539	SAU300572	5873	SAU3c1019_orf_1p	13051
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S1M10000047F06	3541	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000047F07	3542	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000047F08	3543	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000047F09	3544	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000047F10	3545	SAU201571	5824	SAU2c0447_orf_17p	12997
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S1M10000047F12	3547	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000047G01	3548	SAU101369	5434	SAU1c0033_orf_5p	12274
S1M10000047G02	3549	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000047G04	3550	SAU101341	5424	SAU1c0044_orf_38p	12618
S1M10000047G05	3551	SAU100684	5306	SAU1c0044_orf_68p	12632
S1M10000047G05	3551	SAU100685	5307	SAU1c0044_orf_69p	12633
S1M10000047G06	3552	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000047G07	3553	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000047G08	3554	SAU101028	5370	SAU1c0043_orf_7p	12552
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000047H04	3558	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000047H05	3559	SAU102452	5676	SAU1c0045_orf_20p	12674
S1M10000047H06	3560	SAU103038	5757	#N/A	#N/A
S1M10000047H07	3561	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000047H08	3562	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000047H09	3563	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000047H11	3564	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000048A02	3565	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000048A03	3566	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000048A04	3567	SAU103038	5757	#N/A	#N/A
S1M10000048A05	3568	SAU101868	5565	SAU1c0036_orf_23p	12320
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S1M10000048A07	3570	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000048A09	3571	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000048A10	3572	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000048A11	3573	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000048A12	3574	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000048B02	3575	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000048B05	3576	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000048B08	3577	SAU102452	5676	SAU1c0045_orf_20p	12674
S1M10000048B10	3578	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000048B11	3579	SAU103038	5757	#N/A	#N/A
S1M10000048B12	3580	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000048B12	3580	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000048C01	3581	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000048C02	3582	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000048C03	3583	SAU102200	5611	SAU1c0045_orf_168p	12665
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S1M10000048C06	3585	SAU100684	5306	SAU1c0044_orf_68p	12632
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S1M10000048C07	3586	SAU102452	5676	SAU1c0045_orf_20p	12674
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S1M10000048C09	3588	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000048C11	3589	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000048D02	3590	SAU100123	5230	SAU1c0043_orf_189p	12526
S1M10000048D02	3590	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000048D02	3590	SAU103159	5762	SAU1c0045_orf_204p	12670
S1M10000048D02	3590	SAU201827	5837	SAU2c0449_orf_21p	13002
S1M10000048D08	3591	SAU300572	5873	SAU3c1019_orf_1p	13051
S1M10000048D09	3592	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000048D10	3593	SAU302950	5914	SAU3c1512_orf_12p	13160
S1M10000048D12	3594	SAU102599	5706	SAU1c0041_orf_45p	12466
S1M10000048D12	3594	SAU103191	5765	SAU1c0041_orf_44p	12465
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000048E07	3599	SAU100959	5359	SAU1c0042_orf_102p	12485
S1M10000048E08	3600	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000048E10	3601	SAU302950	5914	SAU3c1512_orf_12p	13160
S1M10000048F02	3602	SAU101387	5440	SAU1c0038_orf_52p	12386
S1M10000048F07	3603	SAU101175	5388	SAU1c0031_orf_1p	12213
S1M10000048F08	3604	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000048F09	3605	SAU101793	5534	SAU1c0032_orf_14p	12218
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S1M10000048F12	3607	SAU103038	5757	#N/A	#N/A
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S1M10000048G04	3610	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000048G05	3611	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000048G07	3612	SAU102006	5589	SAU1c0040_orf_107p	12427
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S1M10000048G10	3613	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000048G11	3614	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000048H01	3615	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000048H02	3616	SAU100158	5238	SAU1c0040_orf_80p	12443
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S1M10000048H04	3618	SAU102200	5611	SAU1c0045_orf_168p	12665
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S1M10000048H11	3624	SAU101271	5411	SAU1c0037_orf_90p	12366
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K1M10000044G05	1086	ECO102262	10228	#N/A	#N/A
K1M10000036G08	1076	ECO102447	10247	#N/A	#N/A
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K1M10000043D05	1081	ECO102620	10266	#N/A	#N/A
K1M10000045D10	1088	ECO102620	10266	#N/A	#N/A
K1M10000003C01	1055	ECO103101	10315	#N/A	#N/A
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S4M10000014D07	3706	ECO100757	#N/A	#N/A	#N/A
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S4M10000016A02	3710	ECO100757	#N/A	#N/A	#N/A
S4M10000022E12	3725	ECO100757	#N/A	#N/A	#N/A
S4M10000026E12	3744	ECO100757	#N/A	#N/A	#N/A
S4M10000035E03	3764	ECO100757	#N/A	#N/A	#N/A
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S4M10000020G10	3722	ECO100796	10105	#N/A	#N/A
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S4M10000001C01	3680	ECO103265	10365	#N/A	#N/A
S4M10000024B02	3729	ECO103280	#N/A	#N/A	#N/A
S4M10000020A04	3720	ECO103461	#N/A	#N/A	#N/A
S4M10000002B06	3681	ECO103666	#N/A	#N/A	#N/A
S4M10000019H06	3719	ECO103738	#N/A	#N/A	#N/A
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S4M10000032B12	3752	ECO103935	#N/A	#N/A	#N/A
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S4M10000037A10	3770	ECO103951	#N/A	#N/A	#N/A
S4M10000018D09	3711	ECO104080	#N/A	#N/A	#N/A
S4M10000035F09	3766	EFA101301	#N/A	EFA1c0040_orf_173p	#N/A
S4M10000035F09	3766	EFA102170	#N/A	EFA1c0040_orf_121p	#N/A
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S4M10000036F07	3768	HPY200334	#N/A	#N/A	#N/A
S4M10000001C01	3680	HPY201116	11570	#N/A	#N/A
S4M10000037A10	3770	KPN100467	#N/A	KPN1c0583_orf_2p	#N/A
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S4M10000024B02	3729	KPN101160	#N/A	KPN1c1224_orf_1p	#N/A
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S4M10000012B06	3700	KPN102524	#N/A	#N/A	#N/A
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PA2222	4049	5104
PA2313	4050	5105
PA2398	4051	5106
PA2424	4052	5107
PA2461	4053	5108
PA2470	4054	5109
PA2488	4055	5110
PA2494	4056	5111
PA2584	4057	5112
PA2594	4058	5113
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PA2671	4061	5116
PA2680	4062	5117
PA2684	4063	5118
PA2726	4064	5119
PA2742	4065	5120
PA3006	4066	5121
PA3011	4067	5122
PA3013	4068	5123
PA3041	4069	5124
PA3048	4070	5125
PA3068	4071	5126
PA3121	4072	5127
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PA3154	4074	5129
PA3160	4075	5130
PA3279	4076	5131
PA3280	4077	5132
PA3374	4078	5133
PA3479	4079	5134
PA3484	4080	5135
PA3522	4081	5136
PA3643	4082	5137
PA3703	4083	5138
PA3709	4084	5139
PA3716	4085	5140

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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PA3866	4088	5143
PA3876	4089	5144
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PA3931	4091	5146
PA3984	4092	5147
PA4024	4093	5148
PA4027	4094	5149
PA4037	4095	5150
PA4067	4096	5151
PA4070	4097	5152
PA4081	4098	5153
PA4105	4099	5154
PA4124	4100	5155
PA4125	4101	5156
PA4158	4102	5157
PA4237	4103	5158
PA4242	4104	5159
PA4244	4105	5160
PA4245	4106	5161
PA4246	4107	5162
PA4247	4108	5163
PA4248	4109	5164
PA4249	4110	5165
PA4250	4111	5166
PA4251	4112	5167
PA4252	4113	5168
PA4253	4114	5169
PA4254	4115	5170
PA4256	4116	5171
PA4257	4117	5172
PA4258	4118	5173
PA4259	4119	5174
PA4262	4120	5175
PA4263	4121	5176
PA4264	4122	5177
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PA4269	4124	5179
PA4271	4125	5180
PA4272	4126	5181
PA4316	4127	5182
PA4332	4128	5183
PA4347	4129	5184
PA4363	4130	5185
PA4375	4131	5186
PA4413	4132	5187

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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PA4473	4134	5189
PA4506	4135	5190
PA4512	4136	5191
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PA4576	4138	5193
PA4598	4139	5194
PA4665	4140	5195
PA4681	4141	5196
PA4709	4142	5197
PA4744	4143	5198
PA4771	4144	5199
PA4888	4145	5200
PA4942	4146	5201
PA4997	4147	5202
PA5030	4148	5203
PA5076	4149	5204
PA5088	4150	5205
PA5193	4151	5206
PA5199	4152	5207
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PA5209	4154	5209
PA5248	4155	5210
PA5299	4156	5211
PA5316	4157	5212
PA5388	4158	5213
PA5393	4159	5214
PA5436	4160	5215
PA5443	4161	5216
PA5490	4162	5217
PA5493	4163	5218
PA5507	4164	5219
PA5567	4165	5220
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SAU100059	4169	5224
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SAU100112	4172	5227
SAU100114	4173	5228
SAU100118	4174	5229
SAU100123	4175	5230
SAU100128	4176	5231
SAU100131	4177	5232
SAU100133	4178	5233
SAU100139	4179	5234

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU100141	4181	5236
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SAU100162	4184	5239
SAU100175	4185	5240
SAU100182	4186	5241
SAU100186	4187	5242
SAU100198	4188	5243
SAU100227	4189	5244
SAU100231	4190	5245
SAU100242	4191	5246
SAU100246	4192	5247
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SAU100265	4194	5249
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SAU100272	4196	5251
SAU100275	4197	5252
SAU100300	4198	5253
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SAU100496	4224	5279
SAU100497	4225	5280
SAU100514	4226	5281

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU100521	4228	5283
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SAU100532	4232	5287
SAU100542	4233	5288
SAU100546	4234	5289
SAU100547	4235	5290
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SAU100595	4239	5294
SAU100596	4240	5295
SAU100601	4241	5296
SAU100608	4242	5297
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SAU100736	4261	5316
SAU100738	4262	5317
SAU100741	4263	5318
SAU100745	4264	5319
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SAU100751	4266	5321
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SAU100767	4268	5323
SAU100770	4269	5324
SAU100771	4270	5325
SAU100773	4271	5326
SAU100776	4272	5327
SAU100778	4273	5328

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU100794	4275	5330
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SAU100808	4277	5332
SAU100810	4278	5333
SAU100813	4279	5334
SAU100831	4280	5335
SAU100836	4281	5336
SAU100838	4282	5337
SAU100839	4283	5338
SAU100843	4284	5339
SAU100845	4285	5340
SAU100858	4286	5341
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SAU100865	4288	5343
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SAU100879	4290	5345
SAU100880	4291	5346
SAU100882	4292	5347
SAU100885	4293	5348
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SAU100959	4304	5359
SAU100961	4305	5360
SAU100962	4306	5361
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SAU100970	4310	5365
SAU100996	4311	5366
SAU101006	4312	5367
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SAU101024	4314	5369
SAU101028	4315	5370
SAU101034	4316	5371
SAU101038	4317	5372
SAU101039	4318	5373
SAU101065	4319	5374
SAU101067	4320	5375

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU101084	4322	5377
SAU101085	4323	5378
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SAU101090	4325	5380
SAU101092	4326	5381
SAU101104	4327	5382
SAU101143	4328	5383
SAU101145	4329	5384
SAU101155	4330	5385
SAU101156	4331	5386
SAU101159	4332	5387
SAU101175	4333	5388
SAU101180	4334	5389
SAU101183	4335	5390
SAU101184	4336	5391
SAU101189	4337	5392
SAU101197	4338	5393
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SAU101199	4340	5395
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SAU101224	4342	5397
SAU101226	4343	5398
SAU101231	4344	5399
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SAU101242	4349	5404
SAU101247	4350	5405
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SAU101271	4356	5411
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SAU101293	4359	5414
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SAU101301	4361	5416
SAU101302	4362	5417
SAU101310	4363	5418
SAU101311	4364	5419
SAU101320	4365	5420
SAU101327	4366	5421
SAU101339	4367	5422

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU101344	4371	5426
SAU101346	4372	5427
SAU101347	4373	5428
SAU101350	4374	5429
SAU101351	4375	5430
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SAU101365	4377	5432
SAU101366	4378	5433
SAU101369	4379	5434
SAU101371	4380	5435
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SAU101382	4382	5437
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SAU101387	4385	5440
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SAU101398	4387	5442
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SAU101421	4391	5446
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SAU101436	4394	5449
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SAU101446	4398	5453
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SAU101455	4401	5456
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SAU101492	4410	5465
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SAU101495	4412	5467
SAU101497	4413	5468
SAU101509	4414	5469

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU101545	4419	5474
SAU101546	4420	5475
SAU101549	4421	5476
SAU101551	4422	5477
SAU101554	4423	5478
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SAU101586	4434	5489
SAU101592	4435	5490
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SAU101616	4440	5495
SAU101622	4441	5496
SAU101624	4442	5497
SAU101630	4443	5498
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SAU101637	4445	5500
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SAU101655	4450	5505
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SAU101664	4452	5507
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SAU101679	4454	5509
SAU101681	4455	5510
SAU101682	4456	5511
SAU101685	4457	5512
SAU101717	4458	5513
SAU101724	4459	5514
SAU101726	4460	5515
SAU101727	4461	5516

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU101736	4463	5518
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SAU101752	4467	5522
SAU101754	4468	5523
SAU101756	4469	5524
SAU101771	4470	5525
SAU101772	4471	5526
SAU101777	4472	5527
SAU101781	4473	5528
SAU101782	4474	5529
SAU101784	4475	5530
SAU101790	4476	5531
SAU101791	4477	5532
SAU101792	4478	5533
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SAU101794	4480	5535
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SAU101797	4482	5537
SAU101798	4483	5538
SAU101799	4484	5539
SAU101800	4485	5540
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SAU101802	4487	5542
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SAU101814	4496	5551
SAU101815	4497	5552
SAU101818	4498	5553
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SAU101833	4500	5555
SAU101839	4501	5556
SAU101842	4502	5557
SAU101845	4503	5558
SAU101849	4504	5559
SAU101857	4505	5560
SAU101862	4506	5561
SAU101864	4507	5562
SAU101865	4508	5563

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU101868	4510	5565
SAU101869	4511	5566
SAU101876	4512	5567
SAU101881	4513	5568
SAU101882	4514	5569
SAU101890	4515	5570
SAU101891	4516	5571
SAU101893	4517	5572
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SAU101907	4519	5574
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SAU101910	4521	5576
SAU101915	4522	5577
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SAU102006	4534	5589
SAU102007	4535	5590
SAU102032	4536	5591
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SAU102046	4539	5594
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SAU102132	4550	5605
SAU102142	4551	5606
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SAU102144	4553	5608
SAU102162	4554	5609
SAU102165	4555	5610

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU102201	4557	5612
SAU102222	4558	5613
SAU102231	4559	5614
SAU102232	4560	5615
SAU102233	4561	5616
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SAU102268	4575	5630
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SAU102294	4584	5639
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SAU102389	4601	5656
SAU102390	4602	5657

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU102417	4608	5663
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SAU102420	4610	5665
SAU102422	4611	5666
SAU102423	4612	5667
SAU102433	4613	5668
SAU102434	4614	5669
SAU102437	4615	5670
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SAU102487	4633	5688
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SAU102526	4637	5692
SAU102527	4638	5693
SAU102531	4639	5694
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SAU102554	4644	5699
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SAU102584	4647	5702
SAU102585	4648	5703
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PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU102605	4655	5710
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SAU102671	4674	5729
SAU102674	4675	5730
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SAU102863	4682	5737
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SAU102880	4684	5739
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SAU102939	4692	5747
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SAU102944	4694	5749
SAU102979	4695	5750
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PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU103038	4702	5757
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SAU200731	4738	5793
SAU200740	4739	5794
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SAU200914	4741	5796
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PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU201225	4752	5807
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SAU201301	4754	5809
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SAU201375	4756	5811
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SAU201403	4760	5815
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SAU201654	4774	5829
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SAU201765	4778	5833
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SAU201775	4780	5835
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SAU201952	4784	5839
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SAU201971	4786	5841
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PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU202267	4793	5848
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SAU202736	4796	5851
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SAU202882	4800	5855
SAU202930	4801	5856
SAU202945	4802	5857
SAU202968	4803	5858
SAU203001	4804	5859
SAU203007	4805	5860
SAU203196	4806	5861
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SAU300131	4811	5866
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SAU300269	4814	5869
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SAU300825	4823	5878
SAU300868	4824	5879
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SAU301004	4827	5882
SAU301030	4828	5883
SAU301054	4829	5884
SAU301080	4830	5885
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SAU301133	4832	5887
SAU301148	4833	5888
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PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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SAU301592	4843	5898
SAU301620	4844	5899
SAU301758	4845	5900
SAU301773	4846	5901
SAU301829	4847	5902
SAU301869	4848	5903
SAU301898	4849	5904
SAU302060	4850	5905
SAU302513	4851	5906
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SAU302685	4853	5908
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SAU302699	4855	5910
SAU302805	4856	5911
SAU302901	4857	5912
SAU302931	4858	5913
SAU302950	4859	5914
SAU302956	4860	5915